

101	40	93.8	84	3	US-09-249-448-59	Sequence 59, Appl	174	40	93.8	162	3	US-09-249-471-64	Sequence 64, Appl
102	40	93.8	89	2	US-08-455-380-48	Sequence 48, Appl	175	40	93.8	162	3	US-09-249-472-64	Sequence 64, Appl
103	40	93.8	89	2	US-08-456-397-18	Sequence 48, Appl	176	40	93.8	162	3	US-09-249-472-64	Sequence 64, Appl
104	40	93.8	89	2	US-08-456-397-18	Sequence 48, Appl	177	40	93.8	162	3	US-09-249-451-64	Sequence 64, Appl
105	40	93.8	89	2	US-08-456-397-18	Sequence 48, Appl	178	40	93.8	162	3	US-09-249-451-64	Sequence 64, Appl
106	40	93.8	89	2	US-08-456-397-18	Sequence 48, Appl	179	40	93.8	162	3	US-08-809-455-64	Sequence 64, Appl
107	40	93.8	89	2	US-08-456-397-18	Sequence 48, Appl	180	40	93.8	162	3	US-08-809-455-64	Sequence 64, Appl
108	40	93.8	89	3	US-09-249-471-48	Sequence 48, Appl	181	40	93.8	162	3	US-08-809-455-64	Sequence 64, Appl
109	40	93.8	89	3	US-09-249-472-48	Sequence 48, Appl	182	40	93.8	162	3	US-09-249-461-64	Sequence 64, Appl
110	40	93.8	89	3	US-09-249-451-48	Sequence 48, Appl	183	40	93.8	162	3	US-09-249-461-64	Sequence 64, Appl
111	40	93.8	89	3	US-08-809-455-48	Sequence 48, Appl	184	40	93.8	162	3	US-09-249-448-64	Sequence 64, Appl
112	40	93.8	89	3	US-09-249-461-48	Sequence 48, Appl	185	40	93.8	171	2	US-08-465-380-62	Sequence 62, Appl
113	40	93.8	89	3	US-09-249-448-48	Sequence 48, Appl	186	40	93.8	171	2	US-08-486-397-62	Sequence 62, Appl
114	40	93.8	91	2	US-08-465-380-128	Sequence 128, Appl	187	40	93.8	171	2	US-08-486-397-62	Sequence 62, Appl
115	40	93.8	91	2	US-08-480-478-50	Sequence 50, Appl	188	40	93.8	171	2	US-08-461-965-62	Sequence 62, Appl
116	40	93.8	91	2	US-08-486-397-129	Sequence 128, Appl	189	40	93.8	171	2	US-08-461-965-62	Sequence 62, Appl
117	40	93.8	91	2	US-08-486-397-129	Sequence 128, Appl	190	40	93.8	171	2	US-09-249-471-62	Sequence 62, Appl
118	40	93.8	91	2	US-08-451-965-128	Sequence 128, Appl	191	40	93.8	171	2	US-09-249-472-62	Sequence 62, Appl
119	40	93.8	91	2	US-08-451-965-128	Sequence 128, Appl	192	40	93.8	171	3	US-09-249-451-62	Sequence 62, Appl
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121	40	93.8	91	3	US-09-249-471-128	Sequence 128, Appl	194	40	93.8	171	3	US-09-249-461-62	Sequence 62, Appl
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123	40	93.8	91	3	US-08-809-455-129	Sequence 128, Appl	196	40	93.8	823	4	US-09-651-656-19	Sequence 19, Appl
124	40	93.8	91	3	US-09-249-461-128	Sequence 128, Appl	197	40	93.8	823	4	US-09-650-855-19	Sequence 19, Appl
125	40	93.8	91	3	US-09-249-448-128	Sequence 128, Appl	198	27	94.4	5	2	US-08-465-380-72	Sequence 72, Appl
126	40	93.8	102	2	US-08-465-380-27	Sequence 27, Appl	199	27	94.4	5	2	US-08-496-397-72	Sequence 72, Appl
127	40	93.8	102	2	US-08-496-397-56	Sequence 56, Appl	200	27	94.4	5	2	US-08-496-397-72	Sequence 72, Appl
128	40	93.8	102	2	US-08-496-397-27	Sequence 27, Appl	201	27	94.4	5	2	US-08-461-965-72	Sequence 72, Appl
129	40	93.8	102	2	US-08-496-397-27	Sequence 27, Appl	202	27	94.4	5	2	US-08-461-965-72	Sequence 72, Appl
130	40	93.8	102	2	US-08-451-965-27	Sequence 27, Appl	203	27	94.4	5	2	US-08-461-965-72	Sequence 72, Appl
131	40	93.8	102	2	US-08-451-965-27	Sequence 27, Appl	204	27	94.4	5	2	US-09-249-472-72	Sequence 72, Appl
132	40	93.8	102	2	US-08-634-641-27	Sequence 27, Appl	205	27	94.4	5	3	US-09-249-472-72	Sequence 72, Appl
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135	40	93.8	102	3	US-09-249-471-27	Sequence 27, Appl	208	27	94.4	5	3	US-09-249-461-72	Sequence 72, Appl
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137	40	93.8	102	3	US-08-809-455-27	Sequence 27, Appl	210	27	94.4	7	2	US-08-465-380-81	Sequence 81, Appl
138	40	93.8	102	3	US-09-249-461-27	Sequence 27, Appl	211	27	94.4	7	2	US-08-486-397-81	Sequence 81, Appl
139	40	93.8	102	3	US-09-249-448-27	Sequence 27, Appl	212	27	94.4	7	2	US-09-486-399-81	Sequence 81, Appl
140	40	93.8	108	2	US-08-465-380-24	Sequence 24, Appl	213	27	94.4	7	2	US-08-461-965-81	Sequence 81, Appl
141	40	93.8	108	2	US-08-496-397-53	Sequence 53, Appl	214	27	94.4	7	2	US-08-634-641-81	Sequence 81, Appl
142	40	93.8	108	2	US-08-496-397-24	Sequence 24, Appl	215	27	94.4	7	3	US-09-249-471-81	Sequence 81, Appl
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151	40	93.8	108	3	US-09-249-448-24	Sequence 24, Appl	224	27	94.4	86	2	US-08-145-480-46	Sequence 46, Appl
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158	40	93.8	161	3	US-09-249-471-65	Sequence 65, Appl	231	27	94.4	86	2	US-08-634-641-46	Sequence 46, Appl
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170	40	93.8	162	2	US-08-496-397-63	Sequence 63, Appl	243	27	94.4	86	3	US-09-249-472-46	Sequence 46, Appl
171	40	93.8	162	2	US-08-461-965-63	Sequence 63, Appl	244	27	94.4	86	3	US-09-249-472-46	Sequence 46, Appl
172	40	93.8	162	2	US-08-461-965-63	Sequence 63, Appl	245	27	94.4	86	3	US-09-249-472-46	Sequence 46, Appl
173	40	93.8	162	3	US-09-249-471-63	Sequence 63, Appl	246	27	94.4	86	3	US-09-249-472-46	Sequence 46, Appl

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494	25	78.1	81	2	US-09-219-448-7	Sequence 7, Aff1	467	25	78.1	582	3	US-09-510-649-29
495	25	78.1	81	2	US-08-465-380-22	Sequence 22, Aff1	468	25	78.1	582	4	US-09-231-819-20
496	25	78.1	81	2	US-08-480-478-51	Sequence 51, Aff1	469	25	78.1	603	3	US-08-482-677-8
497	25	78.1	81	2	US-08-486-397-22	Sequence 22, Aff1	470	25	78.1	605	1	US-08-482-677-8
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685	24	75.0	647	2	US-08-155-173B-14	Sequence 14, Appl	758	24	75.0	922	3	US-08-945-086A-14
686	24	75.0	647	2	US-08-465-473B-16	Sequence 16, Appl	759	24	75.0	922	3	US-08-940-086A-20
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688	24	75.0	648	3	US-08-961-083-2	Sequence 2, Appl	761	24	75.0	922	3	US-08-940-086A-20
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897	23	68.8	5	2	US-08-186-397-71	Sequence 71, Appl	970	7	US-09-219-141-71	Sequence 80, Appl
898	23	68.8	5	2	US-08-486-397-71	Sequence 71, Appl	971	7	US-09-219-141-71	Sequence 80, Appl
899	23	68.8	5	2	US-08-461-641-71	Sequence 71, Appl	972	7	US-09-219-141-71	Sequence 80, Appl
900	23	68.8	5	2	US-08-634-641-71	Sequence 71, Appl	973	7	US-09-219-141-71	Sequence 80, Appl
901	23	68.8	5	3	US-09-219-141-71	Sequence 71, Appl	974	7	US-09-219-141-71	Sequence 80, Appl
902	23	68.8	5	3	US-09-219-141-71	Sequence 71, Appl	975	7	US-09-219-141-71	Sequence 80, Appl
903	23	68.8	5	3	US-09-219-141-71	Sequence 71, Appl	976	7	US-09-219-141-71	Sequence 80, Appl

977 22 68.8 78 2 US-08-167-611C-47
 978 22 68.8 78 4 US-08-466-971A-47
 979 22 68.8 78 4 US-08-462-640-47
 980 22 68.8 83 1 US-07-947-375-18
 981 22 68.8 83 1 US-08-321-595A-12
 982 22 68.8 94 1 US-07-989-845-28
 983 22 68.8 94 1 US-07-989-844-12
 984 22 68.8 94 1 US-08-161-041-12
 985 22 68.8 94 1 US-08-240-121-12
 986 22 68.8 94 1 US-08-451-311-12
 987 22 68.8 94 5 PCT-US93-11297-12
 988 22 68.8 94 5 PCT-US93-11298-28
 989 22 68.8 105 3 US-08-407-165-3
 990 22 68.8 118 4 US-08-545-809A-108
 991 22 68.8 119 3 US-09-029-267-14
 992 22 68.8 119 1 US-08-360-125-5
 993 22 68.8 119 2 US-08-450-578-5
 994 22 68.8 119 2 US-09-017-628-5
 995 22 68.8 119 2 US-09-014-890-5
 996 22 68.8 119 4 US-08-450-463-5
 997 22 68.8 119 6 5425942-1
 998 22 68.8 121 4 US-09-142-583A-4
 999 22 68.8 123 2 US-09-462-528A-5
 1000 22 68.8 132 4 US-09-134-801C-4894

ALIGNMENTS

RESULT 1
 US-08-465-480-70
 ? Sequence 70, Application US/08465380
 ? Patent No. 5864894
 ? GENERAL INFORMATION:
 ? APPLICANT: GEORGE P. VLASAK, PATRIC H. STANSSENS,
 ? APPLICANT: JORIS H.L. MEUSSENS, MARC J. LAUWEREYS,
 ? APPLICANT: YVES R. LAROUCHE, LAURENT S. JESPEIRS,
 ? APPLICANT: YANNICK G.J. GANSEMAUS, MATTHEW MOYLE,
 ? APPLICANT: PETER W. BERQUIM
 ? TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICAGULANT
 ? NUMBER OF SEQUENCES: 456
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LYON & LYON
 ? STREET: 633 West Fifth Street
 ? CITY: Suite 4700
 ? STATE: Los Angeles
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C., DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/465-480
 ? FILING DATE: June 5, 1995
 ? CLASSIFICATION: 530
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 16, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 489-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 70:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? FRAGMENT TYPE: internal fragment
 ? US-08-465-480-70

? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? FRAGMENT TYPE: internal fragment
 ? US-08-465-380-70
 Query Match 93.8%; Score 30; DB 2; Length 5;
 Best Local Similarity 100.0%; Prod. No. 20*05;
 Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 DB 1 GYRN 5
 RESULT 2
 US-08-486-397-70
 ? Sequence 70, Application US/08466397
 ? Patent No. 5866542
 ? GENERAL INFORMATION:
 ? APPLICANT: GEORGE P. VLASAK, PATRIC H. STANSSENS,
 ? APPLICANT: JORIS H.L. MEUSSENS, MARC J. LAUWEREYS,
 ? APPLICANT: YVES R. LAROUCHE, LAURENT S. JESPEIRS,
 ? APPLICANT: YANNICK G.J. GANSEMAUS, MATTHEW MOYLE,
 ? APPLICANT: PETER W. BERQUIM
 ? TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICAGULANT
 ? NUMBER OF SEQUENCES: 457
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LYON & LYON
 ? STREET: 633 West Fifth Street
 ? CITY: Suite 4700
 ? STATE: Los Angeles
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C., DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/486-397
 ? FILING DATE: June 5, 1995
 ? CLASSIFICATION: 530
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 16, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 70:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? FRAGMENT TYPE: internal fragment
 ? US-08-486-397-70
 Query Match 92.8%; Score 30; DB 2; Length 5;
 Best Local Similarity 100.0%; Prod. No. 20*05;
 Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 DB 1 GYRN 5

1b 1 GFYRN 5

RESULT 3
US-08-486-399-70
Sequence 70, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-08-486-399-70

Query Match 93.8% Score 30; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 20+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 GFYRN 7
11111
DB 1 GFYRN 5

RESULT 4
US-08-461-965-70
Sequence 70, Application US/08461965
Patent No. 5872068
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-08-461-965-70

Query Match 93.8% Score 40; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 20+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 GFYRN 7
11111
DB 1 GFYRN 5

RESULT 5
US-08-634-611
Sequence 70, Application US/080634611
Patent No. 5872064
GENERAL INFORMATION:
APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Menssens, Joris Hilda Hieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gaussemans, Yannick Georges Joze
APPLICANT: Moy G, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California

1 COUNTRY: U.S.A.
 2 ZIP: 90071
 3 COMPUTER READABLE FORM:
 4 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 5 MEDIUM TYPE: Storage
 6 COMPUTER: IBM Compatible
 7 OPERATING SYSTEM: IBM P.C., DOS 5.0
 8 SOFTWARE: Word Perfect 5.1
 9 CURRENT APPLICATION DATA:
 10 APPLICATION NUMBER: US/08/634,641
 11 FILING DATE: April 19, 1996
 12 PRIOR APPLICATION DATA:
 13 APPLICATION NUMBER: PCT/95/0141
 14 FILING DATE: October 17, 1995
 15 APPLICATION NUMBER: 08/486,499
 16 FILING DATE: June 5, 1995
 17 APPLICATION NUMBER: 08/486,499
 18 FILING DATE: June 5, 1995
 19 APPLICATION NUMBER: 08/465,480
 20 FILING DATE: June 5, 1995
 21 APPLICATION NUMBER: 08/461,965
 22 FILING DATE: June 5, 1995
 23 APPLICATION NUMBER: 08/426,110
 24 FILING DATE: October 18, 1994
 25 ATTORNEY/AGENT INFORMATION:
 26 NAME: BIGGS, SUZANNE L.
 27 REGISTRATION NUMBER: 30,158
 28 REFERENCE: "BET N MOEF" 2:5, 3:6
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: (214) 489-1600
 31 TELEFAX: (214) 489-1600
 32 TELEX: 67-3510
 33 INFORMATION FOR SEQ ID NO: 70:
 34 SEQUENCE CHARACTERISTICS:
 35 LENGTH: 5 amino acids
 36 TYPE: amino acid
 37 TOPOLOGY: linear
 38 MOLECULE TYPE: peptide
 39 FRAGMENT TYPE: internal fragment
 40 US-08 634-641-70

Query Match 93.8%; Score 40; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 20+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 1 GYRN 5

RESULT 6
 US 09 249 471-70
 Sequence 70, Application US/09/249471
 Patent No. 604641

GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Joset
 APPLICANT: Larocche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gaussemans, Yannick Georges Jozet
 APPLICANT: Moyle, Matthew
 APPLICANT: Berquim, Peter W.
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 TITLE OF INVENTION: INHIBITORS AND ANTICAGULANT
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles

1 STATE: California
 2 COUNTRY: U.S.A.
 3 ZIP: 90071
 4 COMPUTER READABLE FORM:
 5 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 6 MEDIUM TYPE: Storage
 7 COMPUTER: IBM Compatible
 8 OPERATING SYSTEM: IBM P.C., DOS 5.0
 9 SOFTWARE: Word Perfect 5.1
 10 CURRENT APPLICATION DATA:
 11 APPLICATION NUMBER: 08/486,499
 12 FILING DATE: June 5, 1995
 13 PRIOR APPLICATION DATA:
 14 APPLICATION NUMBER: 08/486,499
 15 FILING DATE: April 17, 1997
 16 APPLICATION NUMBER: PCT/95/0141
 17 FILING DATE: October 17, 1995
 18 APPLICATION NUMBER: 08/486,499
 19 FILING DATE: June 5, 1995
 20 APPLICATION NUMBER: 08/486,499
 21 FILING DATE: June 5, 1995
 22 APPLICATION NUMBER: 08/465,480
 23 FILING DATE: June 5, 1995
 24 APPLICATION NUMBER: 08/461,965
 25 FILING DATE: June 5, 1995
 26 APPLICATION NUMBER: 08/426,110
 27 FILING DATE: October 18, 1994
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: BIGGS, SUZANNE L.
 30 REGISTRATION NUMBER: 30,158
 31 TELEPHONE: (214) 489-1600
 32 TELEFAX: (214) 489-1600
 33 TELEX: 67-3510
 34 INFORMATION FOR SEQ ID NO: 70:
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 5 amino acids
 37 TYPE: amino acid
 38 TOPOLOGY: linear
 39 MOLECULE TYPE: peptide
 40 FRAGMENT TYPE: internal fragment
 41 US-09-249-471-70

Query Match 93.8%; Score 40; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 20+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 1 GYRN 5

RESULT 7
 US 09 249 472 70
 Sequence 70, Application US/09/249472
 Patent No. 604648

GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Joset
 APPLICANT: Larocche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gaussemans, Yannick Georges Jozet
 APPLICANT: Moyle, Matthew
 APPLICANT: Berquim, Peter W.
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 TITLE OF INVENTION: INHIBITORS AND ANTICAGULANT
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/1231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/445,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/POCKET NUMBER: 216,270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-09-249-472-70

Query Match 93.8%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 1 GYRN 5

RESULT 8
US-09-249-451-70
Sequence 70, Application US/09249451
Patent No. 6087487
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozel
APPLICANT: Moyle, Matthew
TITLE OF INVENTION: NPWATOP-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,451
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/1231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/445,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/POCKET NUMBER: 216,270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-09-249-451-70

Query Match 93.8%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 1 GYRN 5

RESULT 9
US-08-809-455-70
Sequence 70, Application US/08809455
Patent No. 6090916
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozel
APPLICANT: Moyle, Matthew
APPLICANT: Berqum, Peter W.

? TITLE OF INVENTION: MEMBRANE-EXTRACTED SURFING PROTEASE
 ? TITLE OF INVENTION: TRIBUNES AND ANTICAGULANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 456
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LYON & LYON
 ? STREET: 644 West Fifth Street
 ? STREET: Suite 4700
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C., DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/409,455
 ? FILING DATE: April 17, 1997
 ? PRIORITY APPLICATION DATA:
 ? APPLICATION NUMBER: 08/409,455
 ? FILING DATE: October 17, 1995
 ? APPLICATION NUMBER: 08/486,399
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/465,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/461,965
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 18, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BEGG, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? TELEPHONE: (214) 489-1600
 ? TELEFAX: (214) 955-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 70:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: Linear
 ? MOLECULE TYPE: Peptide
 ? FRAGMENT TYPE: Internal Fragment
 ? US-08 409-455-70

Query Match 93.8%; Score 40; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 GFYRN 7
 Db 1 GFYRN 5

RESULT 10
 US 09-249-441-70
 ? Sequence 70, Application US/09/249451
 ? Patent No. 6096877
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasak, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messens, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene
 ? APPLICANT: Jaspers, Laurent Stephane
 ? APPLICANT: Ganssmans, Yvanick Georges Jozef
 ? APPLICANT: Moyls, Matthew

? APPLICANT: Borgum, Peter W.
 ? TITLE OF INVENTION: MEMBRANE-EXTRACTED SURFING PROTEASE
 ? TITLE OF INVENTION: INHIBITORS AND ANTICAGULANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 456
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LYON & LYON
 ? STREET: 644 West Fifth Street
 ? STREET: Suite 4700
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C., DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/249,461
 ? FILING DATE:
 ? PRIORITY APPLICATION DATA:
 ? APPLICATION NUMBER: 08/409,455
 ? FILING DATE: April 17, 1997
 ? APPLICATION NUMBER: 08/486,399
 ? FILING DATE: October 17, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/465,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/461,965
 ? FILING DATE: October 18, 1994
 ? NAME: BEGG, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? TELEPHONE: (214) 489-1600
 ? TELEFAX: (214) 955-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 70:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: Linear
 ? MOLECULE TYPE: Peptide
 ? FRAGMENT TYPE: Internal Fragment
 ? US-09-249-461-70

Query Match 93.8%; Score 40; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 GFYRN 7
 Db 1 GFYRN 5

RESULT 11
 US 09-249-448-70
 ? Sequence 70, Application US/09/249448
 ? Patent No. 6121445
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasak, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messens, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene


```

: APPLICANT: Jespers, Laurent Strophane
: APPLICANT: Gaussemans, Yannick Georges Marie
: APPLICANT: Moyle, Matthew
: APPLICANT: Berquim, Peter W.
: TITLE OF INVENTION: INHIBITORS-EXTRACTED SERINE PROTEASE
: TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
: NUMBER OF SEQUENCES: 356
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: Storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-09-249,448
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/809,455
: FILING DATE: April 17, 1997
: APPLICATION NUMBER: 08/496,394
: FILING DATE: October 17, 1995
: APPLICATION NUMBER: 08/496,394
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/486,397
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/465,380
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/461,465
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/326,110
: FILING DATE: October 18, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: BUGS, SUZANNE L.
: REGISTRATION NUMBER: 30,158
: REFERENCE NUMBER: 21,276
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 70:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal fragment
: US-09-249-448-70

```

```

Query Match 93.8%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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QY 4 GYVEN 7
Db 1 GYVEN 5

```

RESULT 12

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US-08-465-380-79
: Sequence 74, Application US/08465380
: Patent No. 5863894
: GENERAL INFORMATION:
: APPLICANT: Georges P. Vlasak, Patrick H. Stanssens,
: APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,

```

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: APPLICANT: Yves R. Laroche, Laurent St. Jespers,
: APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
: APPLICANT: Peter W. Berquim
: TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 456
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: Storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/508,465,380
: FILING DATE: June 5, 1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/326,110
: FILING DATE: October 18, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: BUGS, SUZANNE L.
: REGISTRATION NUMBER: 30,158
: REFERENCE NUMBER: 21,276
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 79:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal fragment
: FEATURE:
: OTHER INFORMATION: Xaa is located in 1 and 2
: OTHER INFORMATION: is an amino acid, provided
: OTHER INFORMATION: that at least one Xaa is Gly, or
: OTHER INFORMATION: Asp.
: US-08-465-380-79

```

```

Query Match 93.8%; Score 30; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

```

QY 3 GYVEN 7
Db 3 GYVEN 7

```

RESULT 13

```

US-09-196-997-79
: Sequence 79, Application US/08486497
: Patent No. 5866542
: GENERAL INFORMATION:
: APPLICANT: Georges P. Vlasak, Patrick H. Stanssens,
: APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
: APPLICANT: Yves R. Laroche, Laurent St. Jespers,
: APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
: APPLICANT: Peter W. Berquim
: TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 357
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon

```

```

1 STREET: 633 West Fifth Street
2 STREET: Suite 4700
3 CITY: Los Angeles
4 STATE: California
5 COUNTRY: U.S.A.
6 ZIP: 90071
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
9 MEDIUM TYPE: Storage
10 COMPUTER: IBM Compatible
11 OPERATING SYSTEM: IBM P.C. DOS 5.0
12 SOFTWARE: Word Perfect 5.1
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/486,397
15 FILING DATE: June 5, 1995
16 CLASSIFICATION: 530
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/426,110
19 FILING DATE: October 18, 1994
20 ATTORNEY/AGENT INFORMATION:
21 NAME: BIGGS, SUZANNE L.
22 REGISTRATION NUMBER: 40,158
23 REFERENCE/EXCERPT NUMBER: 23,0264
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (213) 489-1600
26 TELEFAX: (213) 955-0440
27 TELEX: 67-3510
28 INFORMATION FOR SEQ ID NO: 79:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 7 amino acids
31 TYPE: amino acid
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 FRAGMENT TYPE: internal fragment
35 FEATURE:
36 OTHER INFORMATION: Xaa in locations 1 and 2
37 OTHER INFORMATION: Is an amino acid, provided
38 OTHER INFORMATION: that at least one Xaa is Glu or
39 OTHER INFORMATION: Asp.
40 US 08-486-397-79

```

```

Query Match 93.88; Score 40; DB 2; Length 7;
Best Local Similarity 100.0%; Prod. No. 20-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 3 GYRN 7

RESULT 14
US-08-486-399-79
Sequence 79, Application US/08/486,397
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: REMAQUE EXTRACTED ANTICAGUANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530

```

```

1 MEDIUM TYPE: Storage
2 COMPUTER: IBM Compatible
3 OPERATING SYSTEM: IBM P.C. DOS 5.0
4 SOFTWARE: Word Perfect 5.1
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/486,399
7 FILING DATE: June 5, 1995
8 CLASSIFICATION: 530
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/426,110
11 FILING DATE: October 18, 1994
12 ATTORNEY/AGENT INFORMATION:
13 NAME: BIGGS, SUZANNE L.
14 REGISTRATION NUMBER: 40,158
15 REFERENCE/EXCERPT NUMBER: 23,0270
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (213) 489-1600
18 TELEFAX: (213) 955-0440
19 TELEX: 67-3510
20 INFORMATION FOR SEQ ID NO: 79:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 7 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 FRAGMENT TYPE: internal fragment
27 FEATURE:
28 OTHER INFORMATION: Xaa in locations 1 and 2
29 OTHER INFORMATION: Is an amino acid, provided
30 OTHER INFORMATION: that at least one Xaa is Glu or
31 OTHER INFORMATION: Asp.
32 US-08-486-399-79

```

```

Query Match 93.88; Score 40; DB 2; Length 7;
Best Local Similarity 100.0%; Prod. No. 20-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 3 GYRN 7

RESULT 15
US-08-461-465-79
Sequence 79, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: REMAQUE EXTRACTED ANTICAGUANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/KEY NUMBER: 319,234
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO. 79:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 FEATURE:
 OTHER INFORMATION: Xaa in locations 1 and 2
 OTHER INFORMATION: is an amino acid, provided
 OTHER INFORMATION: that at least one Xaa is Glu or
 OTHER INFORMATION: Asp.
 US-08-461-965-79

Query Match 93.8%; Score 20; Dg 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 20-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 Db 3 GYRN 7

RESULT 16

US-08-634-641-79
 Sequence 79, Application US/08634641
 Patent No. 5955294

GENERAL INFORMATION:
 APPLICANT: Vlasak, George P.; Vlasak
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Josef
 APPLICANT: Larocche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Rene
 APPLICANT: Moyle, Matthew W.
 APPLICANT: Berquim, Peter W.
 TITLE OF INVENTION: NEMATODE EXTRACTED ANTICAGGLULANT
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: April 19, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/296,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/KEY NUMBER: 319,136
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO. 79:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 FEATURE:
 OTHER INFORMATION: Xaa in locations 1 and 2
 OTHER INFORMATION: is an amino acid, provided
 OTHER INFORMATION: that at least one Xaa is Glu or
 OTHER INFORMATION: Asp.
 US-08-634-641-79

Query Match 93.8%; Score 20; Dg 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 20-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 Db 3 GYRN 7

RESULT 17

US-09-249-471-79
 Sequence 79, Application us/09249471
 Patent No. 6040411

GENERAL INFORMATION:
 APPLICANT: Vlasak, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Josef
 APPLICANT: Larocche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Rene
 APPLICANT: Moyle, Matthew W.
 APPLICANT: Berquim, Peter W.
 TITLE OF INVENTION: NEMATODE EXTRACTED SERINE PROTEASE
 TITLE OF INVENTION: INHIBITORS AND ANTICAGGLULANT
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/249,471


```

GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Staussons, Patrick Eric Hugo
APPLICANT: Messous, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Joset
APPLICANT: Laroche, Yves Rene
APPLICANT: Jaspers, Laurent Stephane
APPLICANT: Gansmaers, Yannick Georges Jozet
APPLICANT: Moylo, Matthew
TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 456
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: 08/461,965
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,499
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,497
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,480
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BLOGS, SUZANNE L.
REGISTRATION NUMBER: 40,158
REFERENCE: 214, 220
TELEPHONE: (214) 489-1600
TELEFAX: (214) 955-0440
TELEX: 67-3510
INFORMATION PER SEQ ID NO: 79
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal fragment
FEATURE:
OTHER INFORMATION: Xaa in locations 1 and 2
OTHER INFORMATION: is an amino acid, provided
OTHER INFORMATION: that at least one Xaa is Glu or
OTHER INFORMATION: Asp.
US 09-249-448-79
Query Match 94.8% Score 40; DB 4; Length 7;
Best Local Similarity 100.0%; Ident. No. 20-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
US 09-249-448-79

```

OTHER INFORMATION: Asp.

US-09-498-556c-79

Query Match 93.8%; Score 30; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2005;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 I I I I I
 Db 3 GYRN 7

RESULT 23

US-08-465-380-47
 Sequence 47, Application US/08465380
 Patent No. 5863894
 GENERAL INFORMATION:
 APPLICANT: George P. Vlasuk, Patric H. Stanssens,
 APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
 APPLICANT: Yves R. Laroche, Laurent S. Jespers,
 APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
 APPLICANT: Peter W. Berquim
 TITLE OF INVENTION: HEMATOIDE EXTRACTED ANTICOAGULANT
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,380

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/AGENT NUMBER: 213,268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-4510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

US-08-465-380-47

QY 3 GYRN 7
 I I I I I
 Db 54 GYRN 58

Query Match 93.8%; Score 30; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 9,4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24

US-08-486-397-47

Sequence 47, Application US/08486397

Patent No. 5866542

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,

APPLICANT: Peter W. Berquim

TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOAGULANT

NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,497

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/AGENT NUMBER: 213,269

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-4510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

US-08-486-397-47

QY 3 GYRN 7
 I I I I I
 Db 54 GYRN 58

Query Match 93.8%; Score 30; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 9,4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25

US-08-486-399-47

Sequence 47, Application US/08486399

Patent No. 5866543

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,

APPLICANT: Peter W. Berquim

TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOAGULANT

NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,497

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/426,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/AGENT NUMBER: 213,269

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-4510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

US-08-486-399-47

```

1  NUMBER OF SEQUENCES: 356
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Lyon & Lyon
4  STREET: 644 West Fifth Street
5  CITY: Los Angeles
6  STATE: California
7  COUNTRY: U.S.A.
8  ZIP: 90071
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
11 MEDIUM TYPE: storage
12 COMPUTER: IBM Compatible
13 OPERATING SYSTEM: IBM P.C. DOS 5.0
14 SOFTWARE: Word Perfect 5.1
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/486,494
17 FILING DATE: June 5, 1995
18 CLASSIFICATION: 530
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/426,110
21 FILING DATE: October 18, 1994
22 ATTORNEY/AGENT INFORMATION:
23 NAME: RIGGS, SUZANNE L.
24 REGISTRATION NUMBER: 40,158
25 PREFERRED CORRESPONDENCE ADDRESS: 213,223
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (213) 489-1600
28 TELEFAX: (213) 955-0440
29
30 INFORMATION FOR SEQ ID NO: 47:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 78 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: peptide
36 ORIGINAL SOURCE:
37 ORGANISM: Ancylostoma caninum
38 US 08-486-399-47

```

Query Match 94.00% Score 40; DB 2; Length 78;

Best Local Similarity 100.00; Pred. No. 9, 4;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 3;

QY 3 GYRN 7

|||||

DB 54 GYRN 58

```

RESULT 26
US-08-461-965-47
Sequence 47, Application US/08461965
Patent No. 5872098

```

```

1  GENERAL INFORMATION:
2  APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
3  APPLICANT: Joris H.L. Meusens, Marc J. Lauwereys,
4  APPLICANT: Yves R. Laroche, Laurent S. Jespers,
5  APPLICANT: Yannick G.J. Gansomans, Matthew Moyle,
6  APPLICANT: Peter W. Berquim
7  TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
8  TITLE OF INVENTION: PROTEIN
9  NUMBER OF SEQUENCES: 456
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Lyon & Lyon
12 STREET: 644 West Fifth Street
13 CITY: Los Angeles
14 STATE: California
15 COUNTRY: U.S.A.
16 ZIP: 90071
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
19 MEDIUM TYPE: storage
20 OPERATING SYSTEM: IBM P.C. DOS 5.0
21 SOFTWARE: Word Perfect 5.1
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: 08/426,110
24 FILING DATE: April 19, 1996
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08/403,641

```

```

1  COMPUTER: IBM Compatible
2  OPERATING SYSTEM: IBM P.C. DOS 5.0
3  SOFTWARE: Word Perfect 5.1
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: 08/461,965
6  FILING DATE: June 5, 1995
7  CLASSIFICATION: 530
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: 08/426,110
10 FILING DATE: October 18, 1994
11 ATTORNEY/AGENT INFORMATION:
12 NAME: RIGGS, SUZANNE L.
13 REGISTRATION NUMBER: 40,158
14 PREFERRED CORRESPONDENCE ADDRESS: 213,223
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (213) 489-1600
17 TELEFAX: (213) 955-0440
18
19 INFORMATION FOR SEQ ID NO: 47:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 78 amino acids
22 TYPE: amino acid
23 TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 ORIGINAL SOURCE:
26 ORGANISM: Ancylostoma caninum
27 US-08-461-965-47

```

Query Match 94.00% Score 40; DB 2; Length 78;

Best Local Similarity 100.00; Pred. No. 9, 4;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

|||||

DB 54 GYRN 58

RESULT 27

US-08-634-641-47

Sequence 47, Application US/0864641

Patent No. 5955294

```

1  GENERAL INFORMATION:
2  APPLICANT: Vlasuk, George P. Vlasuk
3  APPLICANT: Stanssens, Patrick Eric Budo
4  APPLICANT: Meusens, Joris Hilda Lieveh
5  APPLICANT: Lauwereys, Marc Josef
6  APPLICANT: Laroche, Yves Rene
7  APPLICANT: Jespers, Laurent Stephane
8  APPLICANT: Gansomans, Yannick Georges Josef
9  APPLICANT: Moyle, Matthew
10 APPLICANT: Berquim, Peter W.
11 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
12 TITLE OF INVENTION: PROTEIN
13 NUMBER OF SEQUENCES: 356
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: Lyon & Lyon
16 STREET: 644 West Fifth Street
17 CITY: Los Angeles
18 STATE: California
19 COUNTRY: U.S.A.
20 ZIP: 90071
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
23 MEDIUM TYPE: storage
24 OPERATING SYSTEM: IBM P.C. DOS 5.0
25 SOFTWARE: Word Perfect 5.1
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: 08/426,110
28 FILING DATE: April 19, 1996
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/403,641

```


? FILING DATE: October 17, 1995
 ? APPLICATION NUMBER: 08/486,399
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,395
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,395
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: October 18, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? REFERENCE CHECK NUMBER: 219/136
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-3510
 ? INFORMATION FOR SEQ ID NO: 47:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 78 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? ORIGINAL SOURCE:
 ? ORGANISM: Ancylostoma caninum
 ? US-08-634-641-47

Query Match 93.8% Score 30; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYPN 7
 Db 54 GYPN 58

RESULT 28
 US-09-249-471-47
 ? Sequence 47, Application US/09249471
 ? Patent No. 6040441
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasuk, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messers, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene
 ? APPLICANT: Jespers, Laurent Stephane
 ? APPLICANT: Gasemans, Yvanick Georges Jozef
 ? APPLICANT: Moyle, Matthew
 ? APPLICANT: Berquim, Peter W.
 ? TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 ? TITLE OF INVENTION: INHIBITORS AND ANTICAGULANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 356
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: 1906 5 Lye
 ? STREET: 634 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/249,471
 ? FILING DATE:

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/809,455
 ? FILING DATE: April 17, 1997
 ? APPLICATION NUMBER: 08/809,455
 ? FILING DATE: October 17, 1995
 ? APPLICATION NUMBER: 08/486,399
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,395
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: October 18, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? REFERENCE CHECK NUMBER: 219/136
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-3510
 ? INFORMATION FOR SEQ ID NO: 47:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 78 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? ORIGINAL SOURCE:
 ? ORGANISM: Ancylostoma caninum
 ? US-09-249-471-47

Query Match 93.8% Score 30; DB 3; Length 78;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYPN 7
 Db 54 GYPN 58

RESULT 29
 US-09-249-472-47
 ? Sequence 47, Application US/09249472
 ? Patent No. 6046318
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasuk, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messers, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene
 ? APPLICANT: Jespers, Laurent Stephane
 ? APPLICANT: Gasemans, Yvanick Georges Jozef
 ? APPLICANT: Moyle, Matthew
 ? APPLICANT: Berquim, Peter W.
 ? TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 ? TITLE OF INVENTION: INHIBITORS AND ANTICAGULANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 156
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: 1906 5 Lye
 ? STREET: 634 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0

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Query Match: 94.8%; Score 30; DB 3; Length 78;
Best Local Similarity 100.0%; Prod. No. 9.3;
Match 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 GYRN 7
    11111
1D 54 GYRN 58

RESULT 31
US-08-009-455-47
: Sequence 47, Application 43708080455
: Patent No. 6090916
: GENERAL INFORMATION:
: APPLICANT: Viasek, George Phillip
: APPLICANT: Stauss, Patrick Eric Bruno
: APPLICANT: Messous, Louis Hilda (Irene)
: APPLICANT: Lauwerys, Marc Joseph
: APPLICANT: Laroche, Yves Rene
: APPLICANT: Jospers, Laurent Stephane
: APPLICANT: Ganssems, Yambick Georges Jozele
: APPLICANT: Moyle, Matthew
: APPLICANT: Bequim, Peter W.
: TITLE OF INVENTOR: REMAINTS EXTRACTION PROCESS
: TITLE OF INVENTOR: PHARMACEUTICALS AND ARTICLES
: TITLE OF INVENTOR: PROTEIN
: NUMBER OF SEQUENTS: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 613 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles

```

STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,455
FILING DATE: April 17, 1997
PCT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 06/446,369
FILING DATE: June 5, 1995
APPLICATION NUMBER: 04/187,507
FILING DATE: June 5, 1995
APPLICATION NUMBER: 04/466,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/461,265
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/226,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE CHECK NUMBER: 216,276
TRICOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67 3510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-809-455-47

Query Match 93.8%, Score 30; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 3 GFYRN 7
IIIIII
Db 54 GFYRN 58

RESULT 32

US-09-249-461-47
Sequence 47, Application US/09249461
Patent No. 6096877
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stausens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon 5 1700
STREET: 633 West Fifth Street

STREET: Suite 4706
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: 07,000,1321
FILING DATE: October 17, 1995
APPLICATION NUMBER: 06/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/463,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE CHECK NUMBER: 216,270
TRICOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67 3510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-461-47

Query Match 93.8%, Score 30; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 3 GFYRN 7
IIIIII
Db 54 GFYRN 58

RESULT 33

US-09-249-448-47
Sequence 47, Application US/09249448
Patent No. 6121435
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stausens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN

1 NUMBER OF SEQUENCES: 456
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESSEE: Lyon & Lyon
 4 STREET: 644 West Fifth Street
 5 CITY: Los Angeles
 6 STATE: California
 7 COUNTRY: U.S.A.
 8 ZIP: 90071
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 11 MEDIUM TYPE: storage
 12 COMPUTER: IBM Compatible
 13 OPERATING SYSTEM: IBM P.C. DOS 5.0
 14 SOFTWARE: Word Perfect 5.1
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US/09/249,448
 17 FILING DATE: 1995
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 08/486,399
 20 FILING DATE: April 17, 1994
 21 APPLICATION NUMBER: PCT/93/21231
 22 FILING DATE: October 17, 1995
 23 APPLICATION NUMBER: 08/486,399
 24 FILING DATE: June 5, 1995
 25 APPLICATION NUMBER: 08/486,397
 26 FILING DATE: June 5, 1995
 27 APPLICATION NUMBER: 08/465,380
 28 FILING DATE: June 5, 1995
 29 APPLICATION NUMBER: 08/461,965
 30 FILING DATE: June 5, 1995
 31 APPLICATION NUMBER: 08/426,110
 32 FILING DATE: October 18, 1994
 33 ATTORNEY/AGENT INFORMATION:
 34 NAME: BIGGS, SUZANNE L.
 35 REGISTRATION NUMBER: 30,158
 36 REFERENCE/APPYET NUMBER: 214,279
 37 TELECOMMUNICATION INFORMATION:
 38 TELEPHONE: (213) 489-1600
 39 TELEFAX: (213) 955-0440
 40 TELEX: 67-3510
 41 INFORMATION FOR SEQ ID NO: 47:
 42 LENGTH: 78 amino acids
 43 TYPE: amino acid
 44 TOPOLOGY: linear
 45 MOLECULE TYPE: peptide
 46 ORIGINAL SOURCE:
 47 ORGANISM: Ancylostoma caninum
 48 US 09 249-448-47

Query Match 94.8% Score 30; DB 3; Length 78;
 Best Local Similarity 100.0%; Prod. No. 9.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 GYRN 7
 DB 54 GYRN 58

RESULT 34
 US-08-465-380-25
 1 Sequence 25, Application: US/08465380
 2 Patent No. 5863894
 3 GENERAL INFORMATION:
 4 APPLICANT: George P. Vlasuk, Patrick H. Stausseus,
 5 APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
 6 APPLICANT: Yves R. Laroche, Laurent S. Jespers,
 7 APPLICANT: Yvanick G.J. Gaussemans, Matthew Moyle,
 8 APPLICANT: Peter W. Berquam
 9 TITLE OF INVENTION: REMAINDER-EXTRACTED ANTICOAGULANT
 10 NUMBER OF SEQUENCES: 456

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Lyon & Lyon
 3 STREET: 644 West Fifth Street
 4 CITY: Los Angeles
 5 STATE: California
 6 COUNTRY: U.S.A.
 7 ZIP: 90071
 8 COMPUTER READABLE FORM:
 9 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 10 MEDIUM TYPE: storage
 11 COMPUTER: IBM Compatible
 12 OPERATING SYSTEM: IBM P.C. DOS 5.0
 13 SOFTWARE: Word Perfect 5.1
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: 08/38/465,380
 16 FILING DATE: June 5, 1995
 17 CLASSIFICATION: 540
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 08/226,110
 20 FILING DATE: October 18, 1994
 21 ATTORNEY/AGENT INFORMATION:
 22 NAME: BIGGS, SUZANNE L.
 23 REGISTRATION NUMBER: 30,158
 24 REFERENCE/APPYET NUMBER: 214,268
 25 TELECOMMUNICATION INFORMATION:
 26 TELEPHONE: (213) 489-1600
 27 TELEFAX: (213) 955-0440
 28 TELEX: 67-3510
 29 INFORMATION FOR SEQ ID NO: 25:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 82 amino acids
 32 TYPE: amino acid
 33 TOPOLOGY: linear
 34 MOLECULE TYPE: peptide
 35 ORIGINAL SOURCE:
 36 ORGANISM: Ancylostoma caninum
 37 US-08-465-380-25

Query Match 93.8% Score 40; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9.8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 GYRN 7
 DB 51 GYRN 55

RESULT 35
 US-08-465-380-49
 1 Sequence 49, Application: US/08465380
 2 Patent No. 5863894
 3 GENERAL INFORMATION:
 4 APPLICANT: George P. Vlasuk, Patrick H. Stausseus,
 5 APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
 6 APPLICANT: Yves R. Laroche, Laurent S. Jespers,
 7 APPLICANT: Yvanick G.J. Gaussemans, Matthew Moyle,
 8 APPLICANT: Peter W. Berquam
 9 TITLE OF INVENTION: REMAINDER-EXTRACTED ANTICOAGULANT
 10 NUMBER OF SEQUENCES: 456

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Lyon & Lyon
 3 STREET: 644 West Fifth Street
 4 CITY: Los Angeles
 5 STATE: California
 6 COUNTRY: U.S.A.
 7 ZIP: 90071
 8 COMPUTER READABLE FORM:
 9 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 10 MEDIUM TYPE: storage
 11 COMPUTER: IBM Compatible

```

1 OPERATING SYSTEM: IBM P.C. DOS 5.0
2 SOFTWARE: Word Perfect 5.1
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: 08/326,110
5 FILING DATE: June 5, 1995
6 CLASSIFICATION: 530
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 08/326,110
9 FILING DATE: October 18, 1994
10 ATTORNEY/AGENT INFORMATION:
11 NAME: BIGGS, SUZANNE L.
12 REGISTRATION NUMBER: 30,158
13 REFERENCE/LOCKIT NUMBER: 213,269
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (213) 489-1600
16 TELEFAX: (213) 955-0440
17 TELEX: 67-3510
18 INFORMATION FOR SEQ ID NO: 49:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 82 amino acids
21 TYPE: amino acid
22 TOPOLOGY: linear
23 MOLECULE TYPE: peptide
24 ORIGINAL SOURCE:
25 ORGANISM: Ancylostoma canalicum
26 US-08-465-380-49

```

```

Query Match      93.8%  Score 30; DB 2; Length 82;
Best Local Similarity 100.0%  Prod. No. 9.8;
Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0.

```

```

QY 3 GYRN 7
    11111
DB 51 GYRN 55

```

```

RESULT 36
US-08-480-478-54
Sequence 54, Application 05/08486478
Patent No. 5864009
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
APPLICANT: HUGO STANSENS; JORIS HILDA
APPLICANT: LIEVEN MESSERS; MARC JOZEF
APPLICANT: LAURENCE; YVES RENE LAROCHE;
APPLICANT: LAURENT STEPHANE JESPEERS; and
APPLICANT: YANNICK GEORGES JOZEF
APPLICANT: GANSEMAN
TITLE OF INVENTION: NEMATODE EXTRACTED ANTI
TITLE OF INVENTION: COAGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:

```

```

1 NAME: BIGGS, SUZANNE L.
2 REGISTRATION NUMBER: 30,158
3 REFERENCE/LOCKIT NUMBER: 213,269
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (213) 489-1600
6 TELEFAX: (213) 955-0440
7 TELEX: 67-3510
8 INFORMATION FOR SEQ ID NO: 50:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 82 amino acids
11 TYPE: amino acid
12 TOPOLOGY: linear
13 MOLECULE TYPE: peptide
14 ORIGINAL SOURCE:
15 ORGANISM: Ancylostoma canalicum
16 US-08-465-380-49

```

```

Query Match      93.8%  Score 30; DB 2; Length 82;
Best Local Similarity 100.0%  Prod. No. 9.8;
Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0.

```

```

QY 3 GYRN 7
    11111
DB 51 GYRN 55

```

```

RESULT 37
US-08-486-497-25
Sequence 25, Application 05/08486497
Patent No. 5866542
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK; PATRICK ERIC STANSENS;
APPLICANT: JORIS HILDA; MESSERS, MARC JOZEF;
APPLICANT: YVES R. LAROCHE; LAURENT S. JESPEERS;
APPLICANT: YANNICK G.J. GANSEMAN; Matthew Woyle;
APPLICANT: Peter W. Remum
TITLE OF INVENTION: NEMATODE EXTRACTED ANTI-
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/326,486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/LOCKIT NUMBER: 213,269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma canalicum

```

US-08-486-499-25

Query Match 94.8%; Score 30; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 5; Conservatv 0; Mismatches 0; Gaps 0;

QY 4 GYRN 7

|||||

Db 51 GYRN 55

RESULT 38

US-08-486-497-49

: Sequence 49; Application US/08486497

: Patent No. 5866542

: GENERAL INFORMATION:

: APPLICANT: George P. Vlasek, Patric H. Stanssens,

: APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,

: APPLICANT: Yves R. Laroche, Laurent S. Jespers,

: APPLICANT: Yvanick G.J. Ganssems, Matthew Moyle,

: APPLICANT: Peter W. Berquim

: TITLE OF INVENTION: NEMATODE EXTRACTED ANTICAGULANT

: NUMBER OF SEQUENCES: 357

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Lyon & Lyon

: STREET: 643 West Fifth Street

: CITY: Los Angeles

: STATE: California

: COUNTRY: U.S.A.

: ZIP: 90071

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

: MEDIUM TYPE: storage

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: IBM P.C. DOS 5.0

: SOFTWARE: Word Perfect 5.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: June 5, 1995

: CLASSIFICATION: 530

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: October 18, 1994

: ATTORNEY/AGENT INFORMATION:

: NAME: BIGGS, SUZANNE L.

: REGISTRATION NUMBER: 30,158

: REFERENCE/SEQUENT NUMBER: 21,7266

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (213) 489-1600

: TELEFAX: (213) 955-0440

: TELEX: 67-3510

: INFORMATION FOR SEQ ID NO: 49:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 82 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

: ORIGINAL SOURCE:

: ORGANISM: Ancylostoma ceylanicum

US-08-486-497-49

Query Match 94.8%; Score 30; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 5; Conservatv 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7

|||||

Db 51 GYRN 55

RESULT 39

US-08-486-499-25

: Sequence 25; Application US/08486499

: Patent No. 5866543

: GENERAL INFORMATION:

: APPLICANT: George P. Vlasek, Patric H. Stanssens,

: APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,

: APPLICANT: Yves R. Laroche, Laurent S. Jespers,

: APPLICANT: Yvanick G.J. Ganssems, Matthew Moyle,

: APPLICANT: Peter W. Berquim

: TITLE OF INVENTION: NEMATODE EXTRACTED ANTICAGULANT

: NUMBER OF SEQUENCES: 356

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Lyon & Lyon

: STREET: 643 West Fifth Street

: CITY: Los Angeles

: STATE: California

: COUNTRY: U.S.A.

: ZIP: 90071

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

: MEDIUM TYPE: storage

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: IBM P.C. DOS 5.0

: SOFTWARE: Word Perfect 5.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: June 5, 1995

: CLASSIFICATION: 530

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: October 18, 1994

: ATTORNEY/AGENT INFORMATION:

: NAME: BIGGS, SUZANNE L.

: REGISTRATION NUMBER: 30,158

: REFERENCE/SEQUENT NUMBER: 21,7270

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (213) 489-1600

: TELEFAX: (213) 955-0440

: TELEX: 67-3510

: INFORMATION FOR SEQ ID NO: 25:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 82 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

: ORIGINAL SOURCE:

: ORGANISM: Ancylostoma ceylanicum

US-08-486-499-25

Query Match 94.8%; Score 30; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 5; Conservatv 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7

|||||

Db 51 GYRN 55

RESULT 40

US-08-486-499-49

: Sequence 49; Application US/08486499

: Patent No. 5866543

: GENERAL INFORMATION:

: APPLICANT: George P. Vlasek, Patric H. Stanssens,

: APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,

: APPLICANT: Yves R. Laroche, Laurent S. Jespers,

: APPLICANT: Yvanick G.J. Ganssems, Matthew Moyle,

: APPLICANT: Peter W. Berquim

: TITLE OF INVENTION: NEMATODE EXTRACTED ANTICAGULANT

: NUMBER OF SEQUENCES: 356

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/AGENT NUMBER: 213,273
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO. 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma ceylanicum
US-08-486-399-49

```

```

Query Match 93.8% Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Pref. No. 5, 8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 51 GYRN 55

RESULT 41
US-08-461-965-25
Sequence 25, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mousens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158

```

```

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/AGENT NUMBER: 213,243
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma ceylanicum
US-08-461-965-25

Query Match 93.8% Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Pref. No. 9, 8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 51 GYRN 55

RESULT 42
US-08-461-965-49
Sequence 49, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mousens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158

```

1 REFERENCE: 54: 09-110A-54
 2 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: (213) 489 1600
 4 TELEFAX: (213) 955-0440
 5 TELEX: 67-4510
 6 INFORMATION FOR SEQ ID NO: 49:
 7 SEQUENCE CHARACTERISTICS:
 8 LENGTH: 82 amino acids
 9 TYPE: amino acid
 10 TOPOLOGY: linear
 11 MOLECULE TYPE: peptide
 12 ORIGINAL SOURCE:
 13 ORGANISM: Anacyclostoma coplanicum
 14 US 08-461-965-45

Query Match 93.8%; Score 30; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9.8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 11111
 DB 51 GYRN 55

RESULT 44
 US-08-426-110A-54
 1 Sequence 54: Application US/09/25111A
 2 Patent No. 5945275
 3 GENERAL INFORMATION:
 4 APPLICANT: GEORGE P. VLASAK; PATRICK ERIC
 5 APPLICANT: HUGO STANSENS; JORIS HILDA
 6 APPLICANT: LIEVEN MESSERS; MARC JOYEF
 7 APPLICANT: LAURENCE YVES BENE LAKECHIE;
 8 APPLICANT: LAURENT STEPHANE JESPEERS; and
 9 APPLICANT: YANNICK GEORGES JOYEF
 10 APPLICANT: GANSEMAN
 11 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
 12 TITLE OF INVENTION: COAGULANT PROTEIN
 13 NUMBER OF SEQUENCES: 86
 14 CORRESPONDENCE ADDRESS:
 15 ADDRESSEE: LYON 5 LYON
 16 STREET: 633 West Fifth Street
 17 CITY: Los Angeles
 18 STATE: California
 19 COUNTRY: U.S.A.
 20 ZIP: 90071

21 COMPUTER READABLE FORM:
 22 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 23 MEDIUM TYPE: storage
 24 COMPUTER: IBM Compatible
 25 OPERATING SYSTEM: IBM P.C. DOS 5.0
 26 SOFTWARE: FastSeq Version 1.5
 27 CURRENT APPLICATION DATA:
 28 APPLICATION NUMBER: US/08/326,110A
 29 FILING DATE: 18 October 1994
 30 CLASSIFICATION: 530
 31 PRIOR APPLICATION DATA:
 32 APPLICATION NUMBER:
 33 FILING DATE:
 34 ATTORNEY/AGENT INFORMATION:
 35 NAME: ROSEN, ROYALGE L.
 36 REGISTRATION NUMBER: 30,159
 37 REFERENCE: 54: 09-110A-54
 38 TELECOMMUNICATION INFORMATION:
 39 TELEPHONE: (213) 489-1600
 40 TELEFAX: (213) 955-0440
 41 TELEX: 67-4510
 42 INFORMATION FOR SEQ ID NO: 54:
 43 SEQUENCE CHARACTERISTICS:
 44 LENGTH: 82 amino acids
 45 TYPE: amino acid
 46 TOPOLOGY: linear

US-08-426-110A-54

Query Match 93.8%; Score 30; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9.8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 11111
 DB 51 GYRN 55

RESULT 44
 US-08-644-641-25
 1 Sequence 25: Application US/08/644641
 2 Patent No. 5955294
 3 GENERAL INFORMATION:
 4 APPLICANT: VLASAK, George P. Vlasak
 5 APPLICANT: STANSENS, Patrick Eric. Hugo
 6 APPLICANT: MESSERS, Joris Hilda. Lieven
 7 APPLICANT: LAURENCE, Yves Rene
 8 APPLICANT: JESPEERS, Laurent Stephane
 9 APPLICANT: GANSEMAN, Yannick Georges. Joyef
 10 APPLICANT: Joyef, Matthew
 11 APPLICANT: Bertram, Peter W.
 12 TITLE OF INVENTION: NEMATODE EXTRACTED ANTI-
 13 TITLE OF INVENTION: PROTEIN
 14 NUMBER OF SEQUENCES: 356
 15 CORRESPONDENCE ADDRESS:
 16 ADDRESSEE: LYON 5 LYON
 17 STREET: 633 West Fifth Street
 18 CITY: Los Angeles
 19 STATE: California
 20 COUNTRY: U.S.A.
 21 ZIP: 90071

22 COMPUTER READABLE FORM:
 23 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 24 MEDIUM TYPE: storage
 25 COMPUTER: IBM Compatible
 26 OPERATING SYSTEM: IBM P.C. DOS 5.0
 27 SOFTWARE: Word Perfect 5.1
 28 CURRENT APPLICATION DATA:
 29 APPLICATION NUMBER: US/08/644,641
 30 FILING DATE: April 19, 1996
 31 PRIOR APPLICATION DATA:
 32 APPLICATION NUMBER: 157,735/5,132A1
 33 FILING DATE: October 17, 1995
 34 APPLICATION NUMBER: 08/486,499
 35 FILING DATE: June 5, 1995
 36 APPLICATION NUMBER: 08/486,497
 37 FILING DATE: June 5, 1995
 38 APPLICATION NUMBER: 08/465,480
 39 FILING DATE: June 5, 1995
 40 APPLICATION NUMBER: 08/461,965
 41 FILING DATE: June 5, 1995
 42 APPLICATION NUMBER: 08/426,110
 43 FILING DATE: October 18, 1994
 44 ATTORNEY/AGENT INFORMATION:
 45 NAME: ROSEN, ROYALGE L.
 46 REGISTRATION NUMBER: 30,159
 47 REFERENCE: 54: 09-110A-54
 48 TELECOMMUNICATION INFORMATION:
 49 TELEPHONE: (213) 489 1600
 50 TELEFAX: (213) 955-0440
 51 TELEX: 67-4510
 52 INFORMATION FOR SEQ ID NO: 25:
 53 SEQUENCE CHARACTERISTICS:
 54 LENGTH: 82 amino acids
 55 TYPE: amino acid
 56 TOPOLOGY: linear
 57 MOLECULE TYPE: peptide
 58 ORIGINAL SOURCE:

ORGANISM: Ancylostoma ceylanicum
US-08-634-641-25

Query Match 93.8% Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIII
Db 51 GYRN 55

RESULT 45

US-08-634-641-49
Sequence 45, Application: US:08634541
Patent No. 5955294

GENERAL INFORMATION:

APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Mensons, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 59, 59, 634, 641

FILING DATE: April 19, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FCT/9395/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/426,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: HIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 219/136

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO. 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 82 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:
ORGANISM: Ancylostoma ceylanicum
US-08-634-641-49

Query Match 92.8% Score 90; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIII
Db 51 GYRN 55

Search completed: April 30, 2003, 14:37:17
Job time: 27.3727 secs

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GenCore version 5.1.4_p5_4578
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Run on April 20, 2003, 13:47:03, Search time 26.0727 seconds
(without alignments)
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Maximum bh seq length: 200000000
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Post-processing: Minimum Match 08

Listing first 1000 summaries
Maximum Match 100%

Database : Published_Applications_AA:*

— 54 —

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3	30	93.8	268	05-09-864-898-44	Sequence 44, Appl
4	30	93.8	1564	05-09-801-768-244	Sequence 244, App
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ALIGNMENTS

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? Patent No. US20020147140A1
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: none
? CURRENT APPLICATION NUMBER: 09/0764877
? PRIOR APPLICATION DATA REMOVED - refer to PAM or file wrapper
? NUMBER OF SEQ ID NOS: 4031
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 1934
? LENGTH: 1387
? TYPE: PRI
? ORGANISM: Homo sapiens
US-09-764-877-1934

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Best local Similarity 100.0%  Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB  62 GYRN 66

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RESULT 2
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? Sequence 4828: Application US/09748626
? Patent No. US20020197095A1
? GENERAL INFORMATION:
? APPLICANT: NAKAGAWA, SAPOUSHI
? APPLICANT: MIZOGUCHI, HIROSHI
? APPLICANT: ANDO, SEIKO

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? APPLICANT: HAYASHI, MIKIRO
? APPLICANT: CHAI, KEIKO
? APPLICANT: YOKOI, HARUHIKO
? APPLICANT: IATOH, NAOKO
? APPLICANT: SUMOH, AKIHIRO
? APPLICANT: KIKAWA, MASAO
? APPLICANT: CHAI, ZHI
? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
? FILE REFERENCE: 249-125
? CURRENT APPLICATION NUMBER: 09/074828
? PRIOR FILING DATE: 2000-12-18
? PRIOR FILING DATE: 2000-12-18
? PRIOR FILING DATE: 2000-04-07
? PRIOR FILING DATE: 2000-08-04
? NUMBER OF SEQ ID NOS: 7059
? SOFTWARE: Patent In Ver. 3.0
? SEQ ID NO: 3828
? LENGTH: 260
? TYPE: PRI
? ORGANISM: Corynebacterium glutamicum
US-09-748-626-4828

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Query Match          94.8%  Score 30; DB 9; Length 260
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DB  105 GYRN 109

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RESULT 3
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? Patent No. US20020127656A1
? GENERAL INFORMATION:
? APPLICANT: Lloyd, K. Stephen
? APPLICANT: McCulloch, Amanda K.
? TITLE OF INVENTION: DNA REPAIR POLYPEPTIDES AND METHODS OF USE
? FILE REFERENCE: 265,00170101
? CURRENT APPLICATION NUMBER: 09/0864866
? PRIOR FILING DATE: 2000-05-24
? PRIOR FILING DATE: 2000-05-24
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: Patent In Version 3.0
? SEQ ID NO: 43
? LENGTH: 268
? TYPE: PRI
? ORGANISM: Micrococcus luteus
US-09-864-866-43

```

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Query Match          94.8%  Score 30; DB 10; Length 268
Best local Similarity 100.0%  Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  3 GYRN 7
DB  95 GYRN 94

```

```

RESULT 4
US-09-801-368-244
? Sequence 244: Application US/09801368
? Patent No. US20020128250A1
? GENERAL INFORMATION:
? APPLICANT: Busby, Robert
? APPLICANT: Call, Brian
? APPLICANT: Hecht, Peter

```

APPLICANT: Holtzman, Doug
 APPLICANT: Madden, Kevin
 APPLICANT: Maxon, Mary
 APPLICANT: Milne, Todd
 APPLICANT: RO. US2002012850A1/000001/000001
 APPLICANT: Royer, John
 APPLICANT: Salama, Scott
 APPLICANT: Sherman, Amir
 APPLICANT: Silva, Jeff
 APPLICANT: Summers, Eric
 TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 FILE REFERENCE: 109272.147
 CURRENT APPLICATION NUMBER: US2002012850A1/000001/000001
 CURRENT FILING DATE: 2001-03-07
 PRIOR APPLICATION NUMBER: US 09/487,558
 PRIOR FILING DATE: 2000-01-19
 PRIOR APPLICATION NUMBER: US 60/160,587
 PRIOR FILING DATE: 1999-10-20
 NUMBER OF SEQ ID NOS: 440
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 244
 LENGTH: 1564
 TYPE: PRT
 ORGANISM: Streptomyces cerevisiae
 US-09-498-556c-79

Query Match 93.99; Score 27; DP 10; Length 1564;
 Best local similarity 100.0%; Prod. No. 1-00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7
 Db 1363 GYEN 1367

RESULT 5
 US-09-864-761-45609
 Sequence 45609, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rack, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aomic-X-1
 CURRENT APPLICATION NUMBER: US 09/487,558
 CURRENT FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: US 56/488,312
 PRIOR FILING DATE: 2000-09-04
 PRIOR APPLICATION NUMBER: US 60/207,477
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: US 09/532,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/006656
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006657
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006658
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006659
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006660
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006661
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/244,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 60/224,204
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 15117
 SOFTWARE: Automatic sequence List and Enzyme vers. 1.1
 SEQ ID NO: 45609
 LENGTH: 79
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC014644.4
 OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
 OTHER INFORMATION: HUMAN H11: 6174247.1, EVALUATION: 2.50e-01
 OTHER INFORMATION: SWISSPROT HIT: P34133, EVALUATION: 3.10e-01
 US-09-864-761-45609

Query Match 84.4%; Score 27; DP 10; Length 79;
 Best local similarity 80.0%; Prod. No. 1-00;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7
 Db 72 GYEN 76

RESULT 6
 US-09-925-302-855
 Sequence 455, Application US/09925302
 Patent No. US20020044941A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Models Acids, Proteins and Antibodies
 FILE REFERENCE: PA104
 CURRENT APPLICATION NUMBER: US 09/925,302
 CURRENT FILING DATE: 2001-06-11
 PRIOR APPLICATION NUMBER: PCT/US01/006659
 PRIOR FILING DATE: 2000-04-08
 PRIOR APPLICATION NUMBER: PCT/US01/006660
 PRIOR FILING DATE: 1999-04-12
 NUMBER OF SEQ ID NOS: 896
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO: 855
 LENGTH: 173
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (159)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (168)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-302-855

Query Match 84.4%; Score 27; DP 10; Length 173;
 Best local similarity 80.0%; Prod. No. 1-00;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7

```

111:1
Db 70 GFYKN 74

RESULT 7
US-09-858 546-5
Sequence 5, Application US/09/858546
Patent No. US20020172995A1
GENERAL INFORMATION:
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
FILE REFERENCE: CL001242
CURRENT APPLICATION NUMBER: US/09/858,546
CURRENT FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 260
TYPE: PRT
ORGANISM: Human
US-09-858 546-5

Query Match 84.4%; Score 27; DB 9; Length 260;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYKN 7
111:1
Db 121 GFYKN 125

RESULT 8
US-09-813-718-16
Sequence 16, Application US/09/813718
Publication No. US20020192566A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-04-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 392
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human minor
OTHER INFORMATION: TrpRS treatment in PET20B
US-09-813-718-16

Query Match 84.4%; Score 27; DB 9; Length 392;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYKN 7
111:1
Db 154 GFYKN 159

RESULT 9
US-09-813-718-14
Sequence 14, Application US/09/813718
Publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl tRNA Synthetase Polypeptides Useful For

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TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-04-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 415
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: supermini TrpRS in PET20B
US-09-813-718-14

Query Match 84.4%; Score 27; DB 9; Length 415;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYKN 7
111:1
Db 177 GFYKN 181

RESULT 10
US-09-813-718-12
Sequence 12, Application US/09/813718
Publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: the Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-04-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 447
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human mini
OTHER INFORMATION: TrpRS in PET20B
US-09-813-718-12

Query Match 84.4%; Score 27; DB 9; Length 447;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYKN 7
111:1
Db 199 GFYKN 203

RESULT 11
US-10-126-467B-2
Sequence 2, Application US/10/126467B
Publication No. US20030059797A1
GENERAL INFORMATION:
APPLICANT: Paley, Elona
TITLE OF INVENTION: ANIMAL MODEL FOR ALZHEIMER'S DISEASE
FILE REFERENCE: PALL-111
CURRENT APPLICATION NUMBER: US/10/126,467B
CURRENT FILING DATE: 2002-11-19
PRIORITY APPLICATION NUMBER: 60/284,980
PRIORITY FILING DATE: 2001-04-19
PRIORITY APPLICATION NUMBER: 09/518,895
PRIORITY FILING DATE: 2000-02-28
PRIORITY APPLICATION NUMBER: 09/484,869
PRIORITY FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 6

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SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
LENGTH: 471
TYPE: PPT
ORGANISM: Homo sapiens
US-10-126-467B-2

Query Match 84.4%; Score 27; DB 9; Length 471;
Best Local Similarity 80.0%; Pred. No. 5,5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 246 GYRN 250

RESULT 12

US-09-925-302-558
Sequence: PPT, Application US/09/05918
Patent No. US2002004494A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: P104
CURRENT APPLICATION NUMBER: US/09/05918
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-04-08
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 558
LENGTH: 475
TYPE: PPT
ORGANISM: Homo sapiens
US-09-925-302-558

Query Match 84.4%; Score 27; DB 10; Length 475;
Best Local Similarity 80.0%; Pred. No. 5,5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 250 GYRN 254

RESULT 13

US-09-813-718-10
Sequence: PPT, Application US/09/813718
Publication No. US2002018266A1

GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
TITLE OF INVENTION: Human Aminoacyl tRNA Synthetase Polypeptides Useful For
THE REGULATION OF ANGIOGENESIS
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10
LENGTH: 484
TYPE: PPT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: full-length trpRS in pR120H

Query Match 84.4%; Score 27; DB 9; Length 484;
Best Local Similarity 80.0%; Pred. No. 5,6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 246 GYRN 250

RESULT 14

US-10-108-605-171
Sequence: PPT, Application US/10/108605
Patent No. US2002016094A1

GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kambar, Kim
TITLE OF INVENTION: REGULAR ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

FILE REFERENCE: 11138
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/761,142
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 171
LENGTH: 530
TYPE: PPT
ORGANISM: Drosophila melanogaster
US-10-108-605-171

Query Match 84.4%; Score 27; DB 9; Length 530;
Best Local Similarity 80.0%; Pred. No. 6,1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 192 GYRN 186

RESULT 15

US-09-858-546-2
Sequence: PPT, Application US/09/858546
Patent No. US2002017295A1

GENERAL INFORMATION:
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: REGULAR ACID SEQUENCES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: C1001242
CURRENT FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 530
TYPE: PPT
ORGANISM: Human
US-09-858-546-2

Query Match 84.4%; Score 27; DB 9; Length 530;
Best Local Similarity 80.0%; Pred. No. 6,1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 391 GYRN 395

RESULT 16

US-09-808-602-82
Sequence: PPT, Application US/09/808602

? APPLICANT: Rosen et al.
 ? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antisense
 ? FILE REFERENCE: P410
 ? CURRENT APPLICATION NUMBER: US/09/764,855
 ? CURRENT FILING DATE: 2001-01-17
 ? Prior application data removed - consult P410 or file wrapper
 ? NUMBER OF SEQ ID NOS: 334
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO 130
 ? LENGTH: 67
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-09-764-855-130

Query Match 78.1% Score 25; DB 10; Length 67;
 Best Local Similarity 80.0%; Prod. No. 2.1e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYNN 7
 IIII
 Db 44 GYNN 48

RESULT 20
 US-10-140-164-32
 ? Sequence 32, Application US/10140164
 ? Publication No. US20030072736A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Baker et al.
 ? TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR16
 ? FILE REFERENCE: PF51401
 ? CURRENT APPLICATION NUMBER: US/10/140,164
 ? CURRENT FILING DATE: 2002-05-08
 ? PRIOR APPLICATION NUMBER: 09/463,956
 ? PRIOR FILING DATE: 2000-08-10
 ? PRIOR APPLICATION NUMBER: 60/148,348
 ? PRIOR FILING DATE: 1999-08-12
 ? PRIOR APPLICATION NUMBER: 60/148,683
 ? PRIOR FILING DATE: 1999-08-13
 ? PRIOR APPLICATION NUMBER: 60/148,870
 ? PRIOR FILING DATE: 1999-08-13
 ? PRIOR APPLICATION NUMBER: 60/148,758
 ? PRIOR FILING DATE: 1999-08-16
 ? PRIOR APPLICATION NUMBER: 60/149,181
 ? PRIOR FILING DATE: 1999-08-17
 ? PRIOR APPLICATION NUMBER: 60/149,453
 ? PRIOR FILING DATE: 1999-08-18
 ? PRIOR APPLICATION NUMBER: 60/149,458
 ? PRIOR FILING DATE: 1999-08-19
 ? NUMBER OF SEQ ID NOS: 76
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 32
 ? LENGTH: 74
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-10-140-164-32

Query Match 78.1% Score 25; DB 9; Length 74;
 Best Local Similarity 80.0%; Prod. No. 2.1e-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYNN 7
 IIII
 Db 62 GYNN 66

RESULT 21
 US-10-140-164-61
 ? Sequence 51, Application US/10140164
 ? Publication No. US20030072736A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Baker et al.
 ? TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR16

? FILE REFERENCE: PF51401
 ? CURRENT APPLICATION NUMBER: US/10/140,164
 ? CURRENT FILING DATE: 2002-05-08
 ? PRIOR APPLICATION NUMBER: 09/463,956
 ? PRIOR FILING DATE: 2000-08-10
 ? PRIOR APPLICATION NUMBER: 60/148,348
 ? PRIOR FILING DATE: 1999-08-12
 ? PRIOR APPLICATION NUMBER: 60/148,683
 ? PRIOR FILING DATE: 1999-08-13
 ? PRIOR APPLICATION NUMBER: 60/148,870
 ? PRIOR FILING DATE: 1999-08-13
 ? PRIOR APPLICATION NUMBER: 60/148,758
 ? PRIOR FILING DATE: 1999-08-16
 ? PRIOR APPLICATION NUMBER: 60/149,181
 ? PRIOR FILING DATE: 1999-08-17
 ? PRIOR APPLICATION NUMBER: 60/149,453
 ? PRIOR FILING DATE: 1999-08-18
 ? PRIOR APPLICATION NUMBER: 60/149,458
 ? PRIOR FILING DATE: 1999-08-19
 ? NUMBER OF SEQ ID NOS: 76
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 61
 ? LENGTH: 74
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-10-140-164-61

Query Match 78.1% Score 25; DB 9; Length 74;
 Best Local Similarity 80.0%; Prod. No. 2.1e-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYNN 7
 IIII
 Db 62 GYNN 66

RESULT 22
 US-09-939-980-409
 ? Sequence 409, Application US/09949980
 ? Patent No. US2002082334A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Black, Richard
 ? Burnham, Martin
 ? Hodson, John
 ? Knowles, David
 ? Lonetto, Michael
 ? Nicholas, Richard
 ? Pratt, Julie
 ? Reickard, Richard
 ? Rosenberq, Martin
 ? Ward, Judith
 ? TITLE OF INVENTION: Novel Prokaryotic Polypeptides,
 ? NUMBER OF SEQUENCES: 534
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: SmithKline Beecham Corporation
 ? STREET: 709 Swedeland Road
 ? CITY: King of Prussia
 ? STATE: PA
 ? COUNTRY: USA
 ? ZIP: 19406-0949
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM compatible
 ? OPERATING SYSTEM: DOS
 ? SOFTWARE: FastSeq for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: us/09/949,980
 ? FILING DATE: 27 Aug 2001
 ? CLASSIFICATION: unknown
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/946,165
 ? FILING DATE: unknown

```

1 ATTORNEY/AGENT INFORMATION
2 NAME: Gianni, Edward R
3 REPRESENTATION NUMBER: 60/047,501
4 REFERENCE NUMBER: 199549
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: 610-270-4478
7 TELEFAX: 610-270-5090
8 TELEX: Unknown
9
10 INFORMATION FOR SEQ ID NO: 409:
11     SEQUENCE CHARACTERISTICS:
12         LENGTH: 139 amino acids
13         TYPE: amino acid
14         STRANDEDNESS: single
15         TOPOLOGY: linear
16
17     MOLECULE TYPE: Protein
18
19     SEQUENCE DESCRIPTION: SEQ ID NO: 409:
20 US-09 948-940-409
21
22 Query Match      79.1%; Score 25; DB 10; Length 139;
23 Best Local Similarity 89.0%; Prod. No. 430-02;
24 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
25
26 QY 4 GIVEN 7
27 DI 55 GIVEN 59
28
29 RESULT 24
30 US-09 981-876-178
31     Sequence 178; Application US/09/981876
32     Patent No. 6,520,019 A1
33     GENERAL INFORMATION:
34     APPLICANT: Kosco et al
35     TITLE OF INVENTION: 70 Human Secreted Proteins
36     FILE REFERENCE: P200101
37     CURRENT APPLICATION NUMBER: US/09/981,876
38     CURRENT FILING DATE: 2001-10-19
39     PRIOR APPLICATION NUMBER: 09/148,545
40     PRIOR FILING DATE: 1998-07-04
41     PRIOR APPLICATION NUMBER: 60/040,162
42     PRIOR FILING DATE: 1997-03-07
43     PRIOR APPLICATION NUMBER: 60/040,333
44     PRIOR FILING DATE: 1997-03-07
45     PRIOR APPLICATION NUMBER: 60/040,621
46     PRIOR FILING DATE: 1997-03-07
47     PRIOR APPLICATION NUMBER: 60/040,161
48     PRIOR FILING DATE: 1997-03-07
49     PRIOR APPLICATION NUMBER: 60/040,626
50     PRIOR FILING DATE: 1997-03-07
51     PRIOR APPLICATION NUMBER: 60/040,444
52     PRIOR FILING DATE: 1997-03-07
53     PRIOR APPLICATION NUMBER: 60/040,436
54     PRIOR FILING DATE: 1997-03-07
55     PRIOR APPLICATION NUMBER: 60/040,163
56     PRIOR FILING DATE: 1997-03-07
57     PRIOR APPLICATION NUMBER: 60/047,615
58     PRIOR FILING DATE: 1997-05-24
59     PRIOR APPLICATION NUMBER: 60/047,638
60     PRIOR FILING DATE: 1997-05-24
61     PRIOR APPLICATION NUMBER: 60/047,597
62     PRIOR FILING DATE: 1997-05-24
63     PRIOR APPLICATION NUMBER: 60/047,502
64     PRIOR FILING DATE: 1997-05-24
65     PRIOR APPLICATION NUMBER: 60/047,633
66     PRIOR FILING DATE: 1997-05-24
67     PRIOR APPLICATION NUMBER: 60/047,694
68     PRIOR FILING DATE: 1997-05-24
69     PRIOR APPLICATION NUMBER: 60/047,617
70     PRIOR FILING DATE: 1997-05-24
71     PRIOR APPLICATION NUMBER: 60/047,618
72     PRIOR FILING DATE: 1997-05-24
73     PRIOR APPLICATION NUMBER: 60/047,583
74     PRIOR FILING DATE: 1997-05-24
75
76     PRIOR APPLICATION NUMBER: 60/047,592
77     PRIOR FILING DATE: 1997-05-24
78     PRIOR APPLICATION NUMBER: 60/047,501
79     PRIOR FILING DATE: 1997-05-24
80     PRIOR APPLICATION NUMBER: 60/047,584
81     PRIOR FILING DATE: 1997-05-24
82     PRIOR APPLICATION NUMBER: 60/047,500
83     PRIOR FILING DATE: 1997-05-24
84     PRIOR APPLICATION NUMBER: 60/047,587
85     PRIOR FILING DATE: 1997-05-24
86     PRIOR APPLICATION NUMBER: 60/047,492
87     PRIOR FILING DATE: 1997-05-24
88     PRIOR APPLICATION NUMBER: 60/047,598
89     PRIOR FILING DATE: 1997-05-24
90     PRIOR APPLICATION NUMBER: 60/047,613
91     PRIOR FILING DATE: 1997-05-24
92     PRIOR APPLICATION NUMBER: 60/047,582
93     PRIOR FILING DATE: 1997-05-24
94     PRIOR APPLICATION NUMBER: 60/047,596
95     PRIOR FILING DATE: 1997-05-24
96     PRIOR APPLICATION NUMBER: 60/047,612
97     PRIOR FILING DATE: 1997-05-24
98     PRIOR APPLICATION NUMBER: 60/047,632
99     PRIOR FILING DATE: 1997-05-24
100    PRIOR APPLICATION NUMBER: 60/047,601
101    PRIOR FILING DATE: 1997-05-24
102    PRIOR APPLICATION NUMBER: 60/043,580
103    PRIOR FILING DATE: 1997-04-11
104    PRIOR APPLICATION NUMBER: 60/043,568
105    PRIOR FILING DATE: 1997-04-11
106    PRIOR APPLICATION NUMBER: 60/043,414
107    PRIOR FILING DATE: 1997-04-11
108    PRIOR APPLICATION NUMBER: 60/043,569
109    PRIOR FILING DATE: 1997-04-11
110    PRIOR APPLICATION NUMBER: 60/043,411
111    PRIOR FILING DATE: 1997-04-11
112    PRIOR APPLICATION NUMBER: 60/043,671
113    PRIOR FILING DATE: 1997-04-11
114    PRIOR APPLICATION NUMBER: 60/043,674
115    PRIOR FILING DATE: 1997-04-11
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118    PRIOR APPLICATION NUMBER: 60/043,412
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127    PRIOR FILING DATE: 1997-06-06
128    PRIOR APPLICATION NUMBER: 60/056,886
129    PRIOR FILING DATE: 1997-06-24
130    PRIOR APPLICATION NUMBER: 60/056,877
131    PRIOR FILING DATE: 1997-08-22
132    PRIOR APPLICATION NUMBER: 60/056,889
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144    PRIOR APPLICATION NUMBER: 60/056,882
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147    PRIOR FILING DATE: 1997-08-22
148    PRIOR APPLICATION NUMBER: 60/056,903

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73	PRIOR FILING DATE: 1947-08-22	

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? FRICK APPLICATION NUMBER: 607048,944
? FIRST FILING DATE: 1997-09-06
? PRIOR APPLICATION NUMBER: 607057,650
? FIRST FILING DATE: 1997-09-05
? PENDING APPLICATION NUMBER: 607056,884
? PRIOR FILING DATE: 1997-08-22
? NUMBER OF SEQ ID NOS: 280
? SOFTWARE: PATENTIN Ver. 2.0
? SEQ ID NO 178
? LENGTH: 155

Query Match      78.1% Score 25: DB 9; Length 155;
Best Local Similarity 80.0%; Pred No. 4 R+0.0;
Matches 4; Conservative 3; Mismatches 1; Indels

QY   3 GGYRN 7
DB    III I
     67 GTTNN 71

RESULT 24
US-09-148-545-178
? Sequence 178, Application US/09148545
? Publication No. 0029029027132A1
? GENERAL INFORMATION:
? APPLICANT: Rosen et al
? TITLE OF INVENTION: 70 Human Secreted Proteins
? FILE REFERENCE: P2001PI
? CURRENT APPLICATION NUMBER: 92756,148,545
? CURRENT FILING DATE: 1998-09-04
? EARLIER APPLICATION NUMBER: 607038,94182
? EARLIER FILING DATE: 1998-03-06
? EARLIER APPLICATION NUMBER: 607046,162
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? EARLIER APPLICATION NUMBER: 607047,594
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 607047,500

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SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 178
 LENGTH: 155

Query Match 78.1% Score 25; DB 9; Length 155;
 Best Local Similarity 80.0% Pred. No. 4 a-a-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7
 ||| |
 DB 67 GFYNN 71

RESULT 25

US-09-815-242-5352
 Sequence 25; Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlson, Karl L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14119

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5452

LENGTH: 239

TYPE: PPT

ORGANISM: Staphylococcus aureus

US-09-815-242-5352

Query Match 78.1% Score 25; DB 10; Length 239;
 Best Local Similarity 80.0% Pred. No. 7.2e-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7
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 DB 92 GFYNN 96

RESULT 26

US-09-815-242-12278
 Sequence 26; Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlson, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12278

LENGTH: 253

TYPE: PPT

ORGANISM: Staphylococcus aureus

US-09-815-242-12278

Query Match 78.1% Score 25; DB 9; Length 253;
 Best Local Similarity 80.0% Pred. No. 7.2e-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7
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 DB 106 GFYNN 110

RESULT 27

US-09-957-187-20

Sequence 27; Application US/09957187

Publication No. US20030054514A1

GENERAL INFORMATION:

APPLICANT: Shinkets, Richard A.

APPLICANT: Lakocheille, William

TITLE OF INVENTION: NAVIL PATHOGENICITIES AND PROTEINS ENCODED THEREBY

FILE REFERENCE: 15966-540 CIP

CURRENT FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/124,667

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: 60/260,781

PRIOR FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: 60/234,092

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: 60/233,798

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/174,485

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20

LENGTH: 302

TYPE: PPT

ORGANISM: Homo sapiens

US-09-957-187-20

Query Match 78.1% Score 25; DB 9; Length 402;
 Best Local Similarity 80.0% Pred. No. 9.1e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYNN 7
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1 PRIOR FILING DATE: 1997-08-22
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3 PRIOR FILING DATE: 1997-08-22
4 PRIOR APPLICATION NUMBER: 60/056,887
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36 PRIOR APPLICATION NUMBER: 60/056,892
37 PRIOR FILING DATE: 1997-08-22
38 PRIOR APPLICATION NUMBER: 60/047,595
39 PRIOR FILING DATE: 1997-05-23
40 PRIOR APPLICATION NUMBER: 60/057,761
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42 PRIOR APPLICATION NUMBER: 60/047,599
43 PRIOR FILING DATE: 1997-05-23
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46 PRIOR APPLICATION NUMBER: 60/047,585
47 PRIOR FILING DATE: 1997-05-23
48 PRIOR APPLICATION NUMBER: 60/047,586
49 PRIOR FILING DATE: 1997-05-23
50 PRIOR APPLICATION NUMBER: 60/047,590
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52 PRIOR APPLICATION NUMBER: 60/047,594
53 PRIOR FILING DATE: 1997-05-23
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55 PRIOR FILING DATE: 1997-05-23
56 PRIOR APPLICATION NUMBER: 60/047,593
57 PRIOR FILING DATE: 1997-05-23
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9 PRIOR APPLICATION NUMBER: 60/057,650
10 PRIOR FILING DATE: 1997-09-05
11 PRIOR APPLICATION NUMBER: 60/056,884
12 PRIOR FILING DATE: 1997-09-22
13 NUMBER OF SEQ ID NOS: 280
14 SOFTWARE: PatentIn Ver. 2.0
15 SEQ ID NO: 236
16 LENGTH: 313

Query Match 79.1%; Score 25; DB 9; Length 313;
Best Local Similarity 80.0%; Pred. No. 9.4e-02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q7 3 GFYRN 7
111 1
16 67 GFYRN 71

RESULT 30
US-09-148 545-236
1 Sequence 236, Application 55/056,8545
2 Publication No. 05203002712A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: 70 Human Secreted Proteins
6 EMBL REFERENCE: E2001P1
7 CURRENT APPLICATION NUMBER: 05/056,212,545
8 CURRENT FILING DATE: 1998-09-04
9 EARLIER APPLICATION NUMBER: 72/3398,041B2
10 EARLIER FILING DATE: 1998-03-06
11 EARLIER APPLICATION NUMBER: 60/040,162
12 EARLIER FILING DATE: 1997-03-07
13 EARLIER APPLICATION NUMBER: 60/040,333
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16 EARLIER FILING DATE: 1997-03-07
17 EARLIER APPLICATION NUMBER: 60/040,161
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99 EARLIER FILING DATE: 1997-05-23
100 EARLIER APPLICATION NUMBER: 60/047,590
101 EARLIER FILING DATE: 1997-05-23
102 EARLIER APPLICATION NUMBER: 60/047,594
103 EARLIER FILING DATE: 1997-05-23
104 EARLIER APPLICATION NUMBER: 60/047,589
105 EARLIER FILING DATE: 1997-05-23
106 EARLIER APPLICATION NUMBER: 60/047,593
107 EARLIER FILING DATE: 1997-05-23
108 EARLIER APPLICATION NUMBER: 60/047,614
109 EARLIER FILING DATE: 1997-05-23
110 EARLIER APPLICATION NUMBER: 60/047,578
111 EARLIER FILING DATE: 1997-04-11
112 EARLIER APPLICATION NUMBER: 60/047,576
113 EARLIER FILING DATE: 1997-04-11
114 EARLIER APPLICATION NUMBER: 60/047,501
115 EARLIER FILING DATE: 1997-05-23
116 EARLIER APPLICATION NUMBER: 60/047,470
117 EARLIER FILING DATE: 1997-04-11
118 EARLIER APPLICATION NUMBER: 60/056,642
119 EARLIER FILING DATE: 1997-08-22
120 EARLIER APPLICATION NUMBER: 60/056,664
121 EARLIER FILING DATE: 1997-08-22
122 EARLIER APPLICATION NUMBER: 60/056,876
123 EARLIER FILING DATE: 1997-08-22
124 EARLIER APPLICATION NUMBER: 60/056,881
125 EARLIER FILING DATE: 1997-08-22
126 EARLIER APPLICATION NUMBER: 60/056,909
127 EARLIER FILING DATE: 1997-08-22
128 EARLIER APPLICATION NUMBER: 60/056,875
129 EARLIER FILING DATE: 1997-08-22
130 EARLIER APPLICATION NUMBER: 60/056,862
131 EARLIER FILING DATE: 1997-08-22
132 EARLIER APPLICATION NUMBER: 60/056,887
133 EARLIER FILING DATE: 1997-08-22
134 EARLIER APPLICATION NUMBER: 60/056,908
135 EARLIER FILING DATE: 1997-08-22
136 EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/067,650
 ; EARLIER FILING DATE: 1997-09-06
 ; EARLIER APPLICATION NUMBER: 60/066,884
 ; EARLIER FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 236
 ; LENGTH: 313

Query Match: 78.1%, Score 25; DP 9; Length 313;
 Best Local Similarity: 80.0%; Pred. No. 1.1e+03;
 Matches: 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 3 GYNN 7
 IIII
 DB 67 GYNN 71

RESULT 31

; Sequence 1289, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: P101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/0800/05998
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1289
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-498-556c-79-1289

Query Match: 78.1%, Score 25; DP 10; Length 318;
 Best Local Similarity: 80.0%; Pred. No. 6.5e+02;
 Matches: 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYNN 7
 IIII
 DB 257 GYNN 261

RESULT 32

; Sequence 2, Application US/09023771
 ; Patent No. US20010036649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Rudolph-Owen, Laura
 ; TITLE OF INVENTION: 26934, A N. US20010036649A1: Cytidine Deaminase-Like
 ; FILE REFERENCE: 35800/213921 US/09/200,371
 ; CURRENT APPLICATION NUMBER: US/09/200,371
 ; CURRENT FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: 60/188,294
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-802-371-2

Query Match: 78.1%, Score 25; DP 10; Length 372;
 Best Local Similarity: 80.0%; Pred. No. 1.1e+03;
 Matches: 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 3 GYNN 7
 IIII
 DB 297 GYNN 301

RESULT 33

; Sequence 2, Application US/09971020
 ; Patent No. US20020108143A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sano, Hiroshi
 ; APPLICANT: Kusano, Tomonobu
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; FILE REFERENCE: 026350-068
 ; CURRENT APPLICATION NUMBER: US/09/971,020
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2000-407,149
 ; PRIOR FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Coffea arabica
 US-09-971-020-7

Query Match: 78.1%, Score 25; DP 10; Length 372;
 Best Local Similarity: 80.0%; Pred. No. 1.1e+03;
 Matches: 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 3 GYNN 7
 IIII
 DB 354 GYNN 358

RESULT 34

; Sequence 2, Application US/09971020
 ; Patent No. US20020108143A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sano, Hiroshi
 ; APPLICANT: Kusano, Tomonobu
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; FILE REFERENCE: 026350-068
 ; CURRENT APPLICATION NUMBER: US/09/971,020
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2000-407,149
 ; PRIOR FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 385
 ; TYPE: PRT
 ; ORGANISM: Coffea arabica
 US-09-971-020-3

Query Match: 78.1%, Score 25; DP 10; Length 385;
 Best Local Similarity: 80.0%; Pred. No. 1.1e+03;
 Matches: 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 3 GYNN 7
 IIII
 DB 367 GYNN 371

```

RESULT 35
US 09-471-020-5
: Sequence 5, Application US/09471020
: Patent No. US20020108149A1
: GENERAL INFORMATION:
: APPLICANT: Kusano, Tomonobu
: APPLICANT: Kusano, Tomonobu
: TITLE OF INVENTION: Theorizing Synthesis Polypeptide of Coffee Plant and the Gene
: FILE REFERENCE: 026459-068
: CURRENT APPLICATION NUMBER: US/09-498-556c
: PRIOR FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: JP 2000-307,149
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 385
: TYPE: PRT
: ORGANISM: Coffea arabica
US 09-471-020-5

Query Match 78.1%; Score 25; DB 10; Length 385;
Best local Similarity 80.0%; Pred. No. 1,1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GFYRN 7
Db 467 GFYNN 471

RESULT 36
US 10-002-050-10
: Sequence 10, Application US/10000450
: Publication No. US20030032095A1
: GENERAL INFORMATION:
: APPLICANT: Shimkets, Richard
: APPLICANT: Fernandes, Elma
: APPLICANT: Vernet, Corine
: APPLICANT: Yang, Melilla
: APPLICANT: Holdoq, Ferenc
: APPLICANT: Herrmann, John
: TITLE OF INVENTION: No. US20020151494A1 Nucleic Acid Sequences Encoding Human Semaphorin
: FILE REFERENCE: 15466-554 Cuts 54 CON-514
: CURRENT APPLICATION NUMBER: US/10-002-050
: PRIOR FILING DATE: 2001-11-02
: PRIOR APPLICATION NUMBER: 09/604,286
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/140,584
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 10
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US 10-002-050-10

Query Match 78.1%; Score 25; DB 9; Length 411;
Best local Similarity 80.0%; Pred. No. 1,2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GFYRN 7
Db 234 GFYNN 238

RESULT 37
US 10-002-304-10
: Sequence 10, Application US/10002304
: Publication No. US20030046185A1
: GENERAL INFORMATION:
: APPLICANT: Shimkets, Richard
: APPLICANT: Fernandes, Elma
: APPLICANT: Vernet, Corine
: APPLICANT: Yang, Melilla
: APPLICANT: Holdoq, Ferenc
: APPLICANT: Herrmann, John
: TITLE OF INVENTION: No. US20020151494A1 Amino Acid Sequences for Human Semaphorin
: FILE REFERENCE: 15466-554 Cuts 54 CON-512
: CURRENT APPLICATION NUMBER: US/10-002-304
: PRIOR FILING DATE: 2001-11-02
: PRIOR APPLICATION NUMBER: 09/604,286
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/140,584
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 10
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US 10-002-304-10

Query Match 78.1%; Score 25; DB 12; Length 411;
Best local Similarity 80.0%; Pred. No. 1,2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GFYRN 7
Db 234 GFYNN 238

RESULT 39
US 10-118-495-3
: Sequence 3, Application US/10118495
: Publication No. US20030074688A1
: GENERAL INFORMATION:
: APPLICANT: Hennings, Christoph

```


APPLICANT: Rickhof, Wayne
APPLICANT: Klug, Rouven
TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
FILE REFERENCE: MSU-06897
CURRENT APPLICATION NUMBER: US/10/118,495
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: 60/290,912
PRIOR FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 416
TYPE: PRT
ORGANISM: Rhodobacter sphaeroides
US-10-118-495-3

Query Match 78.1%; Score 25; DB 9; Length 416;
Best Local Similarity 80.0%; Pred. No. 1,2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYPRN 7
IIII:
DB 167 GYPRH 171

RESULT 40

Sequence 81 Application US/060999615
Patent No. US2002064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHAPYDZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDAPSANAN, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/04/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-615-81

Query Match 78.1%; Score 25; DB 10; Length 419;
Best Local Similarity 80.0%; Pred. No. 1,4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYPRN 7
IIII:
DB 114 GYFRS 118

RESULT 41

US-10-007-271-4
Sequence 4 Application US/10007271
Patent No. US20020164766A1
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: A NOVEL HUMAN METALLOPROTEINASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-107601
CURRENT APPLICATION NUMBER: US/10/007,271
PRIOR FILING DATE: 2001-10-22
CURRENT APPLICATION NUMBER: 60/242,303
PRIOR FILING DATE: 2000-10-22
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 441
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Colabtools sequence
US 10 607 271 4

Query Match 78.1%; Score 25; DB 9; Length 441;
Best Local Similarity 80.0%; Pred. No. 1,3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYPRN 7
IIII:
DB 142 GYFRS 146

RESULT 42

US-10-002-050-20
Sequence 29 Application US/10302050
Publication No. US20030032095A1
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard
APPLICANT: Fernandes, Elma
APPLICANT: Vernet, Corine
APPLICANT: Yanq, Meijia
APPLICANT: Boldot, Ferenc
APPLICANT: Hertmann, John
TITLE OF INVENTION: NO. US20030032095A1 Nucleic Acid Sequences Encoding Human S
FILE REFERENCE: 15966 554 Cura 54 CGN 814
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/110,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
US 10 002-050-20

Query Match 78.1%; Score 25; DB 9; Length 464;
Best Local Similarity 80.0%; Pred. No. 1,4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYPRN 7
IIII:
DB 287 GYFRS 291

RESULT 43

US 10 002-304-20
Sequence 29 Application US/10002404
Publication No. US20030036185A1
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard
APPLICANT: Fernandes, Elma
APPLICANT: Vernet, Corine
APPLICANT: Yanq, Meijia
APPLICANT: Boldot, Ferenc
APPLICANT: Hertmann, John
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 Cura-54 CGN-58
CURRENT APPLICATION NUMBER: US/10/002,404
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/110,584
PRIOR FILING DATE: 1999-06-23

1 NUMBER OF SEQ ID NOS: 49
 2 SOFTWARE: Patent In Ver. 2.0
 3 SEQ ID NO: 20
 4 LENGTH: 464
 5 TYPE: PRT
 6 ORGANISM: Homo sapiens
 7 US 10-004-152-20

Query Match 78.1% Score 25; Db 9; Length 464;

Best local similarity 80.0% Pred. 80.14e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7

11111

Db 287 GFYNN 291

RESULT 44

US-10-004-152-20

1 Sequence 20, Application US/19994152

2 Patent No. US20020151494A1

3 GENERAL INFORMATION:

4 APPLICANT: Shimkets, Richard

5 APPLICANT: Fernandes, Elma

6 APPLICANT: Vernet, Corine

7 APPLICANT: Yang, Mingli

8 APPLICANT: Boldoa, Ferenc

9 APPLICANT: Bergman, Tom

10 TITLE OF INVENTION: No. 9520220151494A1 Amino Acid Sequences for Human Somatostatin

11 FILE REFERENCE: 15966-554 Ciba-54 CON 312

12 CURRENT APPLICATION NUMBER: 95/18/003,152

13 PRIOR APPLICATION NUMBER: 2001-11-02

14 PRIOR FILING DATE: 2000-06-22

15 PRIOR APPLICATION NUMBER: 60/140,584

16 PRIOR FILING DATE: 1999-06-23

17 NUMBER OF SEQ ID NOS: 49

18 SOFTWARE: Patent In Ver. 2.0

19 SEQ ID NO: 20

20 LENGTH: 464

21 TYPE: PRT

22 ORGANISM: Homo sapiens

23 US-10-004-152-20

Query Match 78.1% Score 25; Db 19; Length 464;

Best local similarity 80.0% Pred. 80.14e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7

11111

Db 287 GFYNN 291

RESULT 45

US-09-498-295A-114

1 Sequence 114, Application US/19994152

2 Patent No. US20020156096A1

3 GENERAL INFORMATION:

4 APPLICANT: Ashkenazi, Avi

5 APPLICANT: Pakar-Kevita, E.

6 APPLICANT: Botstein, David

7 APPLICANT: Desnoyers, Luc

8 APPLICANT: Eaton, Dan

9 APPLICANT: Ferrara, Napoleon

10 APPLICANT: Filvaroff, Ellen

11 APPLICANT: Fong, Sherman

12 APPLICANT: Gao, Wei-Guang

13 APPLICANT: Gerber, Hanspeter

14 APPLICANT: Gottson, Mary E.

15 APPLICANT: Goddard, Audrey

16 APPLICANT: Godowski, Paul J.

17 APPLICANT: Grimaldi, J. Christopher

18 APPLICANT: Gurney, Austin L.

1 APPLICANT: Hillan, Kenneth J.
 2 APPLICANT: Klijivis, Ivar J.
 3 APPLICANT: Kuo, Sophia S.
 4 APPLICANT: Napier, Mary A.
 5 APPLICANT: Pan, James
 6 APPLICANT: Pao, Nicholas F.
 7 APPLICANT: Roy, Margaret Ann
 8 APPLICANT: Shelton, David L.
 9 APPLICANT: Stewart, Timothy A.
 10 APPLICANT: Tumas, Daniel
 11 APPLICANT: Williams, P. Mickey
 12 APPLICANT: Wood, William L.
 13 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 14 TITLE OF INVENTION: Acids Encoding the Same
 15 FILE REFERENCE: P2640P1C11
 16 CURRENT APPLICATION NUMBER: 95/25,778,255A
 17 CURRENT FILING DATE: 2001-10-15
 18 PRIOR APPLICATION NUMBER: 09/418585
 19 PRIOR FILING DATE: 2001-07-30
 20 PRIOR APPLICATION NUMBER: 60/092250
 21 PRIOR FILING DATE: 1997-10-17
 22 PRIOR APPLICATION NUMBER: 60/064249
 23 PRIOR FILING DATE: 1997-11-04
 24 PRIOR APPLICATION NUMBER: 60/065411
 25 PRIOR FILING DATE: 1997-11-14
 26 PRIOR APPLICATION NUMBER: 60/066464
 27 PRIOR FILING DATE: 1997-11-21
 28 PRIOR APPLICATION NUMBER: 60/077450
 29 PRIOR FILING DATE: 1998-04-10
 30 PRIOR APPLICATION NUMBER: 60/077642
 31 PRIOR FILING DATE: 1998-04-11
 32 PRIOR APPLICATION NUMBER: 60/077641
 33 PRIOR FILING DATE: 1998-04-11
 34 PRIOR APPLICATION NUMBER: 60/077649
 35 PRIOR FILING DATE: 1998-04-11
 36 PRIOR APPLICATION NUMBER: 60/077791
 37 PRIOR FILING DATE: 1998-04-12
 38 PRIOR APPLICATION NUMBER: 60/078004
 39 PRIOR FILING DATE: 1998-04-14
 40 PRIOR APPLICATION NUMBER: 60/078886
 41 PRIOR FILING DATE: 1998-04-20
 42 PRIOR APPLICATION NUMBER: 60/078946
 43 PRIOR FILING DATE: 1998-04-20
 44 PRIOR APPLICATION NUMBER: 60/078910
 45 PRIOR FILING DATE: 1998-04-20
 46 PRIOR APPLICATION NUMBER: 60/078949
 47 PRIOR FILING DATE: 1998-04-20
 48 PRIOR APPLICATION NUMBER: 60/079294
 49 PRIOR FILING DATE: 1998-04-25
 50 PRIOR APPLICATION NUMBER: 60/079656
 51 PRIOR FILING DATE: 1998-04-26
 52 PRIOR APPLICATION NUMBER: 60/079664
 53 PRIOR FILING DATE: 1998-04-27
 54 PRIOR APPLICATION NUMBER: 60/079689
 55 PRIOR FILING DATE: 1998-04-27
 56 PRIOR APPLICATION NUMBER: 60/079664
 57 PRIOR FILING DATE: 1998-04-27
 58 PRIOR APPLICATION NUMBER: 60/079728
 59 PRIOR FILING DATE: 1998-04-27
 60 PRIOR APPLICATION NUMBER: 60/079786
 61 PRIOR FILING DATE: 1998-04-27
 62 PRIOR APPLICATION NUMBER: 60/079920
 63 PRIOR FILING DATE: 1998-04-30
 64 PRIOR APPLICATION NUMBER: 60/079924
 65 PRIOR FILING DATE: 1998-04-30
 66 PRIOR APPLICATION NUMBER: 60/080195
 67 PRIOR FILING DATE: 1998-04-31
 68 PRIOR APPLICATION NUMBER: 60/080107
 69 PRIOR FILING DATE: 1998-04-31
 70 PRIOR APPLICATION NUMBER: 60/080165
 71 PRIOR FILING DATE: 1998-04-31
 72 PRIOR APPLICATION NUMBER: 60/080194
 73 PRIOR FILING DATE: 1998-04-31

; PRIOR APPLICATION NUMBER: 60/080327
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080329
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081071
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081329
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081819
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081952
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082704
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082700
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083495
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083496
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083499
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083554
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083558
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083559
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083500
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083742
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084441

; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084639
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084640
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084598
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084643
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085423
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085482
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085779
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match: 78.1%, Score 25, DB 9, Length 515;

Best Local Similarity: 80.0%; Prod. No. 1.5e+03;

Matches: 4, Connections: 6, Mismatches: 1, Index: 9, Gaps: 0;

0Y 3 CYRN 7

03 415 SEVNN 319

Search completed: April 30, 2003, 14:44:59

Job time: 51.2727 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Computer

QM protein - protein search, using sw model

Run on: April 30, 2003, 13:31:02 ; Search time 10.5455 Seconds
(without alignments)
36.465 Million cell updates/sec

Title: US-09-498-5560-357
Perfect score: 11
Sequence: 1 LXR 4

Scoring table	Results	Case
0	0	0
1	1	1
2	2	2
3	3	3
4	4	4
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9	9	9
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11	11	11
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96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

Searched: 08/09/2004 16:34:03
 08/09/2004 16:34:03

Total number of hits satisfying chosen parameters: 383294

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 73: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match		length	DB	IP	Description
		Score	%				
1		9	81.8	7	2	E48394	glycoprotein compo
2		9	81.8	7	2	B48394	major lat-globule
3		9	81.9	8	2	P41131	hypothetical prote
4		9	81.8	8	2	T13818	cytochrome oxidase
5		9	81.8	10	2	T13838	cytochrome-c oxid
6		9	81.8	10	2	T14219	cytochrome-c oxid
7		9	81.8	11	2	P40944	dehydrogenase (EC
8		9	81.8	12	2	A42324	cytochrome P450C2
9		9	81.8	13	2	P40293	1q heavy chain (CD
10		9	81.8	14	2	P40111	protein DA100954 -
11		9	81.8	15	2	S36296	ribosomal protein
12		9	81.8	15	2	FA0075	fructose biphosph
13		9	81.8	15	2	P40102	fructose biphosph
14		9	81.8	15	2	B28006	hypothetical prote
15		9	81.8	15	2	P41455	T-cell receptor al
16		9	81.8	16	2	AF0833	p60 leuk-p-tyros
17		9	81.8	16	2	G61414	chromotransin (PC
18		9	81.8	16	2	J05017	insulin-like grow
19		9	81.8	16	2	B41036	collagen alpha 1(X
20		9	81.8	17	2	J40046	ribosomal protein
21		9	81.8	17	2	A43845	ribosomal protein
22		9	81.8	17	2	I54269	vitamin B binding
23		9	81.8	17	2	J62310	hypothetical 2.1K
24		9	81.9	17	2	J62320	hypothetical 2.1K
25		9	81.8	17	2	B61414	chromotransin (EC
26		9	81.8	18	2	S20461	GTP-binding protei
27		9	81.8	18	2	A41877	Leuk-1/yeastina p
28		9	81.8	18	2	A18334	crf1 5' of leuk-1
29		9	81.8	18	2	S31645	hypothetical prote

103	9	81.8	27	2	P44516	homeotic protein H	176	9	81.8	44	2	317434	alcohol dehydrogenase
104	9	81.8	27	2	H44629	homeotic protein H	177	9	81.8	44	2	A3627	homeotic protein H
105	9	81.8	27	2	F48200	homeotic protein H	178	9	81.8	44	2	A65264	homeotic protein H
106	9	81.8	27	2	H44616	homeotic protein H	179	9	81.8	44	2	A65264	homeotic protein H
107	9	81.8	27	2	A44616	homeotic protein H	180	9	81.8	44	2	H95019	hypothetical protein
108	9	81.8	27	2	D48200	homeotic protein H	181	9	81.8	44	2	P82458	hypothetical protein
109	9	81.8	27	2	A48200	homeotic protein H	182	9	81.8	44	2	A44628	hypothetical protein
110	9	81.8	27	2	G44621	homeotic protein H	183	9	81.8	44	2	H97916	degenerate transfer RNA
111	9	81.8	27	2	A44621	homeotic protein H	184	9	81.8	44	2	A44621	hypothetical protein
112	9	81.8	27	2	A44636	homeotic protein H	185	9	81.8	44	2	P95047	hypothetical protein
113	9	81.8	27	2	A44621	homeotic protein H	186	9	81.8	44	2	A44621	hypothetical protein
114	9	81.8	27	2	H44626	homeotic protein H	187	9	81.8	44	2	A44626	hypothetical protein
115	9	81.8	27	2	H44636	homeotic protein H	188	9	81.8	44	2	A45791	hypothetical protein
116	9	81.8	27	2	F44636	homeotic protein H	189	9	81.8	44	2	A45791	hypothetical protein
117	9	81.8	27	2	F44636	homeotic protein H	189	9	81.8	44	2	A45791	hypothetical protein
118	9	81.8	27	2	F44636	homeotic protein H	190	9	81.8	44	2	A45791	hypothetical protein
119	9	81.8	27	2	A44641	homeotic protein H	191	9	81.8	44	2	A33708	thiolase, cell wall
120	9	81.8	27	2	A44636	homeotic protein H	192	9	81.8	44	2	A44636	hypothetical protein
121	9	81.8	27	2	P23444	second envelope st	193	9	81.8	44	2	A61142	pancreatic hormone
122	9	81.8	27	2	H64520	hypothetical prote	194	9	81.8	44	2	A61142	pancreatic hormone
123	9	81.8	27	2	B32112	glutamate-tRNA lig	195	9	81.8	44	2	P6PG	pancreatic hormone
124	9	81.8	28	2	S77854	ribosomal protein	196	9	81.8	44	2	B61142	pancreatic hormone
125	9	81.8	28	2	S51367	alpha-1 type 1 col	197	9	81.8	44	2	P6PG	pancreatic hormone
126	9	81.8	28	2	S51367	alpha-1 type 1 col	198	9	81.8	44	2	P6PG	pancreatic hormone
127	9	81.8	28	2	S51367	alpha-1 type 1 col	199	9	81.8	44	2	P6PG	pancreatic hormone
128	9	81.8	28	2	S51367	alpha-1 type 1 col	200	9	81.8	44	2	P6PG	pancreatic hormone
129	9	81.8	28	2	S51367	alpha-1 type 1 col	201	9	81.8	44	2	P6PG	pancreatic hormone
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131	9	81.8	28	2	S51367	alpha-1 type 1 col	203	9	81.8	44	2	P6PG	pancreatic hormone
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133	9	81.8	28	2	S51367	alpha-1 type 1 col	205	9	81.8	44	2	P6PG	pancreatic hormone
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135	9	81.8	28	2	S51367	alpha-1 type 1 col	207	9	81.8	44	2	P6PG	pancreatic hormone
136	9	81.8	28	2	S51367	alpha-1 type 1 col	208	9	81.8	44	2	P6PG	pancreatic hormone
137	9	81.8	28	2	S51367	alpha-1 type 1 col	209	9	81.8	44	2	P6PG	pancreatic hormone
138	9	81.8	28	2	S51367	alpha-1 type 1 col	210	9	81.8	44	2	P6PG	pancreatic hormone
139	9	81.8	30	2	I39798	gene CYF182 prote	211	9	81.8	44	2	A51315	calcitonin receptor
140	9	81.8	30	2	P22799	protein R069.7.11	212	9	81.8	44	2	P6BP47	calcitonin receptor
141	9	81.8	30	2	P80406	hypothetical prote	213	9	81.8	44	2	P37244	hypothetical prote
142	9	81.8	30	2	P87254	hypothetical prote	214	9	81.8	44	2	P45186	hypothetical prote
143	9	81.8	30	2	P82290	hypothetical prote	215	9	81.8	44	2	P45187	hypothetical prote
144	9	81.8	30	2	S49114	cystic fibrosis tr	216	9	81.8	44	2	P45187	hypothetical prote
145	9	81.8	30	2	C97464	hypothetical prote	217	9	81.8	44	2	P45187	hypothetical prote
146	9	81.8	31	2	C48472	capsid protein VP	218	9	81.8	44	2	P45187	hypothetical prote
147	9	81.8	31	2	P72270	hypothetical prote	219	9	81.8	44	2	P45187	hypothetical prote
148	9	81.8	31	2	A70219	hypothetical prote	220	9	81.8	44	2	P45187	hypothetical prote
149	9	81.8	31	2	B62101	hypothetical prote	221	9	81.8	44	2	P45187	hypothetical prote
150	9	81.8	31	2	S31075	hypothetical prote	222	9	81.8	44	2	P45187	hypothetical prote
151	9	81.8	31	2	A90049	transposase (part	223	9	81.8	44	2	P45187	hypothetical prote
152	9	81.8	32	2	S57780	histone H3	224	9	81.8	44	2	P45187	hypothetical prote
153	9	81.8	32	2	S30754	genome polyprotein	225	9	81.8	44	2	P45187	hypothetical prote
154	9	81.8	32	2	S30756	genome polyprotein	226	9	81.8	44	2	P45187	hypothetical prote
155	9	81.8	32	2	P37482	proline-rich prote	227	9	81.8	44	2	P45187	hypothetical prote
156	9	81.8	32	2	S31611	beta-1,2-glucanase	228	9	81.8	44	2	P45187	hypothetical prote
157	9	81.8	32	2	H72972	hypothetical prote	229	9	81.8	44	2	P45187	hypothetical prote
158	9	81.8	32	2	S12973	hypothetical prote	230	9	81.8	44	2	P45187	hypothetical prote
159	9	81.8	32	2	P82299	hypothetical prote	231	9	81.8	44	2	P45187	hypothetical prote
160	9	81.8	32	2	S22304	hypothetical prote	232	9	81.8	44	2	P45187	hypothetical prote
161	9	81.8	32	2	B38578	protein kinase 1 (233	9	81.8	44	2	P45187	hypothetical prote
162	9	81.8	32	2	C94111	hypothetical prote	234	9	81.8	44	2	P45187	hypothetical prote
163	9	81.8	33	2	A39188	haloalcohol dehalo	235	9	81.8	44	2	P45187	hypothetical prote
164	9	81.8	33	2	D21997	ornithine carbamoy	236	9	81.8	44	2	P45187	hypothetical prote
165	9	81.8	33	2	S41226	transforming prot	237	9	81.8	44	2	P45187	hypothetical prote
166	9	81.8	33	2	P22205	interferon alpha 1	238	9	81.8	44	2	P45187	hypothetical prote
167	9	81.8	33	2	C47214	CK recombination s	239	9	81.8	44	2	P45187	hypothetical prote
168	9	81.8	33	2	P68894	gene TAP1 protein	240	9	81.8	44	2	P45187	hypothetical prote
169	9	81.8	33	2	P87660	hypothetical prote	241	9	81.8	44	2	P45187	hypothetical prote
170	9	81.8	33	2	P84163	hypothetical prote	242	9	81.8	44	2	P45187	hypothetical prote
171	9	81.8	33	2	H82078	hypothetical prote	243	9	81.8	44	2	P45187	hypothetical prote
172	9	81.8	33	2	C92064	hypothetical prote	244	9	81.8	44	2	P45187	hypothetical prote
173	9	81.8	33	2	A58543	CD41 homology cha	245	9	81.8	44	2	P45187	hypothetical prote
174	9	81.8	33	2	A60222	myelin basic prote	246	9	81.8	44	2	P45187	hypothetical prote
175	9	81.8	33	2	F93713	hypothetical prote	247	9	81.8	44	2	P45187	hypothetical prote

249	9	81.8	41	2	B24910	prolactin tyrosine	322	9	81.8	47	2	D25156	hypothetical prote
250	9	81.8	41	2	B27697	hypothetical prote	323	9	81.8	47	2	F06872	hypothetical prote
251	9	81.8	41	2	F02150	hypothetical prote	324	9	81.8	47	2	E09910	hypothetical prote
252	9	81.8	41	2	F04377	muscle cytochrome	325	9	81.8	47	2	A09875	hypothetical prote
253	9	81.8	41	2	T16051	hypothetical prote	326	9	81.8	47	2	S31005	gene 60 protein
254	9	81.8	41	2	A14536	T cell receptor al	327	9	81.8	47	2	F02473	hypothetical prote
255	9	81.8	41	2	F00048	hypothetical prote	328	9	81.8	47	2	A18947	RNA binding repres
256	9	81.8	41	2	B07367	hypothetical prote	329	9	81.8	47	2	B08410	hypothetical prote
257	9	81.8	41	2	I08022	hypothetical prote	330	9	81.8	47	2	F07560	hypothetical prote
258	9	81.8	41	2	S28633	ribosomal protein	331	9	81.8	48	4	A17735	hemoglobin A1-g be
259	9	81.8	42	2	I05241	hemocyt protein B	332	9	81.8	48	2	C060505	hemoglobin A1-g be
260	9	81.8	42	2	F07850	hypothetical prote	333	9	81.8	48	2	C73486	ribosomal protein
261	9	81.8	42	2	A08805	hypothetical prote	334	9	81.8	48	2	B42871	ribosomal protein
262	9	81.8	42	2	A05509	hypothetical prote	335	9	81.8	48	2	T06246	teritin A - softe
263	9	81.8	42	2	C05868	hypothetical prote	336	9	81.8	48	2	T06450	hemocyt protein A
264	9	81.8	43	2	S24641	cytochrome-b5 redu	337	9	81.8	48	2	S84911	protein division cy
265	9	81.8	43	2	I18824	aldolase C - New	338	9	81.8	48	2	F02473	cell division cy
266	9	81.8	43	2	I45150	aldolase C - do	339	9	81.8	48	2	F06486	hypothetical prote
267	9	81.8	43	2	I77472	aldolase C - do	340	9	81.8	48	2	C05560	hypothetical prote
268	9	81.8	43	2	S48626	translation elonga	341	9	81.8	48	2	B06779	hypothetical prote
269	9	81.8	43	2	B24711	kinase-related pro	342	9	81.8	48	2	B02189	phosphatidylserine
270	9	81.8	43	2	G22009	4E221 protein K	343	9	81.8	48	2	H02409	hypothetical prote
271	9	81.8	43	2	J00404	hypothetical fork	344	9	81.8	48	2	S12588	cytochrome protein
272	9	81.8	43	2	E22271	hypothetical prote	345	9	81.8	48	2	A11305	hypothetical prote
273	9	81.8	43	2	T09051	hypothetical prote	346	9	81.8	48	2	S24534	hypothetical prote
274	9	81.8	43	2	S70536	probable acetylase	347	9	81.8	49	2	C055781	lamin alpha chai
275	9	81.8	43	2	A10876	conserved hypobol	348	9	81.8	49	2	A02122	hypothetical prote
276	9	81.8	44	1	R0P834	ribosomal protein	349	9	81.8	49	2	F70070	conserved hypobol
277	9	81.8	44	1	E0P834	ribosomal protein	350	9	81.8	49	2	T12228	ARA stress lipolip
278	9	81.8	44	1	G0P834	regulatory protein	351	9	81.8	49	2	C05572	hemocyt protein
279	9	81.8	44	2	C04396	ribosomal protein	352	9	81.8	49	2	C05815	calpain I - rat (1
280	9	81.8	44	2	E04107	ribosomal protein	353	9	81.8	49	2	C05815	hypothetical prote
281	9	81.8	44	2	A02951	50S ribosomal prot	354	9	81.8	49	2	C05815	hypothetical prote
282	9	81.8	44	2	S70250	phosphatase II pro	355	9	81.8	49	2	B04912	hypothetical prote
283	9	81.8	44	2	I17730	ATP mutase type Ia	356	9	81.8	50	2	C05597	aspartate protease
284	9	81.8	44	2	S22541	a 2-2 protein in	357	9	81.8	50	2	C11325	9K protein - potat
285	9	81.8	44	2	T09722	hypothetical prote	358	9	81.8	50	2	S70534	2,4 dichlorophenol
286	9	81.8	44	2	E05814	unknown protein en	359	9	81.8	50	2	S09097	hemocyt protein C
287	9	81.8	45	1	E0P834	early protein qf5	360	9	81.8	50	2	T08226	protein tyrosine k
288	9	81.8	45	2	S05119	probable serine pr	361	9	81.8	50	2	B05131	hypothetical prote
289	9	81.8	45	2	F00139	H-2 class I histon	362	9	81.8	50	2	F00731	hypothetical prote
290	9	81.8	45	2	A00081	50S ribosomal prot	363	9	81.8	50	2	G00974	hypothetical prote
291	9	81.8	45	2	R04158	ribosomal protein	364	9	81.8	50	2	C05557	hypothetical prote
292	9	81.8	45	2	S05509	metallothionein b	365	9	81.8	50	2	I05117	hypothetical prote
293	9	81.8	45	2	P01316	hemocyt protein b	366	9	81.8	50	2	C05521	hypothetical prote
294	9	81.8	45	2	P01218	hemocyt protein b	367	9	81.8	50	2	C04004	hypothetical prote
295	9	81.8	45	2	P01217	hemocyt protein b	368	9	81.8	50	2	S48115	hypothetical prote
296	9	81.8	45	2	B07562	hypothetical prote	369	9	81.8	50	2	B26114	hypothetical prote
297	9	81.8	45	2	R04158	hypothetical prote	370	9	81.8	50	2	C71457	hypothetical prote
298	9	81.8	45	2	T01877	hypothetical prote	371	9	81.8	50	2	B02859	hypothetical prote
299	9	81.8	45	2	B46012	p52 (p53) hemolys	372	9	81.8	50	2	A02716	unknown protein en
300	9	81.8	46	1	P0P834	ribosomal protein	373	9	81.8	50	2	H05821	unknown protein en
301	9	81.8	46	2	T06965	ribosomal protein	374	9	81.8	51	2	F00479	cell division cycl
302	9	81.8	46	2	B02517	50S ribosomal p	375	9	81.8	51	2	S47138	cell surface gly
303	9	81.8	46	2	A00407	50S ribosomal prot	376	9	81.8	51	2	C70154	ribosomal protein
304	9	81.8	46	2	F01208	50S ribosomal subu	377	9	81.8	51	2	I05119	hemocyt protein
305	9	81.8	46	2	P00051	translation initia	378	9	81.8	51	2	H05119	hypothetical prote
306	9	81.8	46	2	T07088	probable IS elemen	379	9	81.8	51	2	D70534	hypothetical prote
307	9	81.8	46	2	B03474	hemocyt protein b	380	9	81.8	51	2	T07012	hypothetical prote
308	9	81.8	46	2	B00921	hypothetical prote	381	9	81.8	51	2	C05576	acetylcholinestera
309	9	81.8	46	2	A15571	hypothetical prote	382	9	81.8	51	2	C05592	hypothetical prote
310	9	81.8	46	2	T06245	probable aminotran	383	9	81.8	51	2	D07989	hypothetical prote
311	9	81.8	46	2	T16460	hypothetical prote	384	9	81.8	51	2	A01456	hypothetical prote
312	9	81.8	46	2	B06054	50S ribosomal subu	385	9	81.8	51	2	A01849	hypothetical prote
313	9	81.8	47	1	S05732	ribosomal protein	386	9	81.8	51	2	M01391	hypothetical prote
314	9	81.8	47	1	J01154	ribosomal protein	387	9	81.8	51	2	A01840	hypothetical prote
315	9	81.8	47	2	T06800	sialoprotein reduct	388	9	81.8	52	1	A01321	phospholamban - la
316	9	81.8	47	2	P00483	cell division cycl	389	9	81.8	52	1	S07638	phospholamban - la
317	9	81.8	47	2	S22651	protease subunit	390	9	81.8	52	1	A13057	phospholamban - no
318	9	81.8	47	2	G07316	ribosomal protein	391	9	81.8	52	1	B49324	phospholamban - ra
319	9	81.8	47	2	C75308	ribosomal protein	392	9	81.8	52	1	A29922	phospholamban - do
320	9	81.8	47	2	E04931	50S ribosomal prot	393	9	81.8	52	1	S05540	phospholamban - pi
321	9	81.8	47	2	S02300	protein related	394	9	81.8	52	1	R07129	phospholamban - pi

395	9	81.8	52	1	RVBOMA	stable plasmid inh	468	9	81.8	55	2	A56203	hypothetical prote
396	9	81.8	52	2	S19416	chlorophyll a/b-bi	469	9	81.8	55	2	RV0064	hypothetical OR pr
397	9	81.8	52	2	S00401	kok protein - Esch	470	9	81.8	55	1	CH0006	cytochrome b-ox co
398	9	81.8	52	2	P00491	cell division cycl	471	9	81.8	54	2	P00819	probable tropomoe
399	9	81.8	52	2	P05124	hypothetical prote	472	9	81.8	54	2	Q00295	SMAD2 dehydrogase
400	9	81.8	52	2	P03006	hypothetical prote	473	9	81.8	55	2	P01996	protein tyrosine k
401	9	81.8	52	2	G82496	hypothetical prote	474	9	81.8	56	2	I51161	protein-tyrosine k
402	9	81.8	52	2	P06527	cystic fibrosis tr	475	9	81.8	54	2	I55300	SPRY3 - human (H
403	9	81.8	52	2	P06062	hypothetical prote	476	9	81.8	54	2	P01440	concomoid, third d
404	9	81.8	52	2	H09097	hypothetical prote	477	9	81.8	54	2	S46471	55 heavy chain V-r
405	9	81.8	52	2	A07995	hypothetical prote	478	9	81.8	56	2	A01135	ribosomal protein
406	9	81.8	52	2	A06078	hypothetical prote	479	9	81.8	54	2	A11493	ribosomal protein
407	9	81.8	52	2	A01593	hypothetical prote	480	9	81.8	54	2	P00241	SLC3A1 - mouse (M
408	9	81.8	52	2	A01980	transposase, asloap	481	9	81.8	54	2	P06424	protein kinase APL
409	9	81.8	52	2	A02566	hypothetical prote	482	9	81.8	54	2	P07600	hypothetical prote
410	9	81.8	52	2	A12999	hypothetical prote	483	9	81.8	56	2	B83079	hypothetical prote
411	9	81.8	52	2	S72965	ribosomal protein	484	9	81.8	56	2	B81042	hypothetical prote
412	9	81.8	52	2	S22125	gene K protein p	485	9	81.8	56	2	P04739	hydrophobic protei
413	9	81.8	52	2	S18013	protein-tyrosine k	486	9	81.8	56	2	P02610	hypothetical prote
414	9	81.8	52	2	S18014	protein-tyrosine k	487	9	81.8	56	2	P02613	hypothetical prote
415	9	81.8	52	2	P00072	hypothetical prote	488	9	81.8	54	2	P01256	hypothetical prote
416	9	81.8	52	2	A00462	hypothetical prote	489	9	81.8	56	2	H02647	hypothetical prote
417	9	81.8	52	2	P02634	hypothetical prote	490	9	81.8	54	2	A07816	hypothetical prote
418	9	81.8	52	2	B01221	hypothetical prote	491	9	81.8	56	2	P05368	probable PIIA2 fil
419	9	81.8	52	2	J05105	hypothetical 5.8K	492	9	81.8	56	2	A00071	hypothetical prote
420	9	81.8	52	2	P02975	finger protein (el	493	9	81.8	54	2	A03202	hypothetical prote
421	9	81.8	52	2	P02384	hypothetical prote	494	9	81.8	54	2	A02153	hypothetical prote
422	9	81.8	52	2	P02721	hypothetical prote	495	9	81.8	56	2	P01999	protein tyrosine k
423	9	81.8	52	2	P02813	hypothetical prote	496	9	81.8	57	2	P01893	protein tyrosine k
424	9	81.8	52	2	H02812	hypothetical prote	497	9	81.8	57	2	P01887	protein tyrosine k
425	9	81.8	52	2	B05745	unknown protein, ch	498	9	81.8	57	2	P01498	protein tyrosine k
426	9	81.8	52	2	A00696	hypothetical prote	499	9	81.8	57	2	P02627	protein tyrosine k
427	9	81.8	52	2	A01981	hypothetical prote	500	9	81.8	57	2	P04284	relaxin, chain IIa
428	9	81.8	52	2	A01438	hypothetical prote	501	9	81.8	57	2	H00879	1a kappa chain V r
429	9	81.8	52	2	P07459	hypothetical prote	502	9	81.8	57	2	P04213	40S ribosomal prot
430	9	81.8	52	2	A02676	hypothetical prote	503	9	81.8	57	2	P02634	alpha-interferon -
431	9	81.8	52	2	A04777	ribM protein - Esc	504	9	81.8	57	2	P04977	carbon storage req
432	9	81.8	52	2	P01994	protein tyrosine k	505	9	81.8	57	2	P01998	protein tyrosine k
433	9	81.8	52	2	S44965	H+ transporting tw	506	9	81.8	57	2	H04366	hypothetical prote
434	9	81.8	52	2	P01493	ovomacoid (PSI ty	507	9	81.8	57	2	P03080	hypothetical prote
435	9	81.8	52	2	S03819	hemolysin, Proteu	508	9	81.8	57	2	P01226	hypothetical prote
436	9	81.8	52	2	S45255	YjX protein homol	509	9	81.8	57	2	P04031	hypothetical prote
437	9	81.8	52	2	P07552	protein-tyrosine k	510	9	81.8	57	2	S22425	hypothetical prote
438	9	81.8	52	2	P00836	BipA-like protein	511	9	81.8	57	2	P06183	hypothetical prote
439	9	81.8	52	2	H01933	hypothetical prote	512	9	81.8	57	2	P02787	hypothetical prote
440	9	81.8	52	2	P01414	filamentous hemag	513	9	81.8	57	2	A02708	hypothetical prote
441	9	81.8	52	2	P07125	hypothetical prote	514	9	81.8	57	2	A05809	hypothetical prote
442	9	81.8	52	2	A02784	hypothetical prote	515	9	81.8	57	2	P07813	hypothetical prote
443	9	81.8	52	2	P01346	protein tyrosine k	516	9	81.8	57	2	P07827	(P)phop, x-phyloph
444	9	81.8	52	2	P06456	ubiquitin, ribosoma	517	9	81.8	57	2	A00934	hypothetical prote
445	9	81.8	52	2	S20330	calcasulin, - bovi	518	9	81.8	57	2	P07190	hypothetical prote
446	9	81.8	52	2	S70224	probable membrane	519	9	81.8	57	2	P02786	hypothetical prote
447	9	81.8	52	2	S44415	hemocytic protein z	520	9	81.8	57	2	P07891	probable c-phospho
448	9	81.8	52	2	P05093	hypothetical prote	521	9	81.8	58	2	P08663	pyruvate kinase (E
449	9	81.8	52	2	P01155	hypothetical prote	522	9	81.8	58	2	S45111	histone H3 - mouse
450	9	81.8	52	2	A09563	hypothetical prote	523	9	81.8	58	2	A01604	ribosomal protein
451	9	81.8	52	2	P06733	hypothetical prote	524	9	81.8	58	2	A04384	zinc finger protei
452	9	81.8	52	2	S00452	hypothetical prote	525	9	81.8	58	2	S07479	hypothetical prote
453	9	81.8	52	2	P01415	filamentous hemag	526	9	81.8	58	2	H01110	hypothetical prote
454	9	81.8	52	2	P05677	amber mutation sup	527	9	81.8	58	2	P01284	hypothetical prote
455	9	81.8	52	2	P05993	hypothetical prote	528	9	81.8	58	2	P07623	hypothetical prote
456	9	81.8	52	2	P04444	hypothetical prote	529	9	81.8	58	2	P07457	hypothetical prote
457	9	81.8	52	2	S33915	hypothetical prote	530	9	81.8	58	2	B06974	conserved hypethet
458	9	81.8	52	2	S44331	sox protein less	531	9	81.8	58	2	P04389	hypothetical prote
459	9	81.8	52	2	P01500	hypothetical prote	532	9	81.8	58	2	H04534	hypothetical prote
460	9	81.8	52	2	P02845	hypothetical prote	533	9	81.8	58	2	S44575	gene 72 protein
461	9	81.8	52	2	A02823	hypothetical prote	534	9	81.8	58	2	P04359	hypothetical prote
462	9	81.8	52	2	P02960	hypothetical prote	535	9	81.8	58	2	P04970	hypothetical prote
463	9	81.8	52	2	B02584	hypothetical prote	536	9	81.8	58	2	S05890	hypothetical prote
464	9	81.8	52	2	B06601	hypothetical prote	537	9	81.8	58	2	P05940	hypothetical prote
465	9	81.8	52	2	A01074	probable ribosome	538	9	81.8	58	2	P06092	conserved hypethet
466	9	81.8	52	2	A01078	hypothetical prote	539	9	81.8	58	2	P07464	intefining domain
467	9	81.8	52	2	A01592	conserved hypethet	540	9	81.8	58	2	P01299	hypothetical prote

hemocytic protein B
protein P926.27 I
B GRP D protein
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical 8.1k
kleb protein - pla
hypothetical prote
hypothetical prote
hypothetical prote
mob protein D - Er
chemoreceptor prot
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable type III
hypothetical prote

ALIGNMENTS

RESULT 1
E48394
glycoprotein component 16, major fat globule membrane protein (cattle)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: E48394

R:Mather, J.R.; Bandhart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
11-like sequences.

A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: E48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAI>
A:Experimental source: milk
A:Note: Sequence extracted from NMR backbone (NCBIP:131450)
C:Keywords: glycoprotein

Query Match 81.8% Score 9; DB 2; Length 7;
Best Local Similarity 66.7% Pred. No. 2; Re-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 5 LAR 7

RESULT 2
B48394
major fat-globule membrane protein GP 55 - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: B48394

R:Mather, J.R.; Bandhart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
11-like sequences.

A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: B48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAI>
A:Experimental source: milk
A:Note: Sequence extracted from NMR backbone (NCBIP:131454)

Query Match 81.8% Score 9; DB 2; Length 7;
Best Local Similarity 66.7% Pred. No. 2; Re-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 5 LAR 7

RESULT 3
P64131
hypothetical protein B (imported)
C:Species: Pseudomonas aeruginosa (fragment)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: P64131

R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Deposition and characterization of the 4-kilobase region of the genes encoding
gamma for biosynthesis of home dl.

A:Reference number: J1455; MUID:96144254; PMID:8566817
A:Accession: P64131
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <RAW>
A:Cross references: DDBJ:P50474; NID:01217594

A:Note: this ORF is not annotated in GenBank entry P50474, release 114.0

Query Match 81.8% Score 9; DB 2; Length 8;
Best Local Similarity 66.7% Pred. No. 2; Re-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 4 LSR 6

RESULT 4
T13818
cytochrome oxidase subunit I - Atlantic haddock mitochondrion (fragment)
C:Species: mitochondrion Myxine glutinosa (Atlantic haddock)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13818

R:Delattre, C.; Barillet, V.; Fillion, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-814, 1997
A:Title: The main features of the cranial mitochondrial DNA between the NDI and the

A:Reference number: 217775; MUID:97398784; PMID:9254918
A:Accession: T13818

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8

A:Cross references: EMBL:Y09527; NID:92440019; FID:92440019; FID:92440022

C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion

Query Match 81.8% Score 9; DB 2; Length 8;
Best Local Similarity 66.7% Pred. No. 2; Re-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 4 LSR 6

RESULT 5
T13838
cytochrome-c oxidase (E) 1, 2, 3, 1) chain 1 Bipes biporus mitochondrion (fragment)
C:Species: mitochondrion Bipes biporus
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T13838
R:Maxam, J.F.; Lane, W.S.; Arai, H.; Igarashi, Y.; Kodama, T.
Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A:Reference number: 217789; PMID:97153826; PMID:9800757

A:Accession: T14219

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 cAAC

A:Cross-references: EMBL:071925; NID:91753232; FID:91753235; FID:AA049271.1

C:Genetics:

A:Genome: mitochondrion

A:Note: Col

C:Keywords: mitochondrion; oxidoreductase

Query Match 81.8%; Score 9; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 3 LXR 5

RESULT 6

T14219

Cytochrome oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment)

C:Species: Xenosaurus grandis

C>Date: 20 Sep 1999 #sequence_revision 20 Sep 1999 #text_change 21-Jul-2003

C:Accession: T14219

R:Macoy, J.R.; Larson, A.; Arachova, K.B.; Faud, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light strand replication in rearrangement

A:Reference number: 217789; PMID:97153826; PMID:9800757

A:Accession: T14219

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 cAAC

A:Cross-references: EMBL:071233; NID:91753236; FID:AA049271.1; FID:91753275

C:Genetics:

A:Genome: mitochondrion

A:Note: Col

C:Keywords: mitochondrion; oxidoreductase

Query Match 81.8%; Score 9; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 3 LXR 5

RESULT 7

P00034

dextranucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)

C:Species: Streptococcus bovis

C>Date: 21 Feb 1994 #sequence_revision 03-Feb-1994 #text_change 16 Sep 1996

C:Accession: P00034

R:Dezoro, Y.; Tsumori, H.; Kakasa, H.

submitted to JPIID, October 1993

A:Description: Purification and properties of glycyltransferase synthesizing 1,6-alpha

A:Reference number: P00034

A:Accession: P00034

A:Molecule type: protein

A:Residues: 1-11 cEEZ

A:Experimental source: ATCC 9804

C:Keywords: glycyltransferase; Xenosyltransferase

Query Match 81.8%; Score 9; DB 2; Length 11;

Best Local Similarity 66.7%; Pred. No. 1.3e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 8 LXR 10

RESULT 8

A42324

Cytochrome P450c27/25 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31 Mar 1993 #sequence_revision 18 Mar 1993 #text_change 08 Feb-1996

C:Accession: A42324

R:Shayiq, R.M.; Avadhani, N.G.

J. Biol. Chem. 267, 2121-2126, 1992

A:Title: Sequence homogeneity between the 5' terminal regions of mRNAs for rat m

ap.

A:Reference number: A42324; M01L02129422; PMID:1733943

A:Accession: A42324

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-12 cHAs

A:Note: Sequence extracted from R301 backbone (R0818.78404, R0818.78410)

Query Match 81.8%; Score 9; DB 2; Length 12;

Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 4 LXR 6

RESULT 9

P02293

12 heavy chain CDR3 region (clone 4 121) human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03 Sep 1993 #sequence_revision 03 Sep 1993 #text_change 16 Aug-1996

C:Accession: P02293

R:Kishida, M.; Wasserman, E.; Fairhead, B.A.; Shiner, S.; Gaton, A.; Kovari, G.

J. Exp. Med. 173, 495-507, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity a

A:Reference number: P02227; M01D.0118197; PMID:1879182

A:Accession: P02293

A:Molecule type: DNA

A:Residues: 1-13 cYAM>

A:Experimental source: B lymphocyte

C:Keywords: heterodimer; immunoglobulin

Query Match 81.8%; Score 9; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.5e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 1 LXR 3

RESULT 10

PA0111

protein QA100054 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse rat cross)

C>Date: 07 Apr 1995 #sequence_revision 26 May 1995 #text_change 05 Jun 1997

C:Accession: PA0111

R:Kanno, M.; Kawakami, T.; Ishigita, A.

submitted to JPIID, March 1995

A:Reference number: PA0109

A:Accession: PA0111

A:Molecule type: protein

A:Residues: 1-11 cEAM

A:Experimental source: root

Query Match 81.8%; Score 9; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 1 LXR 1

Db 11 LSR 14

RESULT 11
S36896
ribosomal protein S16 - *Mycobacterium bovis* (fragment)
C:Species: *Mycobacterium bovis*
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36896
R:Ohara, N.; Kimura, M.; Hidaishi, Y.; Yamada, T.
FEBS Lett. 441, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from *Mycobacterium bovis*
A:Reference number: S36897; MIM:6409654; PMID:8495419
A:Accession: S36896
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-15 -OH
C:Keywords: protein biosynthesis; ribosome

Query Match 81.8%; Score 9; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSR 4
|
|
Db 6 LSR 8

RESULT 12
PA0075
fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (*Fusarium sporotrichioides*) (fragment)
N:Alternate names: aldolase; fructose-1,6-bisphosphate triosephosphate-lase
C:Species: *Fusarium sporotrichioides*
C:Date: 20 Feb 1995 #sequence_revision 20-Feb-1995 #text_change 20-Mar-2001
C:Accession: PA0075; PA0077
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*
A:Reference number: PA0051
A:Accession: PA0075
A:Molecule type: protein
A:Residues: 1-15 -OH
A:Note: this form (1) had a molecular weight of 40.6K and an isoelectric point of 5.3
A:Accession: PA0077
A:Molecule type: protein
A:Residues: 1-15 -CH2
A:Note: this form (11) had a molecular weight of 31.6K and an isoelectric point of 5.4
C:Keywords: aldolase; lyase; carbon-carbon lyase

Query Match 81.8%; Score 9; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSR 4
|
|
Db 6 LSR 8

RESULT 13
PA0102
fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (*Fusarium sporotrichioides*) (fragment)
C:Species: *Fusarium sporotrichioides*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Mar-2001
C:Accession: PA0102
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*
A:Reference number: PA0051
A:Accession: PA0102
A:Molecule type: protein
A:Residues: 1-15 -OH
C:Keywords: aldolase; lyase; carbon-carbon lyase

Query Match 81.8%; Score 9; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSR 3
|
|
Db 6 LSR 8

RESULT 14
B42800
hypothetical protein (P1 5' region) human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Mar-1995 #sequence_revision 22-Mar-1995 #text_change 30-Sep-1994
C:Accession: B42800
R:Jindal, S.; Dudani, A.K.; Singh, B.; Bailey, C.H.; Gupta, R.S.
Mol. Cell. Biol. 9, 2279-2293, 1989
A:Title: Primary structure of a human mitochondrial protein homologous to the bacteriophage T4 gp10
A:Reference number: A42800; MIM:6414784; PMID:2568384
A:Accession: B42800
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 -JIN
A:Cross-references: GB:M22482

Query Match 81.8%; Score 9; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSR 3
|
|
Db 3 LSR 5

RESULT 15
PH1455
T-cell receptor alpha chain (clone A24/2EF4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1455
R:Casarova, J.L.; Martison, F.; Gaudier, B.; Baria, C.; Bannister, C.; Remault, A.
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex peptides
A:Reference number: PH1430; MIM:64171821; PMID:8436911
A:Accession: PH1455
A:Molecule type: mRNA
A:Residues: 1-15 -ONS
A:Experimental source: cytolytic T-lymphocyte
A:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 81.8%; Score 9; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSR 3
|
|
Db 3 LSR 5

RESULT 16
AF0832
the leader peptide (imported) *Salmonella enterica* subsp. enterica serovar typhimurium
C:Species: *Salmonella enterica* subsp. enterica serovar typhimurium
A:Note: This species has also been called *Salmonella typhi*
C:Date: 09-Mar-2001 #sequence_revision 09-Mar-2001 #text_change 09-Mar-2001
C:Accession: AF0832
R:Parkhill, J.; Dandam, G.; James, K.D.; Thomson, N.K.; Pickard, D.; Wain, J.; Barrell, A.G.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dezelic, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rotherford, K.; Simmons, M.; Skellern, J.; Stephens, A.; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar typhimurium

A:Reference number: AB0602, PMID:11677609
 A:Accession: AF0832
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <FAR>
 A:Cross references: CR A:013402, B:04, C:030945, D:1, E:01, G:010000, H:0304, I:000000
 A:Genetic: STV28534

Query Match 81.8%; Score 9; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 4 LXR 5

RESULT 17

C61414

chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)

C:Species: Pseudemys scripta (slider)

C:Date: 06-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999

C:Accession: C61414

R:Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2: 187-198, 1974

A:Title: Evolution in the fasciatic Staphylococcus species. N-terminal sequence data

A:Reference number: A61414; PMID:76146602; PMID:4807189

A:Accession: C61414

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <BHA>

C:Keywords: hydrolase; protein digestion, serine proteinase

Query Match 81.8%; Score 9; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 13 LXR 15

RESULT 18

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1992

C:Accession: JH0517

R:Coleman, M.E.; Pan, Y.C.E.; Ebertow, T.P.

Biochem Biophys Res Commun. 191: 1131-1136, 1991

A:Title: Identification and NH2 terminal amino acid sequence of three insulin-like growth

A:Reference number: JH0517; PMID:91100719; PMID:1722298

A:Accession: JH0517

A:Molecule type: protein

A:Residues: 1-16 <COL>

A:Experimental source: serum

Query Match 81.8%; Score 9; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 14 LXR 16

RESULT 19

B44036

collagen alpha 1(XII) chain NC3B domain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 19-Oct-1995

C:Accession: B44036

Kobayashi, S.F.; Katsuzaki, A.M.; Marinkovich, E.L.; Kawai, L.K.; Morris, R.P.; Burg
 J. Biol. Chem. 267: 20087-20092, 1992
 A:Title: Identification and partial purification of a large, variant form of type XII
 A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Accession: B44036

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <LUN>

A:Experimental source: skin

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Title: Identification and partial purification of a large, variant form of type XII

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

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A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

A:Reference number: A44036; PMID:93615874; PMID:1400326

RESULT 22

154269
 vitamin D binding protein - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1996 #sequence_revision 01 Nov 1996 #text_change 21-Jul-2000
 C:Accession: 154269

R:Rama, A.; Hochmaler, R.; Muller, B.; Clove, H.
 Hum. Genet. 90, 526-532, 1994

A:Title: Molecular evaluation of an Alu repeat including a polymorphic variable poly(A)
 A:Reference number: 154269; PMID:8481387

A:Accession: 154269

A>Status: preliminary; translated from GH/TMG/0001

A:Molecule type: DNA

A:Residues: 1-17 - EES

A:Cross-references: 8 S44971, NID: J264876, PDB: 1A61872-1, PIR: J42C1572

C:Superfamily: serum albumin serum albumin repeat homolog

Query Match 81.8% Score 9; DB 2; Length 17;

Best Local Similarity 66.7% Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 5 LSR 7

RESULT 23

JQ2310

hypothetical 2.1K protein - tomato chloroplast (strain Toko)

C:Species: chloroplast lycopersicon esculentum (tomato)

C:Date: 10-Mar-1994 #sequence_revision 28 Oct-1994 #text_change 23-Mar-1995

C:Accession: JQ2310

R:Kawaguchi, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A:Reference number: JQ2306

A:Accession: JQ2310

A:Molecule type: DNA

A:Residues: 1-17 - KAW

A:Experimental source: strain Toko

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 81.8% Score 9; DB 2; Length 17;

Best Local Similarity 66.7% Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 15 LSR 17

RESULT 24

JQ2320

hypothetical 2.1K protein - potato chloroplast

C:Species: chloroplast Solanum tuberosum (potato)

C:Date: 10-Mar-1994 #sequence_revision 28 Oct-1994 #text_change 05-Mar-1995

C:Accession: JQ2320; JQ2315

R:Kawaguchi, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A:Reference number: JQ2306

A:Accession: JQ2320

A:Molecule type: DNA

A:Residues: 1-17 - KWI

A:Experimental source: cv. W553 4

A:Accession: JQ2315

A:Molecule type: DNA

A:Residues: 1-17 - KWI

A:Experimental source: cv. 150

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 81.8% Score 9; DB 2; Length 17;

Best Local Similarity 66.7% Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 15 LSR 17

RESULT 25

B61414

chymotrypsin (PC 3.4.21.1) - painted turtle (fragment)

C:Species: Chrysemys picta (painted turtle)

C:Date: 16-Mar-1997 #sequence_revision 16 Dec 1997 #text_change 07 May 1999

C:Accession: B61414

R:Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2, 187-198, 1973

A:Title: Evolution in the pancreatic chymotrypsinogen series. N-terminal sequence det.

A:Reference number: A61414; PMID:76146602; PMID:4807189

A:Accession: B61414

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 - SBHA

C:Keywords: hydrolase; serine proteinase

Query Match 81.8% Score 9; DB 2; Length 17;

Best Local Similarity 66.7% Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 13 LSR 15

RESULT 26

S29491

GTP binding protein ora3 - mutated electric ray (fragment)

C:Species: Torpedo marmorata (mottled electric ray)

C:Date: 22-Nov-1993 #sequence_revision 27 Feb 1997 #text_change 19 Dec 1998

C:Accession: S29491

R:Glenfield, W.; Bennett, J.; Elferink, L.A.; Pels-Boer, P.B.

FEBS Lett. 317, 53-56, 1993

A:Title: Association of three small GTP-binding proteins with cholinergic synaptic ve

A:Reference number: S29485; PMID:94154521; PMID:8428634

A:Accession: S29491

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 - SWL

C:Genetics:

A:Gene: ora3

C:Superfamily: ras transforming protein; translation elongation factor; G-prote

C:Keywords: GTP binding; lipoprotein; membrane trafficking

Query Match 81.8% Score 9; DB 2; Length 18;

Best Local Similarity 66.7% Pred. No. 2.1e+04;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 5 LSR 7

RESULT 27

A41877

Yersinia pseudotuberculosis (fragment)

C:Species: Yersinia pseudotuberculosis

C:Date: 04 Mar 1994 #sequence_revision 18 Nov 1994 #text_change 18 Nov 1994

C:Accession: A41877

R:Rimpilainen, M.; Forsberg, A.; Woll-Watz, H.

J. Bacteriol. 174, 3355-3363, 1992

A:Title: A novel protein, LerQ, involved in the low calcium response of Yersinia pseu

RESULT 33

A60326
cholecystokinin-58 - bovine (fragment)
C:Species: Bos primigenius taurus (cat)lo
C:Date: 21-Oct-1992 #sequence_revision 21 Oct 1992 #text_change 31 Dec 1993
C:Accession: A60326
R:End, J.: 11, H.R.: Valow, R.S.
Repl, Pept. 40, 15-19, 1990
A:Title: Purification of bovine cholecystokinin-58 and sequencing of its N-terminus.
A:Reference number: A60326; MIM:9191599; PMID:2217939
A:Accession: A60326
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <EN6>
C:Keywords: neuropeptide

Query Match 81.8%; Score 9; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2,4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
| |
DB 17 LXR 19

RESULT 34

A60525
lysozyme (EC 3.2.1.17) - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun 2000
C:Accession: A60525
R:Balliday, J.A.; Bell, K.; McKenzie, H.A.; Shaw, D.C.
Comp. Biochem. Physiol. B 95, 773-779, 1990
A:Title: Feline whey proteins: identification, isolation and initial characterization of
A:Reference number: A60525; MIM:9026404; PMID:2344734
A:Accession: A60525
A:Molecule type: protein
A:Residues: 1-29 <HAI>
A:Experimental source: milk
C:Superfamily: Lysozyme C
C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation

Query Match 81.8%; Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2,4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
| |
DB 8 LXR 10

RESULT 35

JP0050
ribosomal protein L30 - Bacillus mesenterium (fragment)
C:Species: Bacillus mesenterium
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03 May 1996
C:Accession: JP0050
Rachli, K.
submitted to JPIID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A:Reference number: JP0050
A:Accession: JP0050
A:Molecule type: protein
A:Residues: 1-20 <ACH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match 81.8%; Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2,4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 8 LXR 10

RESULT 36

JP0051
ribosomal protein L30 - Bacillus cereus (fragment)
C:Species: Bacillus cereus
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03 May 1996
C:Accession: JP0051
Rachli, K.

submitted to JPIID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0051
A:Molecule type: protein
A:Residues: 1-20 <ACH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match 81.8%; Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2,4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
| |
DB 8 LXR 10

RESULT 37

S33001
hypothetical protein - human herpesvirus 4
C:Species: human herpesvirus 4, Epstein Barr virus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct 1999
C:Accession: S33001
R:Parrell, P.J.
submitted to the EMBL Data Library, March 1988
A:Reference number: S32973
A:Accession: S33001
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <PAR>
A:Cross references: EMBL:V01555; NID:059074; FID:CAA4847.1; FID:CA4466

Query Match 81.8%; Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2,4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
| |
DB 7 LXR 9

RESULT 38

PC2084
serine proteinase (EC 3.4.21.1) - Klebsiella pneumoniae (strain 8K-1) (fragment)
C:Species: Klebsiella pneumoniae
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07 May 1999
C:Accession: PC2084
R:Watanabe, Y.; Nishimura, K.; Shibahara, Y.; Kuroda, N.; Morita, S.; Okabe, H.
Biochim. Biophys. Acta 1187, 58-74, 1994
A:Title: Isolation and characterization of a serine proteinase, inactivated in solid
A:Reference number: PC2084; MIM:9424404; PMID:774466
A:Accession: PC2084
A:Molecule type: protein
A:Residues: 1-20 <WAI>
C:Superfamily: This protein shows selective inhibitory activity against the m subunit of
C:Keywords: hydrolase; serine proteinase

Query Match 81.8%; Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2,4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
11
Db 13 LAR 15

RESULT 39

S19616
N:globin - polychaete (Eudistylia vancoveri) (fragment)
N:Alternate names: chlorocruorin
C:Species: Eudistylia vancoveri
C>Date: 19 Mar 1997 #sequence_revision 10 Oct 1997 #text_change 05 Dec 1998
C:Accession: S19616
R:Qabar, A.N.; Stern, M.S.; Wale, P.A.; Chiu, J.T.; Tinkovitch, P.; Wall, J.F.; Zapp, C.H.
J. Mol. Biol. 223, 1129-1129, 1991
A>Title: Hierarchy of globin complexes: The primary structure of the extracellular chain
A:Reference number: S19616
A:Accession: S19616
A:Molecule type: protein
A:Residues: 1-20 (QAB)
A:Complex: dodecamers, each consisting of a trimer of tetramers of globin chains, dodecamer
C:Keywords: calcium; dodecamer; helix; hemotetramer; oxygen carrier

Query Match 81.8% Score 9; DB 2; Length 20;

Best Local Similarity 66.7% Prod. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
11
Db 12 LAR 14

RESULT 40

A61414
N:chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)
C:Species: Chelydra serpentina (snapping turtle)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C:Accession: A61414
R:Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A>Title: Evolution in the pancreatic chymotrypsinogen series. N terminal sequence determined
A:Reference number: A61414; M01D-76146602; P01D-4807193
A:Accession: A61414
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 (BHA)
C:Keywords: hydrolase; protein; protein; serine protease

Query Match 81.8% Score 9; DB 2; Length 20;

Best Local Similarity 66.7% Prod. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
11
Db 13 LAR 15

RESULT 41

A42267
N:J-kappa recombination sequence-binding protein (mouse) (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: A42267; S23798
R:Kawauchi, M.; Oka, C.; Shibayama, S.; Koromilas, A.E.; Matsunami, N.; Hamauchi, Y.; H.
J. Biol. Chem. 267, 4036-4022, 1992
A>Title: Genomic organization of mouse J-kappa recombination signal binding protein (RBS)
A:Reference number: A42267; M01D-92156146; P01D-1742450
A:Accession: A42267
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 (FAW)
A:Cross-references: GR-M01866

Query Match 81.8% Score 9; DB 2; Length 20;

Best Local Similarity 66.7% Prod. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
11
Db 18 LAR 20

RESULT 42

AC0269
N:protein trip operon (baker) peptide YP02209 (imported) - Yersinia pestis (strain C202)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AC0269
R:Franklin, J.; Wren, B.W.; Thomson, R.K.; Tibbitts, R.W.; Holden, M.T.G.; Prentice, M.
G.; Forsberg, A.M.; Chellidurai, T.; Collins, A.; Davies, P.H.; Davis, P.; Fougere, G.
J.; M.; Rutherford, K.; Simmonds, M.; Skellern, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague
A:Reference number: AB0091; M01D-21479413; P01D-11586660
A:Accession: AC0269
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 (KRS)
A:Cross-references: B6-AL250642; F01D-06616151; F01D-01560609; F01D-06616175
C:Genetics:
A:Gene: YP02209

Query Match 81.8% Score 9; DB 2; Length 20;

Best Local Similarity 66.7% Prod. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
11
Db 15 LAR 18

RESULT 43

S16073
N:alanine-tRNA ligase (EC 6.1.1.7) - rat (fragment)
N:Alternate names: alanyl tRNA synthetase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19 Mar 1997 #sequence_revision 24 Oct 1998 #text_change 03-Jun-2002
C:Accession: S16073
R:Dignam, J.D.; Dignam, S.S.; Brumley, L.L.
Euk. J. Biochem. 226, 261-270, 1991
A>Title: Alanyl-tRNA synthetase from Escherichia coli, Romyx mori and Rattus rat S. E.
A:Reference number: S16073; M01D-591245799; P01D-2040280
A:Accession: S16073
A:Molecule type: protein
A:Residues: 1-21 (DIG)
C:Superfamily: alanine-tRNA ligase
C:Keywords: aminoacyl tRNA synthetase; ATP; louse; protein biosynthesis

Query Match 81.8% Score 9; DB 2; Length 21;

Best Local Similarity 66.7% Prod. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
11
Db 19 LAR 20

RESULT 44

JT0581
N:natriuretic peptide-type C (chicken)
C:Species: Gallus gallus (chicken)
C>Date: 17-Apr-1993 #sequence_revision 17 Apr 1992 #text_change 20-Mar-1998
C:Accession: JT0581
R:Arizumi, T.; Mizuno, Y.; Kunitake, K.; Kato, H.
Biochem. Biophys. Res. Commun. 174, 142-148, 1991
A>Title: Isolation and identification of C type natriuretic peptide in chicken brain.
A:Reference number: JT0581; M01D-91114186; P01D-1989595

A:Accession: J10581
 A:Molecule type: protein
 A:Residues: 1-22 -A81-
 A:Experimental source: brain
 C:Superfamily: natriuretic peptide A precursor
 C:Keywords: diuretic; hormone; natriuretic; osmoregulation

Query Match 81.8% Score 9; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 2 LSK 4

RESULT 45

F23744
 insulin-like growth factor-binding protein 4 - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 11-Jan-2000
 C:Accession: F23744
 R:Shimada, S.; Gao, L.; Shimomura, M.; Lind, N.
 Mol. Endocrinol. 5, 938-948, 1991
 A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6
 A:Reference number: F23744; MIM:62049376; PMID:1719383
 A:Accession: F23744
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-22 -SH1-
 C:Superfamily: Insulin-like growth factor binding protein 1, thyroglobulin type 1 repeat

Query Match 81.8% Score 9; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 14 LAR 16

Search completed: April 30, 2003, 13:47:17
 Job time : 24.0455 secs

545	81.8	88	1	YB4D_SCHUPO	013973	schizosacch	618	9	81.8	92	1	RR19_BORPH	P51416	porphyria pu
546	81.8	88	1	YVAL_VACCV	P35231	varcinia vi	619	9	81.8	92	1	RR19_BORPH	P57587	bacteri ap
547	81.8	89	1	AP21_HOMAN	Q96110	homo sapien	620	9	81.8	92	1	RR19_NEIMA	Q91196	neisseria m
548	81.8	89	1	BX22_BOMMO	P15411	bombx mori	621	9	81.8	92	1	RR29_RICCN	Q92472	ricettista
549	81.8	89	1	BX28_BOMMO	P36731	bombx mori	622	9	81.8	92	1	RR19_HUMAN	P13673	homo sapien
550	81.8	89	1	COX1_BOMMO	Q96522	desaphila	623	9	81.8	92	1	RR19_HUMAN	P13673	escherichia
551	81.8	89	1	R43_PLEIA	P06516	bioparasma	624	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
552	81.8	89	1	IMMF_BPHH1	P13772	bacterioph	625	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
553	81.8	89	1	R148_STAAM	Q96050	staphylococ	626	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
554	81.8	89	1	PP0Y_SCHPO	P19009	schizosacch	627	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
555	81.8	89	1	PP0Y_APPPE	Q96050	schizosacch	628	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
556	81.8	89	1	RS14_SIRIN	Q96050	schizosacch	629	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
557	81.8	89	1	Y27A_AERPE	Q96050	schizosacch	630	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
558	81.8	89	1	Y655_SVNY3	P18111	streptococ	631	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
559	81.8	89	1	Y670_GYSA	Q96050	schizosacch	632	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
560	81.8	89	1	YF19_MYCTU	Q96050	schizosacch	633	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
561	81.8	89	1	YF03_BACST	Q96050	schizosacch	634	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
562	81.8	89	1	YF60_SVYBN	P42730	bacillus at	635	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
563	81.8	90	1	LIM1_LILLO	P42730	bacillus at	636	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
564	81.8	90	1	LIM2_LILLO	Q43533	lilium long	637	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
565	81.8	90	1	NUS_EHIME	Q43533	lilium long	638	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
566	81.8	90	1	NUCC_SACCE	Q43533	lilium long	639	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
567	81.8	90	1	PR18_SIPPO	Q43533	lilium long	640	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
568	81.8	90	1	PS16_LACIA	Q43533	lilium long	641	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
569	81.8	90	1	PS16_LISIN	Q43533	lilium long	642	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
570	81.8	90	1	PS16_LISMO	Q43533	lilium long	643	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
571	81.8	90	1	PS16_SVYBN	Q43533	lilium long	644	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
572	81.8	90	1	RS16_SIRIN	Q43533	lilium long	645	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
573	81.8	90	1	VS56_BOMMO	Q43533	lilium long	646	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
574	81.8	90	1	YF58_FOGH1	P42730	bacillus at	647	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
575	81.8	90	1	YV77_SVNY3	P73455	synochocyst	648	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
576	81.8	91	1	BX01_BOMMO	P15410	bombx mori	649	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
577	81.8	91	1	GAIC_BORRU	Q51318	borrelia bu	650	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
578	81.8	91	1	GAIC_HALRI	Q96050	schizosacch	651	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
579	81.8	91	1	NPC2_BZAJA	P53418	bradyrhizob	652	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
580	81.8	91	1	NLT1_PSTAF	P81651	prunus dome	653	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
581	81.8	91	1	NLT1_PRUDO	P82534	prunus dome	654	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
582	81.8	91	1	NLT1_PRUPE	P81402	prunus pers	655	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
583	81.8	91	1	PS15_SIRIN	Q96050	schizosacch	656	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
584	81.8	91	1	R43_PLEIA	Q96050	schizosacch	657	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
585	81.8	91	1	R43_PLEIA	Q96050	schizosacch	658	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
586	81.8	91	1	R43_PLEIA	Q96050	schizosacch	659	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
587	81.8	91	1	R43_PLEIA	Q96050	schizosacch	660	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
588	81.8	91	1	R43_PLEIA	Q96050	schizosacch	661	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
589	81.8	91	1	R43_PLEIA	Q96050	schizosacch	662	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
590	81.8	91	1	R43_PLEIA	Q96050	schizosacch	663	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
591	81.8	91	1	R43_PLEIA	Q96050	schizosacch	664	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
592	81.8	91	1	R43_PLEIA	Q96050	schizosacch	665	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
593	81.8	91	1	R43_PLEIA	Q96050	schizosacch	666	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
594	81.8	91	1	R43_PLEIA	Q96050	schizosacch	667	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
595	81.8	91	1	R43_PLEIA	Q96050	schizosacch	668	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
596	81.8	91	1	R43_PLEIA	Q96050	schizosacch	669	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
597	81.8	91	1	R43_PLEIA	Q96050	schizosacch	670	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
598	81.8	91	1	R43_PLEIA	Q96050	schizosacch	671	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
599	81.8	91	1	R43_PLEIA	Q96050	schizosacch	672	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
600	81.8	91	1	R43_PLEIA	Q96050	schizosacch	673	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
601	81.8	91	1	R43_PLEIA	Q96050	schizosacch	674	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
602	81.8	91	1	R43_PLEIA	Q96050	schizosacch	675	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
603	81.8	91	1	R43_PLEIA	Q96050	schizosacch	676	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
604	81.8	91	1	R43_PLEIA	Q96050	schizosacch	677	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
605	81.8	91	1	R43_PLEIA	Q96050	schizosacch	678	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
606	81.8	91	1	R43_PLEIA	Q96050	schizosacch	679	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
607	81.8	91	1	R43_PLEIA	Q96050	schizosacch	680	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
608	81.8	91	1	R43_PLEIA	Q96050	schizosacch	681	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
609	81.8	91	1	R43_PLEIA	Q96050	schizosacch	682	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
610	81.8	91	1	R43_PLEIA	Q96050	schizosacch	683	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
611	81.8	91	1	R43_PLEIA	Q96050	schizosacch	684	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
612	81.8	91	1	R43_PLEIA	Q96050	schizosacch	685	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
613	81.8	91	1	R43_PLEIA	Q96050	schizosacch	686	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
614	81.8	91	1	R43_PLEIA	Q96050	schizosacch	687	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
615	81.8	91	1	R43_PLEIA	Q96050	schizosacch	688	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
616	81.8	91	1	R43_PLEIA	Q96050	schizosacch	689	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia
617	81.8	91	1	R43_PLEIA	Q96050	schizosacch	690	9	81.8	92	1	RR19_HUMAN	Q92472	escherichia

691	9	81.8	96	1	GATC_BACED	Q9kf29 bacillus ba	764	9	81.8	99	1	GATC_BACED	Q51259 mycobacteri
692	9	81.8	96	1	GATC_BACST	Q9k250 bacillus st	765	9	81.8	99	1	GATC_BACED	Q95382 ralbactera
693	9	81.8	96	1	GATC_BACSU	Q06492 bacillus su	766	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
694	9	81.8	96	1	GATC_DEIRA	Q9ur56 deinoxococ	767	9	81.8	99	1	RKRN_RBPB3	P07243 bacterioph
695	9	81.8	96	1	GATC_NEIMA	Q9jt26 neissococ	768	9	81.8	99	1	RKRN_RBP2	P04132 bacterioph
696	9	81.8	96	1	GATC_NEIMA	Q9jt26 neissococ	769	9	81.8	99	1	RKRN_RBP2	P04132 bacterioph
697	9	81.8	96	1	GATC_PSAF	Q9hr+9 pseudomon	770	9	81.8	99	1	RKRN_RBP2	P04132 bacterioph
698	9	81.8	96	1	GATC_THMA	Q9w794 thermotoga	771	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
699	9	81.8	96	1	HAC6_PPAPE	Q15651 brachydan	772	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
700	9	81.8	96	1	HAC6_SHEEP	Q28601 ovis aries	773	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
701	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	774	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
702	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	775	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
703	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	776	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
704	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	777	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
705	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	778	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
706	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	779	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
707	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	780	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
708	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	781	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
709	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	782	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
710	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	783	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
711	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	784	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
712	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	785	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
713	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	786	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
714	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	787	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
715	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	788	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
716	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	789	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
717	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	790	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
718	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	791	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
719	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	792	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
720	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	793	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
721	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	794	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
722	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	795	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
723	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	796	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
724	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	797	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
725	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	798	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
726	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	799	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
727	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	800	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
728	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	801	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
729	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	802	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
730	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	803	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
731	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	804	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
732	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	805	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
733	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	806	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
734	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	807	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
735	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	808	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
736	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	809	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
737	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	810	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
738	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	811	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
739	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	812	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
740	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	813	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
741	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	814	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
742	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	815	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
743	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	816	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
744	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	817	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
745	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	818	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
746	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	819	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
747	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	820	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
748	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	821	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
749	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	822	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
750	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	823	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
751	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	824	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
752	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	825	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
753	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	826	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
754	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	827	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
755	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	828	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
756	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	829	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
757	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	830	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
758	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	831	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
759	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	832	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
760	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	833	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
761	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	834	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
762	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	835	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere
763	9	81.8	96	1	HAC6_MUSE	P15975 mus mascul	836	9	81.8	99	1	HAFA_RALSO	Q40787 ralbactere

984 9 81.8 106 1 YB91_YEAST P38241 saccharomye
984 9 81.8 106 1 YF02_YEAST P43566 saccharomye
985 9 81.8 106 1 YF02_RH22A Q37184 rhizobacterr
986 9 81.8 107 1 COL_FABIT P42890 oryctolagus
987 9 81.8 107 1 COL_FABIT P29734 mastigoclad
988 9 81.8 107 1 CYP1_MAGLA P26607 cyp133
989 9 81.8 107 1 CYP1_MAGLA P56300 staphylococ
990 9 81.8 107 1 ECLA_STAYX P27311 human adeno
991 9 81.8 107 1 E312_ADE02 P06496 human adeno
992 9 81.8 107 1 H4_MASHA Q91V79 neisseria m
993 9 81.8 107 1 H4_MASHA Q91V79 neisseria m
994 9 81.8 107 1 H4_MASHA Q91V79 neisseria m
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997 9 81.8 107 1 H4_MASHA Q91V79 neisseria m
998 9 81.8 107 1 H4_MASHA Q91V79 neisseria m
999 9 81.8 107 1 H4_MASHA Q91V79 neisseria m
1000 9 81.8 107 1 NPAB_LOGMI P10776 locusta miq

ALIGNMENTS

RESULT 1
RS01_ONCMY 11 AA: 1123 MW: 2312AB6300D73568 CRC64;
ID RS01_ONCMY STANDARD; PRT; 11 AA.
AC PR4287;
DI 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE 408 ribosomal protein S40 (Fragment).
GN FAU.
OS oncorhynchus mykiss (rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID 8022;
[1]
FN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
FC TISSUE: SKIN MUSCLES.
RA Fernandes J.M.O., Smith V.J.,
RT "A novel antimicrobial function for a ribosomal peptide from skin
secretions of rainbow trout.";
FI Submitted (Apr-2002) to the SWISS-PROT data bank
CC -1- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.
CC -1- MASS SPECTROMETRY: MW-6676.6; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE S40E FAMILY OF RIBOSOMAL PROTEINS.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA: 1123 MW: 2312AB6300D73568 CRC64;

Query Match 81.8%; Score 9; ID 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 4,3602;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

ID 6 LAR 6

RESULT 2

ONC1_ONCMY 15 AA: 1580 MW: 830640CE161440 CRC64;
ID ONC1_ONCMY STANDARD; PRT; 15 AA.
AC PR4287;
DI 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE oncorhynchus mykiss (rainbow trout) (Salmo gairdneri).
OS oncorhynchus mykiss (rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

QY NCBI_TaxID 8022;

FN [1]

FC TISSUE: FUNCTION: SUBCELLULAR LOCATION: ANTIBIOTIC SPECIFICITY.

RA Fernandes J.M.O., Smith V.J., Komp G.D.,

RT "A novel antimicrobial function for a ribosomal peptide from skin
secretions of rainbow trout.";
FI Submitted (May-2002) to the SWISS-PROT data bankCC -1- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: SKIN.

KW Antibiotic.

FT NON_TER 4 4 OR 6.

FT NON_TER 9 9 OR 1.

FT NON_TER 15 15

SQ SEQUENCE 15 AA: 1580 MW: 830640CE161440 CRC64;

Query Match 81.8%; Score 9; ID 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 4,3602;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

ID 12 LAR 14

RESULT 3

UC25_MAIZE 15 AA: 1580 MW: 830640CE161440 CRC64;
ID UC25_MAIZE STANDARD; PRT; 15 AA.
AC PR0631;
DI 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-JUN-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D page of isolated coleoptile (Spot 77)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACO clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID 4577;
[1]
FN SEQUENCE.
FC TISSUE: Coleoptile;
RA Tardif P., Riccardi P., Merle C., Panerai P., Huet J., C.,
RA Tardif P., Riccardi P., Merle C., Panerai P., Huet J., C.,
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
FI genome analysis program.
FI genome analysis program.
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P.I. OF THIS UNKNOW
PROTEIN IS: 4.9, ITS MW IS: 41.6 KDa.
DR Maize-2DPAGE; P80631; COLEOPTILE.
DR Maize-2DPAGE; P80631; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1580 MW: 830640CE161440 CRC64;

Query Match 81.8%; Score 9; ID 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 4,3602;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

ID 5 LAR 7

RESULT 4

IBP4_PIG 16 AA: 1680 MW: 830640CE161440 CRC64;
ID IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DI 01-MAR-1992 (Rel. 21, Created)
DI 01-MAR-1992 (Rel. 21, Last sequence update)
DI 15-JUN-1996 (Rel. 37, Last annotation update)

DE Insulin-like growth factor binding protein 4 (IGFBP-4) (Igf-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Eberhart T.D.:
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 1 THYREOGLOBULIN TYPE-I DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
DR PIR; JH0517.
DR InterPro: IPR000867; Ins_lgr_fac_pr
DR InterPro: IPR000716; Thyroglobulin_1
DR PROSITE: PS00322; IGF BINDING; PARTIAL.
DR PROSITE: PS00484; THYREOGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
FT SEQUENCE 16 AA 1744 MW: 400000000.942 9964;
Query Match 81.8%; Score 9; DB 1; Length 16.
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 LXR 3
DB 14 LAR 16
RESULT 5
YAA5_RH-PA
ID YAA5_RH-PA STANDARD: PPT: 19 AA.
AC Q02005;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in AAP 5'-region (Fragment).
OS Rhodospseudomonas palustris.
CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group.
CC Bradyrhizobium group; Rhodospseudomonas
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CGA0009;
RX MEDLINE=92343492; PubMed 1222059;
FA Dispenso M., Thomas C.T., Kim M.F., Furlong J.A., Bilezik J.,
RA Harwood C.S.:
RT "Anaerobic growth of Rhodospseudomonas palustris on 4-hydroxybenzoate
RT is dependent on AadR, a member of the cyclic AMP receptor protein
RT family of transcriptional regulators.";
RL J. Bacteriol. 174:5803-5813(1992).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M92426; AAA26089.1;
CC PIR: A43334; A43334.

KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA 2173 MW: 610400000.1740A CR094;
Query Match 81.8%; Score 9; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 1 LXR 3
DB 6 LAR 8
RESULT 6
LYC_FEL-CA
ID LYC_FEL-CA STANDARD: PPT: 20 AA.
AC P47155;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysocyme C (EC 3.2.1.17) (1.1 beta-D arabinamylase C) (Fragment).
GN LYZ.
OS Felis silvestris catus (Cat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE.
RX TISSUE=Milk;
RX MEDLINE=96234493; PubMed 244744;
RA Halliday J.A., Bell K., McKenzie H.A., Shaw D.C.:
RT "Feline whey proteases: identification, isolation and initial
RT characterization of alpha-lactalbumin, beta-lactoglobulin and
RT Lysocyme.";
RL Comp. Biochem. Physiol. 95B:774-779(1990).
CC -!- FUNCTION: Lysocymes have primarily a bacteriolytic function; those
CC in tissues and body fluids are associated with the monocyte-
CC macrophage system and enhance the activity of immunoproteins.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC heteropolymers of the prokaryotes cell walls.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: Lysocyme C is capable of both hydrolysis and
CC transglucosylation; it shows also a slight esterase activity. It
CC acts rapidly on both peptide substituted and unsubstituted
CC peptidylglutamate and slowly on chitin carboxylates.
CC -!- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
DR PIR; A09525; A09525.
DR HSPR; P11376; 2R0L.
DR InterPro: IPR001916; GH_22.
DR Pfam: PF00962; 179; 1.
DR PROSITE: PS00129; LACTALBUMIN_LYCOSYME; PARTIAL.
KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Milk.
FT NON_TER 20 20
FT SEQUENCE 20 AA 2214 MW: 18923400.9425113 CR094;
Query Match 81.5%; Score 3; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 1 LXR 3
DB 8 LAR 10
RESULT 7
PECX-AZOV
ID PEXX_AZOV; STAN:AKL; PPT: 20 AA.
AC P37863;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE Regulatory protein pexX (Fragment).
GN PEEX.
FT NON_TER 20 20
FT SEQUENCE 20 AA 2214 MW: 18923400.9425113 CR094;
Query Match 81.5%; Score 3; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 1 LXR 3
DB 8 LAR 10

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GN RECX.
OS Azotobacter vinelandii.
ac Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
ac Azotobacter.
OX NCBI_TaxID: 354;
PN 111
RP SEQUENCE FROM N.A.
PX MEDLINE 94225447; PubMed 1563642;
PA Venkatesh T.V., Das H.K.;
PT "The Azotobacter vinelandii recA gene: sequence analysis and
PT regulation of expression.";
RL gene 114:47-53(1992).
RL 121
PN 121
PP IDENTIFICATION.
PX MEDLINE 94218258; PubMed 8165147;
PA de Mel R., Schoofs G., Vanderheyden J.;
PT "A putative regulatory gene downstream of recA is conserved in gram
PT negative and Gram-positive bacteria.";
RL Nucleic Acids Res. 22:1313-1314(1994).
CC 1- FUNCTION: MAY PLAY A REGULATORY ROLE POSSIBLY BY INTERACTING WITH
CC RECA.
CC 1- SIMILARITY: BELONGS TO THE RECX FAMILY.
CC
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CC
DR EMBL: S96898; ; NOT_ANNOTATED_PDS.
FT NON_TER 20 20
SQ SEQUENCE 20 AA: 2111 MW: 6809486336363655 CR054;

Query Match 81.8%; Score 9; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 18 LAR 20

RESULT 8
SYA_RAI
ID SYA_RAI STANDARD; PRI: 21 AA.
AC P50475;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DE Alanyl tRNA synthetase (EC 6.1.1.7) (Alanine tRNA ligase) (AARS)
DE (Fragment).
DE 111
GN AARS.
OS Rattus norvegicus (Rat).
ac Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ac Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID: 10116;
PN 111
RP SEQUENCE.
PX MEDLINE 91449799; PubMed 2949389;
PA Dignam J.D., Dignam S.S., Brumley L.L.;
PT "Alanyl-tRNA synthetase from Escherichia coli, Bombyx mori and Rattus
PT rattus. Existence of common structural features.";
RL Eur. J. Biochem. 198:201-210(1991).
CC 1- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) -> AMP +
CC diphosphate + L-alanyl-tRNA(Ala).
CC 1- SUBUNIT: MONOMER.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC 1- SIMILARITY: BELONGS TO CLASS II AMINO-ACYL tRNA SYNTHETASE FAMILY.
DR InterPro: IPR002106; AA_RNA_Ligase11.
DR PROSITE: PS50860; AA_TRNA_LIGASE_IL1ALA; PARTIAL.

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KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP binding.
FT NON_TER 21 21
SQ SEQUENCE 21 AA: 2293 MW: 174939526043375 CR064;

Query Match 81.8%; Score 9; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 18 LAR 20

RESULT 9
ANPC_CHICK
ID ANPC_CHICK STANDARD; PRI: 22 AA.
AC P21805;
DT 01-MAY-1991 (rel. 18, Created)
DT 01-MAY-1991 (rel. 18, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE C-type natriuretic peptide (CNP).
DE NPCC.
OS Gallus gallus (Chicken).
ac Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ac Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID: 9031;
RN 111
RP SEQUENCE.
PX MEDLINE-91113186; PubMed-1989595;
PA Arimura J.J., Minamide N., Katsawa K., Matsuo H.;
RT "Isolation and identification of C-type natriuretic peptide in
RT chicken brain.";
RL Biochem. Biophys. Res. Commun. 174:142-148(1991).
CC 1- FUNCTION: VASORELAXANT ACTIVITY. HAS A GMP-STIMULATING ACTIVITY.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: BELONGS TO THE NAIURETIC PEPTIDES FAMILY.
DR PIR: JT0581; J10581.
DR InterPro: IPR000663; Natri_peptide.
DR FLAM: F00212; ANP; 1.
DR PRINTS: PR00710; NAIPEPTIDES.
DR SMART: SM00183; NAT_PEP; 1.
DR PROSITE: PS00263; NAIURETIC_PEPID; 1.
KW Vasodilator.
FT DISULFID 6 22
SQ SEQUENCE 22 AA: 2244 MW: 122447860914025 CR064;

Query Match 81.8%; Score 9; DB 1; Length 22;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 2 LSR 4

RESULT 10
GLNA_PHOIP
ID GLNA_PHOIP STANDARD; PRI: 23 AA.
AC P20479;
DT 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 15-FEB-1998 (rel. 37, Last annotation update)
DE Glutamine synthetase (EC 6.3.1.2) (Glutamate ammonia lyase)
DE (Fragment).
OS Phormidium laticum.
ac Bacteria; Cyanobacteria; Oscillatoriales; Phormidiales.
OX NCBI_TaxID: 32060;
RN 111
RP SEQUENCE.
RX MEDLINE-89214011; PubMed-2907514;

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Query Match      81.8% Score 9; DR 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 1; Gaps 0.

QY 1 LXR 3
DB 22 LXR 24

RESULT 14
UBQL_BOVIN
ID UBQL_BOVIN STANDARD; PRT; 25 AA.
AC P23356;
DT 01-NOV-1991 (rel. 20, Created)
DT 01-NOV-1991 (rel. 20, Last annotation update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
DE (P99 9.5) (P99 9.5) (Fragment).
GN UCHL1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cerviiformes; Sumatran; P. 14; P. 3434
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE 9209646; PubMed 1834240;
RA Giannico L., Bianchi R., Cecaroli P., Pula G., Serci G.,
RA Antonelli S., Borchini V., Donato R.;
RA "Neuron-specific" protein gene product 9.5 (P99 9.5) is also
RA expressed in glioma cell lines and its expression depends on cellular
RA growth state.*
RL FEBS Lett. 290:131-134(1991).
CC 1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINATED PROTEINS.
CC THIS ENZYME IS A THIOLESTERASE THAT SPECIFICALLY HYDROLYZES
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC 1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + thiol.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic.
CC 1- TISSUE SPECIFICITY: NEURONS AND CELLS OF THE DIFFUSE
CC NEUROENDOCRINE SYSTEM AND THEIR TUMORS.
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
DR PIR: S17561; S17561.
DR MEROPS: C12.001.
DR InterPro: IP001578; UCHL1.
DR Pfam: PF01088; peptidase_C12; 1.
DR PROSITE: PS00140; UCHL1: PARTIAL.
KW Ubiquitin degradation pathway; Hydrolase; Thiol protease; Multidomain Family.
FT NON_TER 25
SQ SEQUENCE 25 AA: 2812 MW: 26056.00754255 CRC64.

Query Match      81.8% Score 9; DR 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 1; Gaps 0.

QY 1 LXR 3
DB 17 LXR 19

RESULT 15
NTRC_RHLP
ID NTRC_RHLP STANDARD; PRT; 26 AA.
AC P41502;
DT 01-NOV-1995 (rel. 42, Created)
DT 01-NOV-1995 (rel. 42, Last annotation update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Nitrogen assimilation regulatory protein (Fragment).
GN NTRC.
OS Rhizobium leguminosarum (bacterial strain).

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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Rhizobiaceae; Rhizobium.
CX NCBI_TaxID=385;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CR-4;
RX MEDLINE 94018651; PubMed 8412704;
RA Patriarca E.J., Riccio A., Tate R., Colonna-Romano S., Iacovino M.,
RA Delez R.;
RA "The ntrC genes of Rhizobium leguminosarum are part of a complex
RA operon subject to negative regulation.*"
RL Mol. Microbiol. 9:569-577(1993).
CC 1- FUNCTION: MEMBER OF THE TWO COMPONENT REGULATORY SYSTEM NTRC/NTRC-
CC INVOLVED IN THE ACTIVATION OF NITROGEN ASSIMILATORY GENES SUCH AS
CC GLN-AMIDE IS PHOSPHORYLATED BY NTRC AND INTERACTS WITH SIGMA 54.
CC 1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
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DR EMBL: A71435; 1 NOT_ANNOTATED_THIS.
DR PIR: S36203; S36203.
DR InterPro: IP001789; Response-reg.
DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
KW Nitrogen fixation; Transcription regulation; Repressor; Activator;
KW DNA-binding; ATP-binding; Phosphorylation; Sensory transduction.
FT DOMAIN 1-26
FT NON_TER 26
SQ SEQUENCE 26 AA: 2667 MW: 111636.98636004 CRC64.

Query Match      81.8% Score 9; DR 1; Length 26;
Best Local Similarity 66.7%; Pred. No. 8e+02;
Matches 2; Conservative 0; Mismatches 1; Gaps 0.

QY 1 LXR 3
DB 22 LXR 24

RESULT 16
YFHA_KLEFN
ID YFHA_KLEFN STANDARD; PRT; 26 AA.
AC P21710;
DT 01-MAY-1991 (rel. 18, Created)
DT 01-MAY-1991 (rel. 18, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hydrophobic protein in GNR 5' region (Fragment).
GN YFHA.
OS Klebsiella pneumoniae.
CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Klebsiella.
CX NCBI_TaxID=574;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=M5a1;
RX MEDLINE 89201233; PubMed-2907369;
RA Hotell A., Merrick M.;
RA "Identification of the Klebsiella pneumoniae alk genes: nucleotide
RA sequence of wild-type and mutant alleles.*"
RL Mol. Gen. Genet. 215:134-138(1988).
CC 1- FUNCTION: PROBABLE MEMBER OF A TWO COMPONENT REGULATORY SYSTEM
CC YFHA/YFHK.
CC 1- PTE: PHOSPHORYLATED BY YFHK (POTENTIAL).
CC 1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC REGULATORY DOMAINS OF SENSOR TRANSDUCTION SYSTEMS.
CC 1- SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA 54 FACTOR
CC INTERACTION AND BINDING DOMAIN.
CC 1- SIMILARITY: TO EQUIVALENT PROTEIN IN E. COLI.

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CC -----
DR EMRL: X14012; CAA32176.1; -.
DR PIR: S04376; S04376.
DR InterPro: IPR002078; Sig54_interact.
DR PROSITE: PS00675; SIGMA54_INTERACT_1; PARTIAL.
DR PROSITE: PS00676; SIGMA54_INTERACT_2; PARTIAL.
DR PROSITE: PS00698; SIGMA54_INTERACT_3; PARTIAL.
DR PROSITE: PS00695; SIGMA54_INTERACT_4; PARTIAL.
KW Hypothetical protein, sensory transduction, phosphorylation,
KW transcription regulation, DNA-binding, ATP-binding.
FT NON_TER 1
FT SEQUENCE 26 AA; 3198 MW; 510C88BA443BF0C5 CRC64,
SQ SEQUENCE 26 AA; 3198 MW; 510C88BA443BF0C5 CRC64,

Query Match 81.8%; Score 9; DB 1; Length 26;
Best local Similarity 56.7%; Pred. No. gaps 0;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 14 LSR 16

RESULT 17
CXKR_CONFA
ID CXKR_CONFA STANDARD; PRT; 27 AA.
AC P58806;
DI 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Conantokin-R (Con-R).
OS Conus radiatus (Rayed cone).
OC Eukaryota, Metazoa, Mollusca, Gastropoda, Caudofoveata,
OC Nectogastropoda, Conidae, Conidae, Conus.
OX NCBI_TaxID=61198;
FN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RC MEDLINE=20072842; PubMed=10604979;
RA White H S., McCabe P.T., Armstrong H., Doneran S.D., Cruz L.J.,
RA Abogadie F.C., Torres J., Rivier J.E., Paarmann I., Hollmann M.,
RA Olivera B.M.;
RT "In vitro and in vivo characterization of conantokin R, a selective
RT NMDA receptor antagonist isolated from the venom of the fish-hunting
RL snail Conus radiatus."
RL J. Pharmacol. Exp. Ther. 292:425-432(2000).
CC -!- FUNCTION: Induces sleep-like symptoms in young mice. Inhibits
CC N-methyl-D-aspartate (NMDA) receptor-mediated calcium influx in
CC central nervous system neurons.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=3098.
CC -!- SIMILARITY: BELONGS TO THE CONANTOKIN FAMILY.
KW Toxin; Vitamin K; Gamma-carboxyglutamic acid; Calcium.
FT DISULFID 21 25
FT MOD_RES 3 3 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 11 11 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
FT SEQUENCE 27 AA; 292; MW; 25520AA744B2B453 CRC64.

Query Match 81.8%; Score 9; DB 1; Length 27;
Best local Similarity 56.7%; Pred. No. gaps 0;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 14 LSR 16

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DB 12 LAR 14
RESULT 18
SECR_CONFA
ID SECR_CONFA STANDARD; PRT; 27 AA.
AC P20447;
DI 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Secretin.
GN Secretin.
OS Canis familiaris (Dog).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
OX NCBI_TaxID=9615;
FN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RC MEDLINE=87314204; PubMed=626755;
RA Shimomura Y., Iino J., Yalow R.S.;
RT "Effect of secretin, secretin and secretin analogs on
RT the secretin-stimulated formation of NADPH(+) RICH PANCREATIC JUICE
CC -!- FUNCTION: STIMULATES FORMATION OF NADPH(+) RICH PANCREATIC JUICE
CC AND SECRETION OF NADPH(+) RICH BILE AND INHIBITS BIL. PRODUCTION
CC BY THE STOMACH.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR: A27267; A27267.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00123; hormone2; 1.
DR PRINTS: PR00275; GLUCAGON.
DR SMART: SM00670; GLUC_A; 1.
DR PROSITE: PS00269; GLUCAGON; 1.
KW Glucagon family, Hormone, Amidation.
FT MOD_RES 27 27 AMIDATE N.
FT SEQUENCE 27 AA; 3376 MW; 2540158147955B78 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 27;
Best local Similarity 56.7%; Pred. No. gaps 0;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 10 LSR 12

RESULT 19
SECR_RABIT
ID SECR_RABIT STANDARD; PRT; 27 AA.
AC P20447;
DI 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Secretin.
GN Secretin.
OS Cryptolagus cuniculus (Rabbit).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Lagomorpha, Leporidae, Cryptolagus.
OX NCBI_TaxID=9980;
FN [1]
RP SEQUENCE.
RC TISSUE=Small Intestine;
RC MEDLINE=60259941; PubMed=2412988;
RA Gasser D., Buscail L., Gaudin A., Gourlet P., de Neef P., Rathe J.,
RA Robberecht P., Vandemeers P., M.C., Vandemeers A., Christophe J.,
RA "Amino acid sequence of VIP, PHI and secretin from the rabbit small
RT intestine."
RT Peptides 11:123-128(1990).
CC -!- FUNCTION: STIMULATES FORMATION OF NADPH(+) RICH PANCREATIC JUICE
CC AND SECRETION OF NADPH(+) RICH BILE AND INHIBITS BIL. PRODUCTION
CC BY THE STOMACH.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

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DR PIR: C60415; C60415.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00124; Hormone2; 1.
DR PRINTS: PR00275; GLUCAGN.
DR SMART: SM00070; GLUCA; 1.
DR PROSITE: PS00260; GLUCAGN; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 4105 MW; 8BA01580004D5618 CR664;

Query Match 81.8% Score 9; DB 1; Length 27;
Best Local Similarity 66.7%; Pred. No. 9; 3e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 10 LSR 12

RESULT 20
SECR_SHEEP
ID SECR_SHEEP STANDARD; PRT; 27 AA.
AC P31299;
DT 01-JUL-1993 (rel. 26, Created)
DI 01-JUL-1993 (rel. 26, Last annotation update)
DE Secretin.
GN SCT.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID 9940;
RN 1;
RP SEQUENCE.
RC FLSSDE Small intestine;
RX MEDLINE 91239834; PubMed 2034421;
RA Raminjona Y., Vandermiers A., Rohberecht P., Vandermiers-Piret M.C.,
RA Christophe J.;
RT "Purification and amino acid sequence of vasoactive intestinal
RT peptide, peptide histidine isoleucineamide and secretin from the ovine
RT small intestine.";
RC Regal. Pept. 32:169-179(1991).
CC -1- FUNCTION: STIMULATES FORMATION OF NAUSEA(1) RICH PANCREATIC JUICE
CC AND SECRETION OF NAUSEA(2) RICH BILE ACID INHIBITS BIL. PRODUCTION
CC BY THE STOMACH.
CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR: C60072; SESH.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00124; Hormone2; 1.
DR PRINTS: PR00275; GLUCAGN.
DR SMART: SM00070; GLUCA; 1.
DR PROSITE: PS00260; GLUCAGN; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 4056 MW; 2D4015814ED95878 CR664;

Query Match 81.8% Score 9; DB 1; Length 27;
Best Local Similarity 66.7%; Pred. No. 9; 3e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 10 LSR 12

RESULT 21
VIT04_VACCH
ID VIT04_VACCH STANDARD; PRT; 28 AA.
AC 900434;
DT 01 APR 1993 (rel. 25, Created)
DI 01 APR 1993 (rel. 25, Last sequence update)
DE
FT 01 APR 1993 (rel. 25, Last annotation update)
DE 01 FEB 1994 (rel. 28, Last annotation update)

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DE Protein 13 (Fragment).
GN 13L.
OS Vaccinia virus (strain L-1VP).
CC Viruses; dsDNA viruses; ds DNA virus; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
OX NCBI_TaxID 31531;
RN 1;
RP SEQUENCE FROM H.A.
RX MEDLINE 91066899; PubMed 2250685;
RA Ryazanova O.I., Shchegoleva S.N., Mordukhai A.I., Nesterova N.A.,
RA Vityayeva N.H., Gerasimov V.V., Gerasimov A.P., Koltchikov V.A.;
RA Malygin E.G.;
RT "Molecular-biological study of vaccinia virus genome, II.
RT Localization and nucleotide sequence of vaccinia virus genes coding
RT for proteins 46K and 12K.";
RC Mol. Biol. (Mosk) 24:968-976(1990).
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
CC THE LATE PHASE OF INFECTION.
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CC
DR EMBL: X61165; CAA43473.1;
DR FIC: PS0395; PS0395.
KW Early protein; Late protein.
FT NON_TER 1 1
SQ SEQUENCE 28 AA; 3248 MW; CE10813AC544F010 CR664;

Query Match 81.8% Score 9; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 6; 5e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 2 LAR 4

RESULT 22
HSP98_HSP98
ID HSP98_HSP98 STANDARD; PRT; 29 AA.
AC P31540;
DI 01-JUL-1993 (rel. 26, Created)
DI 01-JUL-1993 (rel. 26, Last sequence update)
DI 01-JUL-1993 (rel. 26, Last annotation update)
DE Heat shock protein HSP98 (Fragment).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID 5141;
RN 1;
RP SEQUENCE.
RC STRAIN-74A;
RX MEDLINE 94112646; PubMed 1472534;
RA Vassiliev A.G., Pleasovsky V.I., Ruzicki R.;
RT "Isolation, partial amino acid sequence, and cellular distribution of
RT heat-shock protein hsp98 from Neurospora crassa.";
RC Biochim. Biophys. Acta 1196:1-6(1992).
CC -1- SUBCELLULAR LOCATION: MORE CONCENTRATED IN POLYMERIZABLES THAN
CC IN MONOMERIZABLES, AND PREFERENTIALLY LOCALIZED IN THE LARGE
CC SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE CLPAA/CLPB FAMILY.
DR PIR: S28174; S28174.
DR InterPro: IPR001270; Claparin_c1pA/B.
DR PROSITE: PS00870; CLPAB_1; 1.
DR PROSITE: PS00871; CLPAB_2; PARTIAL.
KW Chaperone; Heat shock; ATP-binding.
FT NON_TER 1 1
FT NON_TER 29 29

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QY SEQUENCE 29 AA: 3194 MW: 514105988129196000
 Query Match 81.8%; Score 9; DB 1; Length 29;
 Best Local Similarity 66.7%; Pred. No. 10000;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 QY 1 LXR 3
 DB 11 LAR 13
 RESULT 23
 Y51_RPT3
 ID Y51_RPT3 STANDARD; PRT; 29 AA.
 AC P20326.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Hypothetical gene 5.1 protein
 GN 5.1.
 OS Bacteriophage T3.
 OC Viruses; dsDNA viruses, no RNA stage, Caudovirales, P4-like viruses;
 OC T3-like viruses.
 OX NCBI_TaxID=10759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Luria;
 RX MEDLINE:90132923; PubMed:2614842;
 RA Beck P.J., Gonzalez S., Ward G.L., Molinoux J.J.;
 RT "Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.5";
 RL J. Mol. Biol. 210:687-701(1989).
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X17255; CAA35142.1; -
 DR PIR: S07513; S07513.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 29 AA: 3229 MW: 77827995617773477634.
 Query Match 81.8%; Score 9; DB 1; Length 29;
 Best Local Similarity 66.7%; Pred. No. 10000;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 QY 1 LXR 3
 DB 20 LIP 22
 RESULT 24
 D10X_D10PP
 ID D10X_D10PP STANDARD; PRT; 31 AA.
 AC P82372;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diuretic hormone class II (diuretic peptide) (DP) (DH(31)).
 OS Diptera punctata (Pacific beetle cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Panchalana; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthoptera; Grylloptera; Blattaria;
 OC Blaberidae; Blaberidae; Diptera
 OX NCBI_TaxID=6984;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Brain, and Corpora cardiaca;
 RX MEDLINE:20300924; PubMed:10841553;
 RA Furuya K, Mitsuoka F, Schragg K.M., Zhang J., Take S.S., Coast G.M.,
 RA Schooley D.A.;

RT "Diuretic hormone class II (diuretic peptide) (DP) (DH(31)).
 RL Proc. Rati. Acad. Sci. U.S.A. 97:6469-6474(2000).
 CC FUNCTIONAL REGULATION OF FLUID SECRETION. STIMULATES PRIMARY URINE
 CC SECRETION BY MALE RATTUS TORPENS 726. TAKES A DOSE-DEPENDENT
 CC STIMULATION OF CAMP LEVELS IN THE TUBULES. HAS A NONSELECTIVE
 CC EFFECT ON NA+/K+ P-ATPase. IN VITRO, FAIRLY HIGHLY REVEALS
 CC INTRACELLULAR CA2+. HAS SYNERGISTIC EFFECTS WITH THE LARGER
 CC DIURETIC HORMONE DH(46) WHICH CO-OCCURS WITH IT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW:2087; MWERR 0.2; METHOD: Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE DIURETIC HORMONE CLASS II FAMILY.
 KW Hormone; Amidation.
 FT M94_PES 31 AMIDATION.
 SQ SEQUENCE 31 AA: 2089 MW: 353118726211846 CRO64;
 Query Match 81.8%; Score 9; DB 1; Length 31;
 Best Local Similarity 66.7%; Pred. No. 10000;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 QY 1 LXR 3
 DB 6 LSR 8
 RESULT 25
 LYC2_HORSE
 ID LYC2_HORSE STANDARD; PRT; 33 AA.
 AC P01710;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-JUN-2002 (Rel. 41, Last annotation update)
 DE Glycoprotein C, spleen iso., me (EC 3.2.1.17) (2.3 beta N-acetylglucosidase
 DE C) (Fragment).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE:94361523; PubMed:8080284;
 RA Grobler J.A., Rao K.R., Parvaz S., Brow K.J.
 DT "Sequences of two highly divergent canine type C glycosylases:
 DT implications for the evolutionary origins of the glycoprotein alpha-
 DT lactalbumin superfamily".
 RL Arch. Biochem. Biophys. 313:360-366(1994).
 CC -1- FUNCTION: Glycosylates proteins, primarily at Asn-linked function; those
 CC in tissues and body fluids are associated with the monocyte
 CC macrophage system and enhance the activity of immunogens (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4 beta linkages between N-
 CC acetyl-D-glucosamine and N-acetylglucosamine acid in peptidoglycan
 CC heteropolymers of the prokaryotes cell walls.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- MISCELLANEOUS: Glycosylase is capable of both hydrolysis and
 CC transglycosylation. It shows also a slight esterase activity. It
 CC acts rapidly on both peptide-substituted and unsubstituted
 CC peptidoglycan, and slowly on chitin oligosaccharides (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 DR HSP: P00595; LYAN.
 DR InterPro: IPR001916; GH_22.
 DR Pfam: PF00062; Iys_1.
 DR PEST: PEST008; LACTALBUMIN_LYSOZYME; PARTIAL.
 KW Glycolase; Glycosylase; Bacteriophage; Bacteriophage family.
 FT M94_PES 33
 SQ SEQUENCE 33 AA: 3742 MW: 785088640551194 CRO64;
 Query Match 81.8%; Score 9; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 10000;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

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QY      1 LXR 3
      1 1
Db      8 LAR 10

RESULT 26
OTCC_PSEPH STANDARD; PRT: 33 AA.
AC P11727;
Dt 01-01-1989 (Rel. 12, Last sequence update)
Dt 15-JUN-2002 (Rel. 41, Last annotation update)
DE ornithine carbamoyltransferase, catalytic (EC 2.3.3.1) (Fragment).
DE (Fragment).
GN Pseudomonas putida.
OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID:404;
RN 11
RP SEQUENCE.
RX MEDLINE:85104799; PubMed:3968046;
RA Falmagne P., Portetelle D., Stalon V.
RT "Immunological and structural relatedness of catabolic ornithine
carbamoyltransferases and the metabolic enzymes of enterobacteria."
J. Bacteriol. 161:714-719(1985).
RN 12
RP SEQUENCE OF 112 FROM N.A.
RC STRAIN ATCC 4459;
RA Wilson S.D., Wand M., Filpula D.;
RT Submitted (Feb-1994) to the EMBL/GenBank/CCP Data Bank
KW CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine
phosphate
+ L-citrulline.
CC -1- PATHWAY: Arginine degradation via arginine deiminase; second step.
CC -1- SUBUNIT: PREVIOUSLY 2-PARAMETER 2K P-DECEMBER90.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ATCASES/GOTASES FAMILY.
CC
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entire require a license agreement (See http://www.ebi.ac.uk/edl/terms)
or send an email to license@isb.sib.ch).
EMBL: 007185; AAA16965.1; -
DR PIR: D21897; D21897.
DR BSSP: P08408; L08T.
DR InterPro: IPR002029; Asp/Gln-Contant.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT INIT_MET 0 0
FT NON_TER 33 33
SQ SEQUENCE 33 AA: 4916 MW: 544806.342 P2:Q87 CRG64;

Query Match 81.8% Score 9; DB 1; Length 33;
Best Local Similarity 66.7% Pred. No. 16-03;
Matches 2; Conservatio 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LXR 3
      1 1
Db      26 LAR 28

RESULT 27
PKL_BICDI STANDARD; PRT: 33 AA.
AC P4401;
Dt 01-FEB-1994 (Rel. 28, Created)
Dt 01-FEB-1994 (Rel. 28, Last sequence update)
Dt 16-MAY-2001 (Rel. 40, Last annotation update)
DE Protein kinase 1 (EC 2.7.1.1) (Fragment).
DE

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DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Pancreatic hormone (pancreatic polypeptide) (PP).
 GN *Chinchilla brevicauda* (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Cystodonta; Chinchillidae;
 OC Chinchilla.
 CX NCBI_TaxID=10152;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pancreas;
 RX MEDLINE 9104537, PubMed 2356678;
 RA Eng J., Kleiman W.A., Chu L.S.;
 RT "Purification of peptide hormones from chinchilla pancreas by
 chemical assay."
 RL Peptides 11:683-685(1990).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NPV / PPV / PYY FAMILY
 PIR: P60413; B60413.
 DR HSSP: P01302; IBB.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3; 1.
 DR PRINTS: PR0278; PANCHORMON.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4215 MW; 761B717670E3309F CRC64;

 Query Match 81.8%; Score 9; DR 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,le=04;
 Matches 2, Conservative 0, Mismatches 1, Indels 0, Gaps 0.

 QY 1 LXR 3
 DB 31 LTR 33

 RESULT 25
 PAHO_DIDMA STANDARD; PRT; 36 AA.
 AC P18107;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (Pancreatic polypeptide) (PP).
 GN PPV.
 OS *Didelphis marsupialis virgata* (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphus.
 CX NCBI_TaxID=9267.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pancreas;
 RX MEDLINE 9016042; PubMed 2645899;
 RA Yu J.-H., Eng J., Rattan S., Yalow R.S.;
 RT "Opossum insulin, glucagon and pancreatic polypeptide: amino acid
 sequences."
 RL Peptides 10:1195-1197(1989).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NPV / PPV / PYY FAMILY.
 PIR: JQ0365; JQ0365.
 DR HSSP: P01302; IBB.
 DR InterPro: IPR001955; Pancreatic_horm.

DR Pfam: PF00159; hormone3; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_1; 1.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_2; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4215 MW; 761B717670E3309F CRC64;

 Query Match 81.8%; Score 9; DR 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,le=04;
 Matches 2, Conservative 0, Mismatches 1, Indels 0, Gaps 0.

 QY 1 LXR 3
 DB 31 LTR 33

 RESULT 36
 PAHO_EUZE STANDARD; PRT; 36 AA.
 AC P48000;
 DT 01-OCT-1994 (Rel. 40, Created)
 DT 01-OCT-1994 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPV.
 OS *Equus zebra* (Mountain zebra), and
 OS *Equus caballus przewalskii* (Przewalski's horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID 9791, 9798.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pancreas;
 EX MEDLINE 9225511; PubMed 1839025;
 RA Brady J.D., Lamber V.A., Gordon J.M.;
 RT "Primary structure of pancreatic polypeptide from four species of
 Perissodactyla (Przewalski's horse, zebra, rhino, tapir)."
 RL Can. Comp. Endocrinol. 84:440-446(1991).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NPV / PPV / PYY FAMILY.
 PIR: A61132; A61132.
 DR PIR: D61132; D61132.
 DR HSSP: P01302; IBB.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3; 1.
 DR PRINTS: PR0278; PANCHORMON.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4215 MW; 761B717670E3309F CRC64;

 Query Match 81.8%; Score 9; DR 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,le=04;
 Matches 2, Conservative 0, Mismatches 1, Indels 0, Gaps 0.

 QY 1 LXR 3
 DB 31 LTR 33

 RESULT 37
 PAHO_EUZE STANDARD; PRT; 36 AA.
 AC P41335;
 DT 01-FEB-1995 (Rel. 41, Created)
 DT 01-FEB-1995 (Rel. 41, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update).
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPT.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
 OX NCBI_TaxID 9465;
 RN [1]
 RP SEQUENCE.
 RC TISSUE: Pancreas;
 EC MEDLINE: 94052825; PubMed: 8244904;
 RA Marks N.J., Shaw C., Hulton D.W., Thim L.;
 RT "The primary structure of pancreatic polypeptide from a primitive
 insectivorous mammal, the European hedgehog (Erinaceus europaeus).";
 RL Regul. Pept. 47:179-185(1993).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PPV / PPT / PYY FAMILY
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3_1.
 DR PRINTS: PR00278; PANCHORMONE.
 DR SMART: SM00309; hormone3_1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 46; 46. AMIDATION.
 SQ SEQUENCE 46 AA; 4234 MW; 76095599148269F CRC64.

 Query Match 81.8%; Score 9; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 4
 DB 31 LTR 33

 RESULT 48
 ID PAHO_MACMU STANDARD; PRT; 46 AA.
 AC P33684;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPT.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Primates; Catarrhini; Cercopithecoidea;
 OX NCBI_TaxID 9544;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE: 91164506; PubMed: 2003150;
 RA Yu J., Xie Y., Edd J., Yalow R.S.;
 RT "Rhesus monkey gastroenteropancreatic hormones: relationship to human
 sequences.";
 RL Regul. Pept. 32:49-55(1991).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PPV / PPT / PYY FAMILY
 DR PIR: C60071; C60071.
 DR BSSP: P01302; 1BBA.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3_1.
 DR PRINTS: PR00278; PANCHORMONE.
 DR SMART: SM00309; hormone3_1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 46; 46. AMIDATION.
 SQ SEQUENCE 46 AA; 4198 MW; 761110671A6-08F CRC64;

 Query Match 81.8%; Score 9; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 4
 DB 31 LTR 33

 RESULT 49
 ID PAH_RABIT STANDARD; PRT; 46 AA.
 AC P41346;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPT.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID 9986;
 RN [1]

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suis.
 OX NCBI_TaxID 9823;
 RN [1]
 RP SEQUENCE.
 RA Chance R.E., Johnson M.S., Hollmann J.A., Lin L. M.;
 RL (in) Baba S., Kaneko I., Yamahara N. (eds.);
 RL "Proinsulin, insulin, c-peptide, pp.419-425, Excerpta Medica,
 Amsterdam (1979)."
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PPV / PPT / PYY FAMILY.
 DR PIR: A01568; PPI1.
 DR BSSP: P01302; 1BBA.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3_1.
 DR PRINTS: PR00278; PANCHORMONE.
 DR SMART: SM00309; PPT; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36; 36. AMIDATION.
 SQ SEQUENCE 46 AA; 4198 MW; 761110671A6-08F CRC64;

 Query Match 81.8%; Score 9; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 4
 DB 31 LTR 33

 RESULT 40
 ID PAH_PIG STANDARD; PRT; 46 AA.
 AC P01300;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPT.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suis.
 OX NCBI_TaxID 9823;
 RN [1]
 RP SEQUENCE.
 RA Chance R.E., Johnson M.S., Hollmann J.A., Lin L. M.;
 RL (in) Baba S., Kaneko I., Yamahara N. (eds.);
 RL "Proinsulin, insulin, c-peptide, pp.419-425, Excerpta Medica,
 Amsterdam (1979)."
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PPV / PPT / PYY FAMILY.
 DR PIR: A01568; PPI1.
 DR BSSP: P01302; 1BBA.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3_1.
 DR PRINTS: PR00278; PANCHORMONE.
 DR SMART: SM00309; PPT; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36; 36. AMIDATION.
 SQ SEQUENCE 46 AA; 4198 MW; 761110671A6-08F CRC64;

 Query Match 81.8%; Score 9; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 4
 DB 31 LTR 33

 RESULT 40
 ID PAH_RABIT STANDARD; PRT; 46 AA.
 AC P41346;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPT.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID 9986;
 RN [1]


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RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94130533; PubMed=8299350;
RA Marks N.J., Shaw C., Halton D.W., Curry W.J., Thim L.;
RI "Rabbit pancreatic polypeptide."
RL Comp. Biochem. Physiol. 106B:883-887(1993).
CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANCERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PPV / PYY / PYY FAMILY.
DR HSSP: P01302; IPIA.
DR InterPro: IPR001955; Pancreatic_hormn.
DR Pfam: PF00159; hormone3; 1.
DR PRINTS: PR00278; PANCCHORMONE.
DR SMART: SM00309; PAH; 1.
DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
DR Hormone: Amidation; Pancreas.
KW MOD_RES 36
FT MOD_RES 36
SQ SEQUENCE 36 AA; 4197 MW; A14M192831A7759D CRC64;

Query Match 81.8%; Score 9; DB 1; Length 36;
Best local Similarity 66.7%; Pred. No. 1; Ltr 33;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

CY 1 LXR 3
DB 1 LTR 33

RESULT 41
PANO_TAPPI
ID PAHO_TAPPI STANDARD; PRT; 36 AA.
AC P39559;
DT 01-OCT-1994 (rel. 30, Created)
DI 01-OCT-1994 (rel. 30, Last sequence update)
DI 16-OCT-2001 (rel. 40, Last annotation update)
DE Pancreatic hormone (pancreatic polypeptide) (PP).
GN PPY.
OS Tapirus pinchoue (Mountain tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=30582;
RN 1
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=92225314; PubMed=1808025;
RA Henry J.S., Lance V.A., Conlon J.M.;
RI "Primary structure of pancreatic polypeptide from four species of
RI Perissodactyla (Perissodactyla: Equidae, Equus, Equus)."
RL Gen. Comp. Endocrinol. 84:440-446(1991).
CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANCERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PPV / PYY / PYY FAMILY.
DR HSSP: P01302; IPIA.
DR InterPro: IPR001955; Pancreatic_hormn.
DR Pfam: PF00159; hormone3; 1.
DR PRINTS: PR00278; PANCCHORMONE.
DR SMART: SM00309; PAH; 1.
DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
DR Hormone: Amidation; Pancreas.
KW MOD_RES 36
FT MOD_RES 36
SQ SEQUENCE 36 AA; 4197 MW; 761B717671A6308F CRC64;

Query Match 81.8%; Score 9; DB 1; Length 36;
Best local Similarity 66.7%; Pred. No. 1; Ltr 33;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

CY 1 LXR 3
DB 1 LTR 33

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Db 1 LTR 33

RESULT 42
PYY_AMICA
ID PYY_AMICA STANDARD; PRT; 36 AA.
AC P29205;
DT 01-DEC-1992 (rel. 24, Created)
DI 01-DEC-1992 (rel. 24, Last sequence update)
DI 15-JUN-2002 (rel. 41, Last annotation update)
DE Peptide YY 1-like (PYY).
GN PYY.
OS Ania calva (Bowlin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amniotes; Anillidae; Ania.
OX NCBI_TaxID=7724;
RN 1
RP SEQUENCE.
RC TISSUE=Pancreas;
FX MEDLINE=9296574; PubMed=2067473;
RA Conlon J.M., Bjornling C., Moon T.W., Yonson J.H., Thim L.;
RI "Neuropeptide Y related peptides from the pancreas of a teleostean
RI (eel), teleostean (koi) and elasmobranch (skate) fish."
RL Peptides 1:221-226(1991).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PPV / PYY / PYY FAMILY.
DR HSSP: P01303; IPIA.
DR InterPro: IPR001955; Pancreatic_hormn.
DR Pfam: PF00159; hormone3; 1.
DR PRINTS: PR00278; PANCCHORMONE.
DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
DR Hormone: Amidation.
KW MOD_RES 36
FT MOD_RES 36
SQ SEQUENCE 36 AA; 4133 MW; 56B4614308060611 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 36;
Best local Similarity 66.7%; Pred. No. 1; Ltr 0;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

CY 1 LXR 4
DB 1 LTR 19

RESULT 43
PYY_PIG
ID PYY_PIG STANDARD; PRT; 36 AA.
AC P01305;
DT 21-JUL-1986 (rel. 01, Created)
DI 21-JUL-1986 (rel. 01, Last sequence update)
DI 16-OCT-2001 (rel. 40, Last annotation update)
DE Peptide YY (PYY) (Peptide tyrosine tyrosine).
GN PYY.
OS Sus scrofa (Pig), and
OS Sus scrofa (Pig), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Canidae; Sus.
OX NCBI_TaxID=9824; 9615;
RN 1
RP SEQUENCE.
RC SPECIES=Pig;
RX MEDLINE=8222168; PubMed=4954409;
RA Tatamoto K.;
RI "Isolation and characterization of peptide YY (PYY), a candidate gut
RI hormone that inhibits pancreatic secretions."
RL J. Biol. Chem. 267:7523-7526(1992).
GN PYY.
KW MOD_RES 36
FT MOD_RES 36
SQ SEQUENCE.
RC SPECIES=Canis familiaris;

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RX MEDLINE 9025984; PubMed 2442986;
 RA Eysselein V.E., Eborlein G.A., Grand D., Schaeffer M., Zehres B.,
 Rein U., Schaeffer D., Goebel H., Davis M., Lee T.D., Shively J.E.,
 Meyer H.E., Kooze J.K., Jr.;
 RI "Structural characterization of canine PYY."
 RL Inptides 11:111-116(1990).
 CC -1 FUNCTION: THIS GDI PERTHSE INHIBITS EXCITATORY SECRETION,
 CC HAS A VASOCONSTRICTORY ACTION AND INHIBITS JEJUNAL AND COLONIC
 CC MOTILITY.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 SIMILARITY: Ref: 1; DB 1; Length 46;
 DR PIR: A01574; YYPG.
 DR PIR: A60416; A60416.
 DR BSSP: P01403; IRON.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3; 1.
 DR PRINTS: PK0278; PANCIF-886-RE.
 DR ProDom: P0001267; Pancreatic_horm; 1.
 DR SMART: SM00309; PAR; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation.
 FT MOD_RES 36
 SQ SEQUENCE 36 AA: 4242 89% 5255386C586JCC8D CRG64.
 Query Match 81.8%; Score 9; DB 1; Length 46;
 Best Local Similarity 66.7%; Pred. No. 1,2e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 4
 DB 17 LSR 19
 RESULT 44
 CGRP_PIG
 ID CGRP_PIG STANDARD PRT 47 AA.
 AC P00880;
 DT 01 JUL 1993 (Ref. 26, Created)
 DT 01 JUL 1993 (Ref. 26, Last sequence update)
 DT 15 JUL 1998 (Ref. 36, Last annotation update)
 DE Calcitonin gene-related peptide (CGRP).
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID 9823;
 RN 111
 RP SEQUENCE.
 RX MEDLINE 87174481; PubMed 4494209;
 RA Kimura S., Saito Y., Kanazawa T., Saito A., Goto K.;
 RI "Isolation and amino acid sequence of calcitonin gene related peptide
 RI from porcine spinal cord."
 RL Neuropeptides 9:75-82(1987).
 CC -1 FUNCTION: CGRP INDUCES VASODILATION. IT ELICITS A VARIETY OF
 CC VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE.
 CC ITS AGONISMS IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR
 CC NEUROMODULATOR ROLE.
 CC -1 SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 DR InterPro: IPR001693; Calcitonin-like.
 DR InterPro: IPR002163; Calcitonin_R.
 DR Pfam: PF00214; Calc_CGRP_LIAPP; 1.
 DR PRINTS: PK00817; CALCITONIN_R.
 DR SMART: SM00113; CALCITONIN; 1.
 DR PROSITE: PS00258; CALCITONIN; 1.
 DR Amidation; Hormone.
 FT DISULFID 2 7
 FT MOD_RES 47 47
 SQ SEQUENCE 47 AA: 4314 89% 5470380243B44A CRG64.
 Query Match 81.8%; Score 9; DB 1; Length 47;
 Best Local Similarity 66.7%; Pred. No. 1,2e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 4
 DB 16 LSR 18
 RESULT 45
 CGRP_RANR1
 ID CGRP_RANR1 STANDARD PRT 47 AA.
 AC P41888;
 DT 01 JUL 1993 (Ref. 26, Created)
 DT 01 JUL 1993 (Ref. 26, Last sequence update)
 DT 15 JUL 1998 (Ref. 36, Last annotation update)
 DE Calcitonin gene-related peptide (CGRP).
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
 OX NCBI_TaxID-8406;
 RN 111
 RP SEQUENCE.
 RX MEDLINE 6224452; PubMed 8442553;
 RA Coulon J.M., Tonon M.-C., Vaudry H.;
 RI "Isolation and structural characterization of calcitonin gene-related
 RI peptide from the brain and intestine of the frog, Rana ridibunda."
 RL Peptides 14:581-586(1993).
 CC -1 FUNCTION: CGRP INDUCES VASODILATION. IT ELICITS A VARIETY OF
 CC VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE.
 CC ITS AGONISMS IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR
 CC NEUROMODULATOR ROLE.
 CC -1 SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 DR InterPro: IPR001693; Calcitonin-like.
 DR InterPro: IPR002163; Calcitonin_R.
 DR Pfam: PF00214; Calc_CGRP_LIAPP; 1.
 DR PRINTS: PK00817; CALCITONIN_R.
 DR SMART: SM00113; CALCITONIN; 1.
 DR PROSITE: PS00258; CALCITONIN; 1.
 DR Amidation; Hormone.
 FT DISULFID 2 7
 FT MOD_RES 47 47
 SQ SEQUENCE 47 AA: 4889 89% 50002746RDE CRG64.
 Query Match 81.8%; Score 9; DB 1; Length 47;
 Best Local Similarity 66.7%; Pred. No. 1,2e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 4
 DB 16 LSR 18

Search completed: April 30, 2003, 13:44:42
 Job time : 16.0909 secs

90	9	81.8	15	16	Q9X144	Q9X144 salmonella	163	9	81.8	22	14	Q91105	Q91105 morone saxa
91	9	81.8	16	2	Q9K414	Q9K414 pseudomonas	164	9	81.8	22	14	Q91106	Q91106 morone saxa
92	9	81.8	16	2	Q9K410	Q9K410 trypanosoma	165	9	81.8	22	14	Q91107	Q91107 morone saxa
93	9	81.8	16	6	Q91R05	Q91R05 bos taurus	166	9	81.8	22	14	Q91108	Q91108 morone saxa
94	9	81.8	16	7	Q91R05	Q91R05 bos taurus	167	9	81.8	23	2	Q92232	Q92232 morone saxa
95	9	81.8	16	7	Q91R05	Q91R05 morone saxa	168	9	81.8	23	5	Q96705	Q96705 trypanosoma
96	9	81.8	16	7	Q91R05	Q91R05 morone saxa	169	9	81.8	23	5	Q96707	Q96707 trypanosoma
97	9	81.8	16	12	Q91R05	Q91R05 morone saxa	170	9	81.8	23	5	Q94781	Q94781 trypanosoma
98	9	81.8	17	4	Q91R05	Q91R05 morone saxa	171	9	81.8	23	5	Q95162	Q95162 morone saxa
99	9	81.8	17	10	Q9R854	Q9R854 lithocarpus	172	9	81.8	23	5	Q95135	Q95135 morone saxa
100	9	81.8	17	10	Q94F00	Q94F00 arabidopsis	173	9	81.8	23	5	Q95136	Q95136 morone saxa
101	9	81.8	18	4	Q90E58	Q90E58 morone saxa	174	9	81.8	23	5	Q95139	Q95139 morone saxa
102	9	81.8	18	4	Q90E58	Q90E58 morone saxa	175	9	81.8	23	11	Q96137	Q96137 morone saxa
103	9	81.8	18	7	Q90E58	Q90E58 morone saxa	176	9	81.8	23	12	Q96495	Q96495 morone saxa
104	9	81.8	18	13	Q90E58	Q90E58 morone saxa	177	9	81.8	23	12	Q96496	Q96496 morone saxa
105	9	81.8	18	15	Q90E58	Q90E58 morone saxa	178	9	81.8	23	12	Q96497	Q96497 morone saxa
106	9	81.8	18	15	Q90E58	Q90E58 morone saxa	179	9	81.8	23	12	Q96498	Q96498 morone saxa
107	9	81.8	18	15	Q90E58	Q90E58 morone saxa	180	9	81.8	23	12	Q96499	Q96499 morone saxa
108	9	81.8	18	15	Q90E58	Q90E58 morone saxa	181	9	81.8	23	12	Q96500	Q96500 morone saxa
109	9	81.8	18	15	Q90E58	Q90E58 morone saxa	182	9	81.8	23	12	Q96501	Q96501 morone saxa
110	9	81.8	19	5	Q90E58	Q90E58 morone saxa	183	9	81.8	23	12	Q96502	Q96502 morone saxa
111	9	81.8	19	5	Q90E58	Q90E58 morone saxa	184	9	81.8	23	12	Q96503	Q96503 morone saxa
112	9	81.8	19	5	Q90E58	Q90E58 morone saxa	185	9	81.8	23	12	Q96504	Q96504 morone saxa
113	9	81.8	19	5	Q90E58	Q90E58 morone saxa	186	9	81.8	23	12	Q96505	Q96505 morone saxa
114	9	81.8	19	11	Q91R05	Q91R05 morone saxa	187	9	81.8	23	12	Q96506	Q96506 morone saxa
115	9	81.8	19	12	Q91R05	Q91R05 morone saxa	188	9	81.8	23	12	Q96507	Q96507 morone saxa
116	9	81.8	19	12	Q91R05	Q91R05 morone saxa	189	9	81.8	23	12	Q96508	Q96508 morone saxa
117	9	81.8	20	2	Q91R05	Q91R05 morone saxa	190	9	81.8	23	12	Q96509	Q96509 morone saxa
118	9	81.8	20	2	Q91R05	Q91R05 morone saxa	191	9	81.8	23	12	Q96510	Q96510 morone saxa
119	9	81.8	20	2	Q91R05	Q91R05 morone saxa	192	9	81.8	23	12	Q96511	Q96511 morone saxa
120	9	81.8	20	2	Q91R05	Q91R05 morone saxa	193	9	81.8	23	12	Q96512	Q96512 morone saxa
121	9	81.8	20	2	Q91R05	Q91R05 morone saxa	194	9	81.8	23	12	Q96513	Q96513 morone saxa
122	9	81.8	20	2	Q91R05	Q91R05 morone saxa	195	9	81.8	23	12	Q96514	Q96514 morone saxa
123	9	81.8	20	2	Q91R05	Q91R05 morone saxa	196	9	81.8	23	12	Q96515	Q96515 morone saxa
124	9	81.8	20	2	Q91R05	Q91R05 morone saxa	197	9	81.8	23	12	Q96516	Q96516 morone saxa
125	9	81.8	21	2	Q91R05	Q91R05 morone saxa	198	9	81.8	23	12	Q96517	Q96517 morone saxa
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127	9	81.8	21	2	Q91R05	Q91R05 morone saxa	200	9	81.8	23	12	Q96519	Q96519 morone saxa
128	9	81.8	21	2	Q91R05	Q91R05 morone saxa	201	9	81.8	23	12	Q96520	Q96520 morone saxa
129	9	81.8	21	2	Q91R05	Q91R05 morone saxa	202	9	81.8	23	12	Q96521	Q96521 morone saxa
130	9	81.8	21	2	Q91R05	Q91R05 morone saxa	203	9	81.8	23	12	Q96522	Q96522 morone saxa
131	9	81.8	21	2	Q91R05	Q91R05 morone saxa	204	9	81.8	23	12	Q96523	Q96523 morone saxa
132	9	81.8	21	2	Q91R05	Q91R05 morone saxa	205	9	81.8	23	12	Q96524	Q96524 morone saxa
133	9	81.8	21	2	Q91R05	Q91R05 morone saxa	206	9	81.8	23	12	Q96525	Q96525 morone saxa
134	9	81.8	21	2	Q91R05	Q91R05 morone saxa	207	9	81.8	23	12	Q96526	Q96526 morone saxa
135	9	81.8	21	2	Q91R05	Q91R05 morone saxa	208	9	81.8	23	12	Q96527	Q96527 morone saxa
136	9	81.8	21	2	Q91R05	Q91R05 morone saxa	209	9	81.8	23	12	Q96528	Q96528 morone saxa
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138	9	81.8	21	2	Q91R05	Q91R05 morone saxa	211	9	81.8	23	12	Q96530	Q96530 morone saxa
139	9	81.8	21	2	Q91R05	Q91R05 morone saxa	212	9	81.8	23	12	Q96531	Q96531 morone saxa
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142	9	81.8	21	2	Q91R05	Q91R05 morone saxa	215	9	81.8	23	12	Q96534	Q96534 morone saxa
143	9	81.8	21	2	Q91R05	Q91R05 morone saxa	216	9	81.8	23	12	Q96535	Q96535 morone saxa
144	9	81.8	21	2	Q91R05	Q91R05 morone saxa	217	9	81.8	23	12	Q96536	Q96536 morone saxa
145	9	81.8	21	2	Q91R05	Q91R05 morone saxa	218	9	81.8	23	12	Q96537	Q96537 morone saxa
146	9	81.8	21	2	Q91R05	Q91R05 morone saxa	219	9	81.8	23	12	Q96538	Q96538 morone saxa
147	9	81.8	21	2	Q91R05	Q91R05 morone saxa	220	9	81.8	23	12	Q96539	Q96539 morone saxa
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149	9	81.8	22	2	Q91R05	Q91R05 morone saxa	222	9	81.8	23	12	Q96541	Q96541 morone saxa
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152	9	81.8	22	2	Q91R05	Q91R05 morone saxa	225	9	81.8	23	12	Q96544	Q96544 morone saxa
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154	9	81.8	22	2	Q91R05	Q91R05 morone saxa	227	9	81.8	23	12	Q96546	Q96546 morone saxa
155	9	81.8	22	2	Q91R05	Q91R05 morone saxa	228	9	81.8	23	12	Q96547	Q96547 morone saxa
156	9	81.8	22	2	Q91R05	Q91R05 morone saxa	229	9	81.8	23	12	Q96548	Q96548 morone saxa
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159	9	81.8	22	2	Q91R05	Q91R05 morone saxa	232	9	81.8	23	12	Q96551	Q96551 morone saxa
160	9	81.8	22	2	Q91R05	Q91R05 morone saxa	233	9	81.8	23	12	Q96552	Q96552 morone saxa
161	9	81.8	22	2	Q91R05	Q91R05 morone saxa	234	9	81.8	23	12	Q96553	Q96553 morone saxa
162	9	81.8	22	2	Q91R05	Q91R05 morone saxa	235	9	81.8	23	12	Q96554	Q96554 morone saxa

[illegible]

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530	9	81.8	31	16	Q9X126	Q9X126 yersinia fe	603	9	81.8	31	16	Q9X126	Q9X126 cala porce
531	9	81.8	31	16	Q9X127	Q9X127 anaerobacteri	604	9	81.8	31	16	Q9X127	Q9X127 hepatitis b
532	9	81.8	32	2	Q9X128	Q9X128 methylobact	605	9	81.8	34	13	Q9X128	Q9X128 motophthal
533	9	81.8	32	2	Q9X129	Q9X129 actinobacteri	606	9	81.8	34	13	Q9X129	Q9X129 trichostema
534	9	81.8	32	2	Q9X130	Q9X130 yersinia fe	607	9	81.8	31	16	Q9X130	Q9X130 vibrio chol
535	9	81.8	32	2	Q9X131	Q9X131 bacillus su	608	9	81.8	34	13	Q9X131	Q9X131 staphylococ
536	9	81.8	32	2	Q9X132	Q9X132 bacillus su	609	9	81.8	35	2	Q9X132	Q9X132 synchocystis
537	9	81.8	32	2	Q9X133	Q9X133 streptococ	610	9	81.8	35	2	Q9X133	Q9X133 bovinura ap
538	9	81.8	32	3	Q9X134	Q9X134 schistosom	611	9	81.8	35	2	Q9X134	Q9X134 pseudomonas
539	9	81.8	32	8	Q9X135	Q9X135 schistosom	612	9	81.8	35	2	Q9X135	Q9X135 pseudomonas
540	9	81.8	32	8	Q9X136	Q9X136 bnf melano	613	9	81.8	35	2	Q9X136	Q9X136 mycobacteri
541	9	81.8	32	8	Q9X137	Q9X137 bnf melano	614	9	81.8	35	2	Q9X137	Q9X137 bacteroides
542	9	81.8	32	8	Q9X138	Q9X138 bnf himala	615	9	81.8	35	2	Q9X138	Q9X138 homo sapien
543	9	81.8	32	8	Q9X139	Q9X139 bnf himala	616	9	81.8	35	2	Q9X139	Q9X139 paramacium
544	9	81.8	32	10	Q9X140	Q9X140 bnf himala	617	9	81.8	35	2	Q9X140	Q9X140 paramacium
545	9	81.8	32	10	Q9X141	Q9X141 matricaria	618	9	81.8	35	2	Q9X141	Q9X141 paramacium
546	9	81.8	32	10	Q9X142	Q9X142 arabidopsis	619	9	81.8	35	2	Q9X142	Q9X142 arabidopsis
547	9	81.8	32	10	Q9X143	Q9X143 brassica na	620	9	81.8	35	2	Q9X143	Q9X143 arabidopsis
548	9	81.8	32	12	Q9X144	Q9X144 lysozyme	621	9	81.8	35	2	Q9X144	Q9X144 arabidopsis
549	9	81.8	32	12	Q9X145	Q9X145 lactate de	622	9	81.8	35	2	Q9X145	Q9X145 arabidopsis
550	9	81.8	32	12	Q9X146	Q9X146 foot and m	623	9	81.8	35	2	Q9X146	Q9X146 arabidopsis
551	9	81.8	32	16	Q9X147	Q9X147 thermotoga	624	9	81.8	35	2	Q9X147	Q9X147 arabidopsis
552	9	81.8	32	16	Q9X148	Q9X148 vibrio chol	625	9	81.8	35	2	Q9X148	Q9X148 arabidopsis
553	9	81.8	32	16	Q9X149	Q9X149 bacillus hu	626	9	81.8	35	2	Q9X149	Q9X149 arabidopsis
554	9	81.8	33	4	Q9X150	Q9X150 homo sapien	627	9	81.8	35	2	Q9X150	Q9X150 arabidopsis
555	9	81.8	33	4	Q9X151	Q9X151 homo sapien	628	9	81.8	35	2	Q9X151	Q9X151 arabidopsis
556	9	81.8	33	4	Q9X152	Q9X152 homo sapien	629	9	81.8	35	2	Q9X152	Q9X152 arabidopsis
557	9	81.8	33	4	Q9X153	Q9X153 homo sapien	630	9	81.8	35	2	Q9X153	Q9X153 arabidopsis
558	9	81.8	33	5	Q9X154	Q9X154 illyanassa o	631	9	81.8	35	2	Q9X154	Q9X154 arabidopsis
559	9	81.8	33	5	Q9X155	Q9X155 anthopleura	632	9	81.8	35	2	Q9X155	Q9X155 arabidopsis
560	9	81.8	33	5	Q9X156	Q9X156 anthopleura	633	9	81.8	35	2	Q9X156	Q9X156 arabidopsis
561	9	81.8	33	5	Q9X157	Q9X157 anthopleura	634	9	81.8	35	2	Q9X157	Q9X157 arabidopsis
562	9	81.8	33	5	Q9X158	Q9X158 anthopleura	635	9	81.8	35	2	Q9X158	Q9X158 arabidopsis
563	9	81.8	33	5	Q9X159	Q9X159 anthopleura	636	9	81.8	35	2	Q9X159	Q9X159 arabidopsis
564	9	81.8	33	5	Q9X160	Q9X160 anthopleura	637	9	81.8	35	2	Q9X160	Q9X160 arabidopsis
565	9	81.8	33	5	Q9X161	Q9X161 anthopleura	638	9	81.8	35	2	Q9X161	Q9X161 arabidopsis
566	9	81.8	33	5	Q9X162	Q9X162 anthopleura	639	9	81.8	35	2	Q9X162	Q9X162 arabidopsis
567	9	81.8	33	5	Q9X163	Q9X163 anthopleura	640	9	81.8	35	2	Q9X163	Q9X163 arabidopsis
568	9	81.8	33	5	Q9X164	Q9X164 anthopleura	641	9	81.8	35	2	Q9X164	Q9X164 arabidopsis
569	9	81.8	33	5	Q9X165	Q9X165 anthopleura	642	9	81.8	35	2	Q9X165	Q9X165 arabidopsis
570	9	81.8	33	5	Q9X166	Q9X166 anthopleura	643	9	81.8	35	2	Q9X166	Q9X166 arabidopsis
571	9	81.8	33	5	Q9X167	Q9X167 anthopleura	644	9	81.8	35	2	Q9X167	Q9X167 arabidopsis
572	9	81.8	33	5	Q9X168	Q9X168 anthopleura	645	9	81.8	35	2	Q9X168	Q9X168 arabidopsis
573	9	81.8	33	5	Q9X169	Q9X169 anthopleura	646	9	81.8	35	2	Q9X169	Q9X169 arabidopsis
574	9	81.8	33	5	Q9X170	Q9X170 anthopleura	647	9	81.8	35	2	Q9X170	Q9X170 arabidopsis
575	9	81.8	33	5	Q9X171	Q9X171 anthopleura	648	9	81.8	35	2	Q9X171	Q9X171 arabidopsis
576	9	81.8	33	5	Q9X172	Q9X172 anthopleura	649	9	81.8	35	2	Q9X172	Q9X172 arabidopsis
577	9	81.8	33	5	Q9X173	Q9X173 anthopleura	650	9	81.8	35	2	Q9X173	Q9X173 arabidopsis
578	9	81.8	33	5	Q9X174	Q9X174 anthopleura	651	9	81.8	35	2	Q9X174	Q9X174 arabidopsis
579	9	81.8	33	5	Q9X175	Q9X175 anthopleura	652	9	81.8	35	2	Q9X175	Q9X175 arabidopsis
580	9	81.8	33	5	Q9X176	Q9X176 anthopleura	653	9	81.8	35	2	Q9X176	Q9X176 arabidopsis
581	9	81.8	33	5	Q9X177	Q9X177 anthopleura	654	9	81.8	35	2	Q9X177	Q9X177 arabidopsis
582	9	81.8	33	5	Q9X178	Q9X178 anthopleura	655	9	81.8	35	2	Q9X178	Q9X178 arabidopsis
583	9	81.8	33	5	Q9X179	Q9X179 anthopleura	656	9	81.8	35	2	Q9X179	Q9X179 arabidopsis
584	9	81.8	33	5	Q9X180	Q9X180 anthopleura	657	9	81.8	35	2	Q9X180	Q9X180 arabidopsis
585	9	81.8	33	5	Q9X181	Q9X181 anthopleura	658	9	81.8	35	2	Q9X181	Q9X181 arabidopsis
586	9	81.8	33	5	Q9X182	Q9X182 anthopleura	659	9	81.8	35	2	Q9X182	Q9X182 arabidopsis
587	9	81.8	33	5	Q9X183	Q9X183 anthopleura	660	9	81.8	35	2	Q9X183	Q9X183 arabidopsis
588	9	81.8	33	5	Q9X184	Q9X184 anthopleura	661	9	81.8	35	2	Q9X184	Q9X184 arabidopsis
589	9	81.8	33	5	Q9X185	Q9X185 anthopleura	662	9	81.8	35	2	Q9X185	Q9X185 arabidopsis
590	9	81.8	33	5	Q9X186	Q9X186 anthopleura	663	9	81.8	35	2	Q9X186	Q9X186 arabidopsis
591	9	81.8	33	5	Q9X187	Q9X187 anthopleura	664	9	81.8	35	2	Q9X187	Q9X187 arabidopsis
592	9	81.8	33	5	Q9X188	Q9X188 anthopleura	665	9	81.8	35	2	Q9X188	Q9X188 arabidopsis
593	9	81.8	33	5	Q9X189	Q9X189 anthopleura	666	9	81.8	35	2	Q9X189	Q9X189 arabidopsis
594	9	81.8	33	5	Q9X190	Q9X190 anthopleura	667	9	81.8	35	2	Q9X190	Q9X190 arabidopsis
595	9	81.8	33	5	Q9X191	Q9X191 anthopleura	668	9	81.8	35	2	Q9X191	Q9X191 arabidopsis
596	9	81.8	33	5	Q9X192	Q9X192 anthopleura	669	9	81.8	35	2	Q9X192	Q9X192 arabidopsis
597	9	81.8	33	5	Q9X193	Q9X193 anthopleura	670	9	81.8	35	2	Q9X193	Q9X193 arabidopsis
598	9	81.8	33	5	Q9X194	Q9X194 anthopleura	671	9	81.8	35	2	Q9X194	Q9X194 arabidopsis
599	9	81.8	33	5	Q9X195	Q9X195 anthopleura	672	9	81.8	35	2	Q9X195	Q9X195 arabidopsis
600	9	81.8	33	5	Q9X196	Q9X196 anthopleura	673	9	81.8	35	2	Q9X196	Q9X196 arabidopsis

[illegible]

[illegible]

966 9 81.8 44 3 Q900D7
 967 9 81.8 44 3 Q900P8
 968 9 81.8 44 3 Q900P7
 969 9 81.8 44 3 Q13013
 970 9 81.8 44 4 Q8WYM8
 971 9 81.8 44 5 Q62013
 972 9 81.8 44 5 Q45XB0
 973 9 81.8 44 6 Q45S82
 974 9 81.8 44 9 Q40064
 975 9 81.8 44 10 Q42153
 976 9 81.8 44 10 Q91NR5
 977 9 81.8 44 11 Q40061
 978 9 81.8 44 11 Q45436
 979 9 81.8 44 12 Q41293
 980 9 81.8 44 12 Q40062
 981 9 81.8 44 12 Q40064
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 998 9 81.8 44 13 Q40064
 999 9 81.8 44 13 Q40064
 1000 9 81.8 44 13 Q40064

ALIGNMENTS

RESULT 1
 Q14458 ID 089965 PRELIMINARY: PRI: 8 AA.
 AC Q14458
 DI 01 NOV 1996 (TREMEL: 01, Created)
 DI 01 MAY 1999 (TREMEL: 10, Last sequence update)
 DI 01 DEC 2001 (TREMEL: 19, Last annotation update)
 DE DNA for consaid cell 1134 (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_FaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 9645520; PubMed-8848806;
 RA James L.A., Galvao D.T., Yamakawa K., Nakamura Y., Stirling C.J.,
 RA Andou K.
 RI "Walking, sleeping and mating with YACS in 3p27: localisation of 5
 RI ESTs including 3 members of the Cystatin gene family and
 RI identification of Cpi islands.";
 RL Genomics 42425-430(1996).
 DR EMBL; X88976; CAA61407.1;
 FT NON-TER R
 SQ SEQUENCE 8 AA: 925 MW: F05411A7476871E6 C8C64;

Query Match 81.8%; Score 9; DB 4; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6,7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
 DB 5 LXR 7

RESULT 2

Q914Y2 ID 0914Y2 PRELIMINARY: PRI: 8 AA.
 AC Q914Y2
 DI 01 MAY 2000 (TREMEL: 13, Created)
 DI 01 MAY 2000 (TREMEL: 13, Last sequence update)
 DI 01 MAY 2000 (TREMEL: 14, Last annotation update)
 DE Col gene product (Fragment).
 OS Astoria pectiniifera (Starfish).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Platyhelminthes; Asterozoa;
 OC Asterozoa; Valvataceae; Valvulida; Asterozoa;
 OX NCBI_FaxID:7594;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 8944669; PubMed-276482;
 DI 01 MAY 2000 (TREMEL: 13, Created)
 DI 01 MAY 2000 (TREMEL: 13, Last sequence update)
 DE Observed TERA gene cluster in starfish mitochondrial DNA.
 RL Cui, Guohua, 15, 193-206(1999).
 RP X894; X16986; CAA34767.1;
 RN [1]
 RP Mitochondrion.
 FT NON-TER R
 SQ SEQUENCE 8 AA: 1114 MW: F0C9D46415B746D6 C8C64;

Query Match 81.8%; Score 9; DB 8; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6,7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
 DB 3 LXR 5

RESULT 3

089965 ID 089965 PRELIMINARY: PRI: 8 AA.
 AC 089965
 DI 01 NOV 1998 (TREMEL: 08, Created)
 DI 01 NOV 1998 (TREMEL: 08, Last sequence update)
 DI 01 NOV 1998 (TREMEL: 08, Last annotation update)
 DE Anoprotet (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_FaxID:10642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 9624452; PubMed-9584961;
 RA Beldorini R., Caldarillo Stetano R., Munoz G., Zocchi M., Mediani M.,
 RA Tosoni A., Ferrante P.
 RI "PCR detection of JC virus DNA in the brain tissue of a 9 year old
 RI child with pleomorphic xanthocystoma.";
 RL J. Neurovirology 4:242-245(1998).
 DR EMBL; AF044517; AAC23945.1;
 FT NON-TER R
 SQ SEQUENCE 8 AA: 1002 MW: F0E929C407426E C8C64;

Query Match 81.6%; Score 9; DB 12; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6,7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
 DB 6 LXR 8

RESULT 4

Q91688 ID 091688 PRELIMINARY: PRI: 9 AA.
 AC Q91688
 DI 01 MAY 2000 (TREMEL: 13, Created)
 DI 01 MAY 2000 (TREMEL: 13, Last sequence update)
 DI 01 MAY 2000 (TREMEL: 13, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).
 GN COL.
 OS Gecko gecko (Tokay gecko).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=36310.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99343648; PubMed=10413626;
 FA Macey J.P., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
 RI "Variant patterns of fragmentation among gekkonid lizards of the
 RI genus *Tenisoni* produced by the Indian collision: A molecular
 RI phylogenetic perspective and an area cladogram for central Asia";
 EL Mol. Phylogenet. Evol. 12:30-32(1999).
 DR EMBL: AF14244; AAL10011; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1189 MW; 428790936411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 2 LTR 4

RESULT 5

ID Q94V18 PRELIMINARY; PRI; 9 AA.
 AC Q94V18;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COL.
 OS Varanus eremias.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=169848;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
 KL Cladistics 17:0-0(2001).
 DR EMBL: AF407495; AAL10040.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1124 MW; 9E80C733640D5731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LTR 5

RESULT 6

ID Q94VH4 PRELIMINARY; PRI; 9 AA.
 AC Q94VH4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COL.
 OS Varanus glauerti.
 OC Mitochondrion.

DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=169841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
 KL Cladistics 17:0-0(2001).
 DR EMBL: AF407560; AAL10054.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1124 MW; 9E80C733640D5731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LTR 5

RESULT 7

ID Q94VE1 PRELIMINARY; PRI; 9 AA.
 AC Q94VE1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COL.
 OS Varanus mertensi.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=62044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
 KL Cladistics 17:0-0(2001).
 DR EMBL: AF407512; AAL10050.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LTR 5

RESULT 8

ID Q94VD8 PRELIMINARY; PRI; 9 AA.
 AC Q94VD8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COL.
 OS Varanus niloticus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=62046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";

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PL Chadiasties 17:0-0(2001).
DR EMBL: AF407514; AAL10096.1; -.
KW Mitochondrion.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1154 MW: 98007346411A731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 9
ID Q94VVC PRELIMINARY: PRT; 9 AA.
AC Q94VVC;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Varanus pilbarensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Sclerozoa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID 62048;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
PL "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
DR EMBL: AF407518; AAL10108.1; -.
KW Mitochondrion.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1004 MW: 8740A5A36411A735 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 10
ID Q9PYK1 PRELIMINARY: PRT; 9 AA.
AC Q9PYK1;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Papovavirus HK (Gardner) early transcription control region
DE (Fragment).
OS Simian virus 12.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID 46771;
RN [1]
RP SEQUENCE FROM N.A.
RA Choke W.F.; Walker D.L.; Peitzman L.R.; Frisque R.J.;
PL "Construction and characterization of hybrid polyomavirus genomes.";
DR EMBL: M14451; AAA06245.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1130 MW: 8701F5B746C40742 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 11
ID Q91HMB PRELIMINARY: PRT; 9 AA.
AC Q91HMB;
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Papovavirus HK (Gardner) derived clone HK99 early transcription
DE control region (Fragment).
OS Simian virus 12.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID 46771;
RN [1]
RP SEQUENCE FROM N.A.
RA Choke W.F.; Walker D.L.; Peitzman L.R.; Frisque R.J.;
PL "Construction and characterization of hybrid polyomavirus genomes.";
DR EMBL: M14452; AAA06236.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1130 MW: 8701F5B746C40742 CRC64;

Query Match 81.8%; Score 9; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 6 LXR 8

RESULT 12
ID Q9T3R6 PRELIMINARY: PRT; 10 AA.
AC Q9T3R6;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Diplolossus bilobatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Sclerozoa; Anguimorpha; Anolis.
OC Diplolossus.
OX NCBI_TaxID 102189;
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R.; Schulte J.A. II; Larson A.; Ballyve P.S.; Ballyve R.;
KA Papadatos J.J.;
PL "Molecular phylogenetics, tRNA evolution, and historical biogeography
PL in anole lizards and related taxonomic families.";
DR EMBL: AF089698; AAO51514.1; -.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1255 MW: 51EED067466411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 1

```

Db 3 LTR 5

RESULT 13

Q9TG47 ID Q9TG47 PRELIMINARY: PRI: 10 AA.
 AC Q9TG47
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Cyt.
 GS Ophisaurus koollikeri.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Anguillidae;
 OC Ophisaurus.
 OX NCBI_TaxID=102194;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99343613; PubMed-10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, rRNA evolution, and historical biogeography
 RT in anigid lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL: AF085621; AAD51563.1;
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55EE80C7336460B7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 30+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

I I

Db 3 LAR 5

RESULT 14

Q9TG38 ID Q9TG38 PRELIMINARY: PRI: 10 AA.
 AC Q9TG38
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Cyt.
 GS Ophisaurus harti.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Anguillidae;
 OC Ophisaurus.
 OX NCBI_TaxID=102193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99343613; PubMed-10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, rRNA evolution, and historical biogeography
 RT in anigid lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL: AF085624; AAD51562.1;
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55EE80C7336460B7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 30+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 3 LTR 5

RESULT 15

Q9TG35 ID Q9TG35 PRELIMINARY: PRI: 10 AA.
 AC Q9TG35
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Cyt.
 GS Ophisaurus attenuatus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Anguillidae;
 OC Ophisaurus.
 OX NCBI_TaxID=102192;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99343613; PubMed-10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, rRNA evolution, and historical biogeography
 RT in anigid lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL: AF085625; AAD51565.1;
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55EE80C7336460B7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 30+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

I I

Db 3 LTR 5

RESULT 16

Q9TG42 ID Q9TG42 PRELIMINARY: PRI: 10 AA.
 AC Q9TG42
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Cyt.
 GS Ophisaurus ventralis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Anguillidae;
 OC Ophisaurus.
 OX NCBI_TaxID=102195;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99343613; PubMed-10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, rRNA evolution, and historical biogeography
 RT in anigid lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL: AF085626; AAD51568.1;
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55EE80C7336460B7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 30+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 LXR 3
  1 1
  3 LXR 5

RESULT 17
Q91FV5 PRELIMINARY: PRT: 10 AA.
AC Q91FV5:
  01-MAY-2000 (TREMBLrel. 13, Created)
  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
  01-MAY-2000 (TREMBLrel. 13, Last annotation update)
  DE Cytochrome c oxidase subunit 1 (Fragment).
  GN Col.
  OS Eublepharus turkmenicus.
  OG Mitochondrion.
  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Lepidosauria; Squamata; ScleroGLOSSa; Gekkota; Eublepharidae;
  OC Eublepharus.
  CX NCBI_TaxID 52219;
  RN [1]
  RP SEQUENCE FROM N.A.
  RX MEDLINE-99444613; PubMed 10414621;
  RA Macey J.R., Schulte J.A. II, Larson A., Janney R.S., Orlov N.,
  RA Papenfuss T.J.;
  RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
  RT in anolis lizards and related taxonomic families.";
  RL Mol. Phylogenet. Evol. 12:250-272(1999).
  DR EMBL: 071345; AA062821.1;
  KW Mitochondrion.
  FT NON_TER 10 10
  SQ SEQUENCE 10 AA: 5DEE80C936411A7 CR664;

  Query Match 81.8%; Score 9; DB 8; Length 10;
  Best Local Similarity 66.7%; Pred. No. 3e+03;
  Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
  1 1
  3 LXR 5

RESULT 18
Q92771 PRELIMINARY: PRT: 10 AA.
AC Q92771:
  01-MAY-1997 (TREMBLrel. 03, Created)
  01-MAY-1997 (TREMBLrel. 03, Last sequence update)
  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
  DE Cytochrome c oxidase subunit 1 (Fragment).
  GN Col.
  OS Xenosaurus grandis.
  OG Mitochondrion.
  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Lepidosauria; Squamata; ScleroGLOSSa; Anouromorpha; Xenosauridae;
  OC Xenosaurus.
  CX NCBI_TaxID 52183;
  RN [1]
  RP SEQUENCE FROM N.A.
  RX MEDLINE-97154826; PubMed 9000757;
  RA Macey J.R., Larson A., Ananjeva N.B., Pan 2., Papenfuss T.J.;
  RT "Two novel gene orders and the role of light-strand replication in
  RT rearrangement of the vertebrate mitochondrial genome.";
  RL Mol. Biol. Evol. 14:91-104(1997).
  DR EMBL: 071345; AA048271.1;
  KW Mitochondrion.
  FT NON_TER 10 10
  SQ SEQUENCE 10 AA: 1176 MW: 56580C905A411A7 CR664;

  Query Match 81.8%; Score 9; DB 8; Length 10;
  Best Local Similarity 66.7%; Pred. No. 3e+03;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXR 3
  1 1
  3 LXR 5

RESULT 19
Q92576 PRELIMINARY: PRT: 10 AA.
AC Q92576:
  01-MAY-1997 (TREMBLrel. 03, Created)
  01-MAY-1997 (TREMBLrel. 03, Last sequence update)
  01-NOV-1998 (TREMBLrel. 08, Last annotation update)
  DE Cytochrome c oxidase subunit 1 (Fragment).
  GN Col.
  OS Rana biporus.
  OG Mitochondrion.
  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Lepidosauria; Squamata; ScleroGLOSSa; Amphibiana; Ranae; Ranae;
  OC NCBI_TaxID 52188;
  RN [1]
  RP SEQUENCE FROM N.A.
  RX MEDLINE-97154826; PubMed 9000757;
  RA Macey J.R., Larson A., Ananjeva N.B., Pan 2., Papenfuss T.J.;
  RT "Two novel gene orders and the role of light-strand replication in
  RT rearrangement of the vertebrate mitochondrial genome.";
  RL Mol. Biol. Evol. 14:91-104(1997).
  DR EMBL: 071345; AA048271.1;
  KW Mitochondrion.
  FT NON_TER 10 10
  SQ SEQUENCE 10 AA: 1176 MW: 56580C905A411A7 CR664;

  Query Match 81.8%; Score 9; DB 8; Length 10;
  Best Local Similarity 66.7%; Pred. No. 3e+03;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LXR 3
  1 1
  3 LXR 5

RESULT 20
Q958K9 PRELIMINARY: PRT: 10 AA.
AC Q958K9:
  01-DEC-2001 (TREMBLrel. 19, Created)
  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
  DE Cytochrome c oxidase subunit 1 (Fragment).
  GN Col.
  OS Rana boylii.
  OG Mitochondrion.

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
 KN NBI_TaxID=160499;
 RP SEQUENCE FROM N.A.
 PX MESLINE=21184290; PubMed 11286499;
 RA Macey J.R., Strassburg J.H., Brissou J.A., Vredenburg V.I.,
 RA Jennings M., Larson A.;
 RT "Molecular Phylogenetics of Western North American Frogs of the Rana
 RT boylei Species Group",
 RL Mol. Phylogenet. Evol. 19:131-142(2001).
 DR EMBL: AF140194; AAK56477 1; -
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1320 MW: 42D380C9D36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LIR 5

RESULT 21
 Q94VF0
 ID Q94VF0 PRELIMINARY; PRI; 10 AA.
 AC Q94VF0
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN COL.
 OS Varanus kinsurum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Lepidosauria; Squamata; Scleroglossa; Ankuimorpha; Varanidae; Varanus.
 OX NBI_TaxID=169845;
 KN [1]
 RP SEQUENCE FROM N.A.
 RA AST J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407509; AAL10041 1; -
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1255 MW: 5BDE90C7A36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LIR 5

RESULT 22
 Q94V05
 ID Q94V05 PRELIMINARY; PRI; 10 AA.
 AC Q94V05;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN COL.
 OS Varanus olivaceus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Lepidosauria; Squamata; Scleroglossa; Ankuimorpha; Varanidae; Varanus.
 OX NBI_TaxID=62047;
 KN [1]

RP SEQUENCE FROM N.A.
 RA AST J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407515; AAL10099 1;
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1234 MW: 5B4C4CA5A36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LIR 5

RESULT 23
 Q94VD2
 ID Q94VD2 PRELIMINARY; PRI; 10 AA.
 AC Q94VD2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN COL.
 OS Varanus panoptes panoptes.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Lepidosauria; Squamata; Scleroglossa; Ankuimorpha; Varanidae; Varanus.
 OX NBI_TaxID=169849;
 KN [1]
 RP SEQUENCE FROM N.A.
 RA AST J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407516; AAL10102 1;
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1239 MW: 5BDE90C4156411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LIR 5

RESULT 24
 Q94VC9
 ID Q94VC9 PRELIMINARY; PRI; 10 AA.
 AC Q94VC9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN COL.
 OS Varanus panoptes panoptes.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Lepidosauria; Squamata; Scleroglossa; Ankuimorpha; Varanidae; Varanus.
 OX NBI_TaxID=169848;
 KN [1]
 RP SEQUENCE FROM N.A.
 RA AST J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407517; AAL10105 1;
 KW Mitochondrion.
 FT NON_TER 10 10

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LIR 5

SQ SEQUENCE 10 AA: 1255 MW: 50EE80C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB #: Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 25

Q94V97 PRELIMINARY: PRT; 10 AA.

AC Q94V97

DT 01-DEC-2001 (TREMELREL: 19, Created)

DT 01-DEC-2001 (TREMELREL: 19, Last sequence update)

DT 01-DEC-2001 (TREMELREL: 19, Last annotation update)

DE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Varanus varius.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; ScleroGLOSSA; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=169854;

RN [1]

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

KL Cladistics 17:0-0(2001).

DR EMBL; AF407530; AAL10142.1; -.

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA: 1255 MW: 50EE80C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB #: Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 26

Q94V85 PRELIMINARY: PRT; 10 AA.

AC Q94V85

DT 01-DEC-2001 (TREMELREL: 19, Created)

DT 01-DEC-2001 (TREMELREL: 19, Last sequence update)

DT 01-DEC-2001 (TREMELREL: 19, Last annotation update)

DE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Varanus varius (Lace monitor).

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; ScleroGLOSSA; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=8559;

RN [1]

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

KL Cladistics 17:0-0(2001).

DR EMBL; AF407534; AAL10154.1; -.

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA: 1255 MW: 50EE90C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB #: Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 27

Q94P08 PRELIMINARY: PRT; 10 AA.

AC Q94P08

DT 01-DEC-2001 (TREMELREL: 19, Created)

DT 01-DEC-2001 (TREMELREL: 19, Last sequence update)

DT 01-DEC-2001 (TREMELREL: 19, Last annotation update)

DE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Varanus scalaris.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; ScleroGLOSSA; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=169852;

RN [1]

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

KL Cladistics 17:0-0(2001).

DR EMBL; AF407527; AAL10143.1; -.

DR EMBL; AF407528; AAL10136.1; -.

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA: 1255 MW: 50EE80C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB #: Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 28

Q9SHN1 PRELIMINARY: PRT; 10 AA.

AC Q9SHN1

DT 01-JUN-2002 (TREMELREL: 21, Created)

DT 01-JUN-2002 (TREMELREL: 21, Last sequence update)

DT 01-JUN-2002 (TREMELREL: 21, Last annotation update)

DE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Bradypodion tateianum.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Aetosauria; Chamaeleonidae;

OC Bradypodion.

OX NCBI_TaxID=179888;

RN [1]

RP SEQUENCE FROM N.A.

RA Townsend T.M.; Larson A.L.;

RT "Nucleolar Phylogenetic and Mitochondrial Genome Evolution in the

Chamaeleonidae (Reptilia, Squamata).";

KL Systematic Zoology 51:1-19; PMID: 12435404; PubMed databases.

DR EMBL; AF448730; AAL90472.1;

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA: 1427 MW: 5E2D60C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB #: Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 3 LXR 5

RESULT 29

QC1R7
ID Q6C1R7 PRELIMINARY: PRT: 11 AA.
AC Q6C1R7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN Sslp (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetia; Saccharomycetes.
OC Saccharomycetia; Saccharomycetes; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STAIN-173;
RA Perez-Ortin J.E.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF239758; AAC15080.1; -;
FT NON_TER 11
SQ SEQUENCE 11 AA: 1274 MW: 1256761407.420374 CRC64;

Query Match 81.8%; Score 9; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 3,3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 9 LXR 11

RESULT 30

077899
ID 077899 PRELIMINARY: PRT: 11 AA.
AC 077899
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Moleleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
FA Malaga-Trillo E.; Zaleska-Raczynska Z.; McAndrew B.; Vincek V.;
RA Figueroa F.; Sultmann H.; Klein J.;
RT "Linkage relationships and haplotype polymorphism among eichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL: AF050009; AAC41348.1; -;
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA: 1349 MW: 81C12D8E7341B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 3,3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 7 LXR 9

RESULT 31

077900
ID 077900 PRELIMINARY: PRT: 11 AA.
AC 077900
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Moleleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
FA Malaga-Trillo E.; Zaleska-Raczynska Z.; McAndrew B.; Vincek V.;
RA Figueroa F.; Sultmann H.; Klein J.;
RT "Linkage relationships and haplotype polymorphism among eichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL: AF050010; AAC41449.1; -;
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA: 1349 MW: 81C12D8E7341B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 3,3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 7 LXR 9

RESULT 32

077901
ID 077901 PRELIMINARY: PRT: 11 AA.
AC 077901
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Moleleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
FA Malaga-Trillo E.; Zaleska-Raczynska Z.; McAndrew B.; Vincek V.;
RA Figueroa F.; Sultmann H.; Klein J.;
RT "Linkage relationships and haplotype polymorphism among eichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL: AF050011; AAC41450.1; -;
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA: 1349 MW: 81C12D8E7341B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 3,3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 7 LXR 9

RESULT 33

077902
ID 077902 PRELIMINARY: PRT: 11 AA.
AC 077902
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 14 (Fragment).
 OS oreochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroides;
 OC Cichlidae; oreochromis.
 CX NCBI_taxid:8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98415113; PubMed:9649549;
 RA Malada-Trillo E., Zaleska-Rotcynska Z., McAndrew B., Vinick V.,
 EA Fiqueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41352.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 8101208E7441B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 44

077903
 ID 077903 PRELIMINARY: PRI: 11 AA.
 AC 077903;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS oreochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroides;
 OC Cichlidae; oreochromis.
 CX NCBI_taxid:8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98415113; PubMed:9649549;
 RA Malada-Trillo E., Zaleska-Rotcynska Z., McAndrew B., Vinick V.,
 EA Fiqueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41352.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 8101208E7441B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 45

077904
 ID 077904 PRELIMINARY: PRI: 11 AA.
 AC 077904;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).

OS oreochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroides;
 OC Cichlidae; oreochromis.
 CX NCBI_taxid:8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98415113; PubMed:9649549;
 RA Malada-Trillo E., Zaleska-Rotcynska Z., McAndrew B., Vinick V.,
 EA Fiqueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41353.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 8101208E7441B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 46

077905
 ID 077905 PRELIMINARY: PRI: 11 AA.
 AC 077905;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS oreochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroides;
 OC Cichlidae; oreochromis.
 CX NCBI_taxid:8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98415113; PubMed:9649549;
 RA Malada-Trillo E., Zaleska-Rotcynska Z., McAndrew B., Vinick V.,
 EA Fiqueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050015; AAC41354.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 8101208E7441B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 47

078121
 ID 078121 PRELIMINARY: PRI: 11 AA.
 AC 078121;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS oreochromis niloticus (Nile tilapia) (tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malada-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL; AF050027; AAC41366.1; -;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA; 1362 MW; 03C12D8EB741B54 CRO64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 56.7%; Pred. No. 4.4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 I 1
 DB 7 LSR 9

RESULT 38

O77916
 ID O77916 PRELIMINARY; PRT; 11 AA.
 AC O77916;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malada-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL; AF050029; AAC41368.1; -;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB741B41 CRO64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 56.7%; Pred. No. 4.4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 I 1
 DB 7 LSR 9

RESULT 39

O77917
 ID O77917 PRELIMINARY; PRT; 11 AA.
 AC O77917;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malada-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL; AF050030; AAC41369.1; -;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA; 1449 MW; 81C12D8EB741B41 CRO64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 56.7%; Pred. No. 4.4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 I 1
 DB 7 LSR 9

RESULT 40

O77921
 ID O77921 PRELIMINARY; PRT; 11 AA.
 AC O77921;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Pseudotropheus sp. "Pseudotropheus tropheus complex".
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
 OC Cichlidae; Pseudotropheus.
 OX NCBI_TaxID=51796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malada-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL; AF050034; AAC41373.1; -;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA; 1449 MW; 81C12D8EB741B41 CRO64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 56.7%; Pred. No. 4.4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 I 1
 DB 7 LSR 9

RESULT 41

O96368
 ID O96368 PRELIMINARY; PRT; 11 AA.
 AC O96368;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Draco blanfordi.
 OG Mitochondrion.

```

oc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidodonta; Squamata; Iguania; Arodonta; Anamniota; Anomalia;
oc Calotes.
ox NBI_LaxID 89021;
rn [1]
rp SEQUENCE FROM N.A.
rx MEDLINE 97154820; PubMed 9000751;
ra Macey J.R., Schulte J.A., Larson A., Ananjeva N.B., Papenfuss T.J.;
rt "Replication slippage may cause parallel evolution in the secondary
ri structures of mitochondrial transfer RNAs.";
rl Mol. Biol. Evol. 14:40-49(1997);
rn [2]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schulte J.A., Larson A., Ananjeva N.B., Papenfuss T.J.;
ra Pothiyarada R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of Transposon Migration: An example using Anolis lizard
ri phylogenetics.";
rl Syst. Biol. 49:244-256(2000);
rn [3]
rp EMBL; AF128477; AA006686.1;
rl NON_TER 11 11
rn SEQUENCE 11 AA; 1441 MW; 48207143641147 CR654;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.78; Pred. No. 3,600;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 4
Ib 4 LSR 6

RESULT 42
Q96540 PRELIMINARY; PRI; 11 AA.
AC Q96540;
DT 01-MAR-2001 (TREMBLE; 16, Created)
DT 01-MAR-2001 (TREMBLE; 16, Last sequence update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Calotes cyclonensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidodonta; Squamata; Iguania; Arodonta; Anamniota; Anomalia;
oc Calotes.
ox NBI_LaxID 118094;
rn [1]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schulte J.A., Larson A., Ananjeva N.B., Papenfuss T.J.;
ra Pothiyarada R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of Transposon Migration: An example using Anolis lizard
ri phylogenetics.";
rl Syst. Biol. 49:244-256(2000);
rn [2]
rp EMBL; AF128477; AA006686.1;
rl NON_TER 11 11
rn SEQUENCE 11 AA; 1441 MW; 48207143641147 CR654;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.78; Pred. No. 3,600;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 4
Ib 4 LSR 6

RESULT 43
Q96547 PRELIMINARY; PRI; 11 AA.
AC Q96547;
DT 01-MAR-2001 (TREMBLE; 16, Created)
DT 01-MAR-2001 (TREMBLE; 16, Last sequence update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Calotes liocephalus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidodonta; Squamata; Iguania; Arodonta; Anamniota; Anomalia;
oc Calotes.
ox NBI_LaxID 118095;
rn [1]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schulte J.A., Larson A., Ananjeva N.B., Papenfuss T.J.;
ra Pothiyarada R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of Transposon Migration: An example using Anolis lizard
ri phylogenetics.";
rl Syst. Biol. 49:244-256(2000);
rn [2]
rp EMBL; AF128477; AA006686.1;
rl NON_TER 11 11
rn SEQUENCE 11 AA; 1441 MW; 48207143641147 CR654;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.78; Pred. No. 3,600;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 4
Ib 4 LSR 6

RESULT 44
Q96544 PRELIMINARY; PRI; 11 AA.
AC Q96544;
DT 01-MAR-2001 (TREMBLE; 16, Created)
DT 01-MAR-2001 (TREMBLE; 16, Last sequence update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Calotes liocephalus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidodonta; Squamata; Iguania; Arodonta; Anamniota; Anomalia;
oc Calotes.
ox NBI_LaxID 118096;
rn [1]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schulte J.A., Larson A., Ananjeva N.B., Papenfuss T.J.;
ra Pothiyarada R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of Transposon Migration: An example using Anolis lizard
ri phylogenetics.";
rl Syst. Biol. 49:244-256(2000);
rn [2]
rp EMBL; AF128477; AA006686.1;
rl NON_TER 11 11
rn SEQUENCE 11 AA; 1441 MW; 48207143641147 CR654;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.78; Pred. No. 3,600;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 4
Ib 4 LSR 6

```

RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.:
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.";
 PL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128485; AAG00692.1; -.
 KW Mitochondrion.
 FT NON_TERR 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 | |
 DB 4 LIR 6

RESULT 45

Q9G631 PRELIMINARY: PRT: 11 AA.
 AC Q9G631;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN cOI.
 GS Calotes nigrilabris.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Brachylophidae;
 OC Calotes.
 OX NCBI_TaxID=118098;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macey J.R., Schulte J.A. II, Larson A.:
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 PA Macey J.P., Schulte J.A. II, Larson A., Anderson M.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.:
 PT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.";
 PL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128486; AAG00695.1; -.
 KW Mitochondrion.
 FT NON_TERR 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 | |
 DB 4 LIR 6

Search completed: April 30, 2003, 13:36:56
 Job time : 56.8182 secs

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GenCore version: 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 30, 2003, 13:32:48 ; Search time 8.72727 seconds

Title: US-09-498-556c-357

Perfect score: 11

Sequence: 1 LXXK 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 762574 seqs, 29422927 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 1000 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_2/blast/1/aa/seqs/seqs.ppt*
- 2: /cgn2_2/blast/1/aa/seqs/seqs.ppt*
- 3: /cgn2_2/blast/1/aa/seqs/seqs.ppt*
- 4: /cgn2_2/blast/1/aa/seqs/seqs.ppt*
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- 6: /cgn2_2/blast/1/aa/seqs/seqs.ppt*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	9	81.8	4	4 US-09-533-889-19
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150	9	81.8	9	4	US-08-657-339A-4	Sequence 4, App1	223	9	81.8	10	2	US-08-556-597-160	Sequence 160, App
151	9	81.8	9	4	US-08-657-339A-10	Sequence 10, App1	224	9	81.8	10	2	US-08-595-014A-72	Sequence 72, App1
152	9	81.8	9	4	US-09-510-748A-35	Sequence 35, App1	225	9	81.8	10	2	US-08-985-126-7	Sequence 7, App1
153	9	81.8	9	4	US-09-510-748A-101	Sequence 101, App	226	9	81.8	10	2	US-08-985-126-8	Sequence 8, App1
154	9	81.8	9	4	US-09-510-748A-147	Sequence 147, App	227	9	81.8	10	2	US-08-985-126-10	Sequence 10, App1
155	9	81.8	9	4	US-09-510-748A-158	Sequence 158, App	228	9	81.8	10	2	US-08-985-126-19	Sequence 19, App1
156	9	81.8	9	4	US-09-510-748A-159	Sequence 159, App	229	9	81.8	10	2	US-08-985-126-24	Sequence 24, App1
157	9	81.8	9	4	US-09-133-521-16	Sequence 16, App1	230	9	81.8	10	2	US-08-985-126-26	Sequence 26, App1
158	9	81.8	9	4	US-09-142-481-11	Sequence 11, App1	231	9	81.8	10	2	US-08-985-126-27	Sequence 27, App1
159	9	81.8	9	4	US-08-457-694A-4	Sequence 4, App1	232	9	81.8	10	2	US-08-985-126-28	Sequence 28, App1
160	9	81.8	9	4	US-08-457-694A-10	Sequence 10, App1	233	9	81.8	10	2	US-08-985-126-29	Sequence 29, App1
161	9	81.8	9	4	US-09-349-797-2	Sequence 2, App1	234	9	81.8	10	2	US-08-985-126-30	Sequence 30, App1
162	9	81.8	9	4	US-08-627-654-110	Sequence 110, App	235	9	81.8	10	2	US-08-985-126-41	Sequence 41, App1
163	9	81.8	9	4	US-08-649-518-140	Sequence 140, App	236	9	81.8	10	2	US-08-985-126-42	Sequence 42, App1
164	9	81.8	9	4	US-09-044-718-59	Sequence 59, App1	237	9	81.8	10	2	US-08-985-126-43	Sequence 43, App1
165	9	81.8	9	4	US-09-160-513-218	Sequence 218, App	238	9	81.8	10	2	US-08-985-126-44	Sequence 44, App1
166	9	81.8	9	4	US-08-459-260A-166	Sequence 166, App	239	9	81.8	10	2	US-08-985-126-45	Sequence 45, App1
167	9	81.8	9	5	PCI-US94-02195-1	Sequence 1, App1	240	9	81.8	10	2	US-08-985-126-46	Sequence 46, App1
168	9	81.8	9	6	5217969-116	Patent No. 5217969	241	9	81.8	10	2	US-08-985-126-47	Sequence 47, App1
169	9	81.8	10	1	US-07-841-997A-31	Sequence 31, App1	242	9	81.8	10	2	US-09-174-060-19	Sequence 19, App1
170	9	81.8	10	1	US-08-166-195A-8	Sequence 8, App1	243	9	81.8	10	2	US-09-149-762A-22	Sequence 22, App1
171	9	81.8	10	1	US-08-166-195A-9	Sequence 9, App1	244	9	81.8	10	3	US-09-149-762A-26	Sequence 26, App1
172	9	81.8	10	1	US-08-166-195A-10	Sequence 10, App1	245	9	81.8	10	3	US-09-149-762A-46	Sequence 46, App1
173	9	81.8	10	1	US-08-166-195A-42	Sequence 42, App1	246	9	81.8	10	3	US-09-149-762A-46	Sequence 46, App1

685	9	81.8	17	4	US-08-832-567-1	Sequence 1, Appl	758	9	81.8	19	4	US-09-357-141-4	Sequence 7, Appl
686	9	81.8	17	4	US-09-138-056-4	Sequence 4, Appl	759	9	81.8	19	4	US-09-566-111-27	Sequence 27, Appl
687	9	81.8	17	4	US-09-138-056-7	Sequence 7, Appl	760	9	81.8	19	4	US-09-201-945-222	Sequence 222, Appl
688	9	81.8	17	4	US-09-138-056-38	Sequence 38, Appl	761	9	81.8	19	4	US-09-201-945-452	Sequence 452, Appl
689	9	81.8	17	4	US-09-138-056-49	Sequence 49, Appl	762	9	81.8	19	4	US-09-533-889-4	Sequence 4, Appl
690	9	81.8	17	4	US-08-896-933-4	Sequence 4, Appl	763	9	81.8	19	4	US-09-053-611-9	Sequence 9, Appl
691	9	81.8	17	4	US-09-177-249-62	Sequence 62, Appl	764	9	81.8	19	4	US-09-053-611-15	Sequence 15, Appl
692	9	81.8	17	4	US-08-605-430-57	Sequence 57, Appl	765	9	81.8	19	4	US-09-500-124-187	Sequence 187, Appl
693	9	81.8	17	4	US-09-025-769-229	Sequence 229, Appl	766	9	81.8	19	4	US-09-441-528-24	Sequence 24, Appl
694	9	81.8	17	4	US-09-314-235-4	Sequence 4, Appl	767	9	81.8	19	4	US-09-441-528-24	Sequence 24, Appl
695	9	81.8	17	4	US-09-227-357-451	Sequence 451, Appl	768	9	81.8	19	4	US-09-441-528-25	Sequence 25, Appl
696	9	81.8	17	4	US-09-336-048-2	Sequence 2, Appl	769	9	81.8	19	4	US-09-441-528-78	Sequence 78, Appl
697	9	81.8	17	4	US-09-148-712-25	Sequence 25, Appl	770	9	81.8	19	4	US-09-441-528-79	Sequence 79, Appl
698	9	81.8	17	4	US-09-122-1248-13	Sequence 13, Appl	771	9	81.8	19	4	US-09-388-548E-41	Sequence 41, Appl
699	9	81.8	17	4	US-08-465-260A-300	Sequence 300, Appl	772	9	81.8	19	4	US-08-465-260A-300	Sequence 300, Appl
700	9	81.8	17	4	US-08-465-260A-125	Sequence 125, Appl	773	9	81.8	19	4	US-08-465-260A-125	Sequence 125, Appl
701	9	81.8	18	1	US-08-279-058B-20	Sequence 20, Appl	774	9	81.8	20	1	US-07-882-923-8	Sequence 8, Appl
702	9	81.8	18	1	US-08-486-135-5	Sequence 5, Appl	775	9	81.8	20	1	US-07-882-923-11	Sequence 11, Appl
703	9	81.8	18	1	US-08-468-956-2	Sequence 2, Appl	776	9	81.8	20	1	US-07-651-719A-22	Sequence 22, Appl
704	9	81.8	18	1	US-08-470-152-5	Sequence 5, Appl	777	9	81.8	20	1	US-07-796-776-14	Sequence 14, Appl
705	9	81.8	18	2	US-08-371-622-83	Sequence 83, Appl	778	9	81.8	20	1	US-07-956-848A-14	Sequence 14, Appl
706	9	81.8	18	2	US-08-374-652-88	Sequence 88, Appl	779	9	81.8	20	1	US-07-956-848A-20	Sequence 20, Appl
707	9	81.8	18	2	US-08-460-502-2	Sequence 2, Appl	780	9	81.8	20	1	US-07-956-848A-47	Sequence 47, Appl
708	9	81.8	18	2	US-08-686-594-1	Sequence 1, Appl	781	9	81.8	20	1	US-07-994-277A-3	Sequence 3, Appl
709	9	81.8	18	2	US-08-686-594-5	Sequence 5, Appl	782	9	81.8	20	1	US-08-289-653-4	Sequence 4, Appl
710	9	81.8	18	2	US-08-686-594-8	Sequence 8, Appl	783	9	81.8	20	1	US-07-794-289E-97	Sequence 97, Appl
711	9	81.8	18	2	US-08-685-589A-144	Sequence 144, Appl	784	9	81.8	20	1	US-07-794-289E-142	Sequence 142, Appl
712	9	81.8	18	2	US-08-468-964B-3	Sequence 3, Appl	785	9	81.8	20	1	US-07-794-289E-149	Sequence 149, Appl
713	9	81.8	18	2	US-07-571-282A-3	Sequence 3, Appl	786	9	81.8	20	1	US-08-190-789A-235	Sequence 235, Appl
714	9	81.8	18	2	US-09-017-205-9	Sequence 9, Appl	787	9	81.8	20	1	US-08-250-789A-191	Sequence 191, Appl
715	9	81.8	18	2	US-09-017-205-10	Sequence 10, Appl	788	9	81.8	20	1	US-08-419-673-13	Sequence 13, Appl
716	9	81.8	18	2	US-08-455-079-21	Sequence 21, Appl	789	9	81.8	20	1	US-08-606-888A-7	Sequence 7, Appl
717	9	81.8	18	2	US-09-353-679A-3	Sequence 3, Appl	790	9	81.8	20	1	US-08-383-173B-252	Sequence 252, Appl
718	9	81.8	18	3	US-08-860-368B-3	Sequence 3, Appl	791	9	81.8	20	1	US-08-465-991A-249	Sequence 249, Appl
719	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	792	9	81.8	20	1	US-08-471-956-14	Sequence 14, Appl
720	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	793	9	81.8	20	1	US-08-471-956-26	Sequence 26, Appl
721	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	794	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
722	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	795	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
723	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	796	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
724	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	797	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
725	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	798	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
726	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	799	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
727	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	800	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
728	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	801	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
729	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	802	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
730	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	803	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
731	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	804	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
732	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	805	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
733	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	806	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
734	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	807	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
735	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	808	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
736	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	809	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
737	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	810	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
738	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	811	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
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740	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	813	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
741	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	814	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
742	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	815	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
743	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	816	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
744	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	817	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
745	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	818	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
746	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	819	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
747	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	820	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
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749	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	822	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
750	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	823	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
751	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	824	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
752	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	825	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
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754	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	827	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
755	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	828	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
756	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	829	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl
757	9	81.8	18	3	US-08-860-368B-6	Sequence 6, Appl	830	9	81.8	20	1	US-08-471-956-47	Sequence 47, Appl

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Sequence 283, Appl
Sequence 18, Appl
Sequence 98, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 3, Appl
Sequence 10, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 32, Appl
Sequence 77, Appl
Sequence 141, Appl
Sequence 138, Appl
Sequence 145, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 123, Appl
Sequence 28, Appl

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981 9 81.8 24 4 05 09 492 631B 10
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984 9 81.8 24 5 02 01 0595 00962 17
985 9 81.8 24 5 02 01 0595 04435 10
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1000 9 81.8 24 1 05 07 794 288B 22

ALIGNMENTS

RESULT 1
US-08-470-847-7
Sequence 7, Application US/08470947
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimmi, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90255-5595
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.20
CURRENT APPLICATION DATA: US/08/470-847
FILING DATE:
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: Shoup, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/AGENT NUMBER: 00630-10501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: peptide

US-08-470-847-7

Query Match: 81.8%, Score 9; BR 1; Length 3;
Best Local Similarity: 66.7%; Pred. No. 1.9e+05;
Matches: 2; Mismatches: 1; Indels: 0;

QY 1 LXR 3
DB 1 LXR 3

RESULT 2

US-08-868-452-7
Sequence 7, Application US/08684527
Patent No. 6352972
GENERAL INFORMATION:
APPLICANT: Marcell E. Nimmi
APPLICANT: Frederick L. Hall
APPLICANT: Lingtao Wu
APPLICANT: Bo Han
APPLICANT: Edwin Shors
TITLE OF INVENTION: HORME MORPHOGENETIC PROTEINS AND THEIR
TITLE OF INVENTION: USE IN BONE GROWTH
FILE REFERENCE: 17972-11
CURRENT APPLICATION NUMBER: US/08/868,452C
CURRENT FILING DATE: 1997-06-04
REMARK OF SEQ ID NO: 51
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 7
LENGTH: 3
TYPE: PRT
REMARK: Human
US-08-868-452-7

Query Match: 81.8%; Score 9; BR 4; Length 3;
Best Local Similarity: 66.7%; Pred. No. 1.9e+05;
Matches: 2; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 LXR 3

DB 1 LXR 3

RESULT 3

US-08-288-405A-4
Sequence 4, Application US/08288405A
Patent No. 5556009
GENERAL INFORMATION:
APPLICANT: Chandy, Kaniandhara G.
APPLICANT: Kaiman, Katalin
APPLICANT: Chandy, Griscela
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5556009 Voltage Gated Potassium Channel
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ficht, Holbach, Test, Albritton & Herbert
ADDRESSEE: Attn: Walter H. Broder
STREET: 4 Embarcadero Center, Suite 400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/288,405A
FILING DATE: 10-AUG-1994
CLASSIFICATION: 4.45
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,431
 FILING DATE: 04-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/POCKET NUMBER: A-56844-1/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 498-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-288-405A-4

Query Match 81.8%; Score 9; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 DB 2 LAR 4

RESULT 4
 US-08-336-443A-36
 Sequence 36; Application US/0833643A
 Patent No. 5677144
 GENERAL INFORMATION:
 APPLICANT: Ulrich, Axel
 APPLICANT: Altes, Frank
 TITLE OF INVENTION: CCK-2, A No. 5677144-el Receptor Tyrosine Kinase
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/336,443A
 FILING DATE: 08-NOV-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/POCKET NUMBER: 769; 055
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 769-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-336-443A-36

Query Match 81.8%; Score 9; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 2 LSR 4

RESULT 5
 US-09-142-078-19
 Sequence 19; Application US/09142078
 Patent No. 6172641
 GENERAL INFORMATION:
 APPLICANT: Morale, R. Tyler
 APPLICANT: Zhou, Li-Ming
 APPLICANT: Layer, Richard L.
 TITLE OF INVENTION: Use of Conantokins
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rothwell, Fiqd, Ernst & Kutz, P.C.
 STREET: 555 Thirteenth Street, N.W., Suite 701-E
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/142,078
 FILING DATE: 10-FEB-1999
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: W0 US97/12652
 FILING DATE: 21-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/762,077
 FILING DATE: 06-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/684,750
 FILING DATE: 22-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Thuen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/POCKET NUMBER: 2414-145.A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 793-6040
 TELEFAX: 202-783-6041
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: Internal
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 4
 OTHER INFORMATION: Note "Xaa is
 OTHER INFORMATION: gamma-carboxyglutamic acid"
 US-09-142-078-19

Query Match 81.8%; Score 9; DB 4; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 DB 1 LAR 4

RESULT 6
 US-09-357-141-19
 Sequence 19; Application US/09357141
 Patent No. 6277825

```

: GENERAL INFORMATION:
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: McCabe, R. Tyler
: APPLICANT: Layer, Richard L.
: APPLICANT: Zhou, Li-Ming
: TITLE OF INVENTION: Use of Conantokins for Treating Pain
: FILE REFERENCE: 2314-171
: CURRENT APPLICATION NUMBER: US/09/357,141
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: US 09/293,277
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: US 09/142,078
: PRIOR FILING DATE: 1999-02-10
: PRIOR APPLICATION NUMBER: W/ 09/57,12552
: PRIOR FILING DATE: 1997-07-21
: PRIOR APPLICATION NUMBER: US 08/762,377
: PRIOR FILING DATE: 1996-12-06
: PRIOR APPLICATION NUMBER: US 09/694,752
: PRIOR FILING DATE: 1996-07-22
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: Patent In Vol. 2.0
: SEQ ID NO 19
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Coelus radiatus
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (4)
: OTHER INFORMATION: Xaa is gamma-carboxyglutamic acid.
: US-09-457-141-19

Query Match 81.8%; Score 9; DB 4; Length 4;
Best Local Similarity 66.7%; Prod No 1 9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 1 LAR 3

RESULT 7
US-09-533-889-19
: Sequence 19, Application US/09/533889
: Patent No. 6,499,574
: GENERAL INFORMATION:
: APPLICANT: McCabe, R. Tyler
: APPLICANT: Zhou, Li-Ming
: APPLICANT: Layer, Richard L.
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: TITLE OF INVENTION: Use of Conantokins
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Potlwell, Fwy. East & Kartz, P.O.
: STREET: 555 Thirtieth Street, N.W., Suite 701 E
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09/694,989
: FILING DATE: 23 MAR 2000
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/342,679
: FILING DATE: 10-FEB-1999
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: W/ 09/57,12552

```

```

: FILING DATE: 21 JUL 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/762,477
: FILING DATE: 06-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/684,750
: FILING DATE: 22 JUL 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Thuen, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: EXERCISE OF RIGHT NUMBER: 2111366A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-783-6040
: TELEFAX: 202-783-6041
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 amino acids
: TYPE: amino acid
: SYNOPSIS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: Internal
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Xaa is
: OTHER INFORMATION: gamma-carboxyglutamic acid"
: US-09-533-889-19

Query Match 81.8%; Score 9; DB 4; Length 4;
Best Local Similarity 66.7%; Prod No 1 9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 1 LAR 3

RESULT 8
US-07-626-923A-12
: Sequence 12, Application US/07/626923A
: GENERAL INFORMATION:
: APPLICANT: Yoshimura, Akihiko
: APPLICANT: Lombardi, Gregory D.
: APPLICANT: Ledish, Harvey
: TITLE OF INVENTION: MUTANT HIV NUCLEOTIDE AND USES
: TITLE OF INVENTION: THEREFOR
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAMILTON, BROOK, SMITH & KEYNOLDS, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02174
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 07/926,923A
: FILING DATE: 18 December 1990
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Ghandan, Patricia
: REGISTRATION NUMBER: 22,227
: EXERCISE OF RIGHT NUMBER: 2111366A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 861-4240
: TELEFAX: (617) 861-9540
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:

```


LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-626-923A-12

Query Match 81.8% Score 9; DB 1; Length 5;
 Best Local Similarity 66.7% Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 I I
 Db 1 LSR 3

RESULT 9
 US-08-357-264-5
 : Sequence 5, Application US/08357264
 : Patent No. 5541077
 : GENERAL INFORMATION:
 : APPLICANT: BURNIE MR., James P.
 : APPLICANT: MATTHEWS MS., Ruth C.
 : TITLE OF INVENTION: FUNGAL STRESS PROTEINS
 : NUMBER OF SEQUENCES: 1
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cushman, Darby & Cushman
 : STREET: 1100 New York Avenue, N.W.
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20005-3918
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/357,264
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/152669
 : FILING DATE: 16-NOV-1993
 : APPLICATION NUMBER: US 663897
 : FILING DATE: 14-MAR-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: KOKULIS, Paul N.
 : REGISTRATION NUMBER: 16773
 : TELEPHONE: 202-861-3000
 : TELEFAX: 202-861-3000
 : TELEX: 5714627 CUSH
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 US-08-357-264-5

Query Match 81.8% Score 9; DB 1; Length 5;
 Best Local Similarity 66.7% Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 I I
 Db 1 LSR 3

RESULT 10
 US-08-456-840-48
 : Sequence 38, Application US/08456248

Patent No. 5597908
 : GENERAL INFORMATION:
 : APPLICANT: Label-Peters, W. C.
 : APPLICANT: Butler, Sandra M.
 : TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
 : NUMBER OF SEQUENCES: 48
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: AVE No. 5597908e1
 : STREET: 122 Placer Drive
 : CITY: Rockville
 : STATE: Maryland
 : COUNTRY: US
 : ZIP: 20850
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/456,840
 : FILING DATE: 01 JUN-1995
 : CLASSIFICATION: 536
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 09/266,407
 : FILING DATE: 27 JUN-1994
 : APPLICATION NUMBER: US 09/172,461
 : FILING DATE: 21-DEC-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Gormley, Mary E.
 : REGISTRATION NUMBER: 44,409
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 301-258-5200
 : TELEFAX: 301-977-0847
 : INFORMATION FOR SEQ ID NO: 38:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 US-08-456-840-48

Query Match 31.8% Score 9; DB 1; Length 5;
 Best Local Similarity 56.7% Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 I I
 Db 1 LSR 3

RESULT 11
 US-08-672-514-5
 : Sequence 5, Application US/08672514
 : Patent No. 5686248
 : GENERAL INFORMATION:
 : APPLICANT: HORNIE MR., James P.
 : APPLICANT: MATTHEWS MS., Ruth C.
 : TITLE OF INVENTION: FUSAL STRESS PROTEINS
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cushman, Darby & Cushman
 : STREET: 1100 New York Avenue, N.W.
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20005-3918
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/672,514

```

1 FILING DATE: 28-JUN-1996
2 CLASSIFICATION: 445
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 08/152,659
5 FILING DATE: 16-NOV-1991
6 APPLICATION NUMBER: US 08/152,669
7 FILING DATE: 16-NOV-1993
8 APPLICATION NUMBER: US 66,897
9 FILING DATE: 14-MAR-1993
10 ATTORNEY/AGENT INFORMATION:
11 NAME: KOKULIS, PAUL N.
12 REGISTRATION NUMBER: 16773
13 REFERENCE CITATION NUMBER: 08/152,659
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 202 861-4000
16 TELEFAX: 202 922-0944
17
18 INFORMATION FOR SEQ ID NO: 5:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 5 amino acids
21 TYPE: amino acid
22 TOPOLOGY: linear
23 MOLECULE TYPE: peptide
24 US-08-672-514-5

```

```

Query Match      81.8%  Score 9;  DB 1;  Length 5;
Best Local Similarity 66.7%  Pred. No. 1.9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Gaps 0;

```

```

QY 1 LXR 3
1 1
DB 1 LXR 3

```

```

RESULT 12
US-07-789-184-173
1 Sequence 173, Application US/07789184
2 Patent No. 5688768
3 GENERAL INFORMATION:
4 APPLICANT: CUREBLIN, SHAWN R.
5 TITLE OF INVENTION: RESPERANT THERAPEUTIC AND
6 TITLE OF INVENTION: RELATED PHARMACEUTICALS
7 NUMBER OF SEQUENCES: 223
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: MORRISON & FORSTER
10 STREET: 755 Palo Alto Road
11 CITY: Palo Alto
12 STATE: California
13 COUNTRY: USA
14 ZIP: 94304 1018
15 COMPUTER READABLE FORM:
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent In Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/07789,184
21 FILING DATE: 19911107
22 CLASSIFICATION: 514
23 ATTORNEY/AGENT INFORMATION:
24 NAME: MIRASHIGE, KATE H.
25 REGISTRATION NUMBER: 29,969
26 REFERENCE CITATION NUMBER: 08/000-0000, 20
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (415) 814-5600
29 TELEFAX: (415) 494-0792
30 TELEX: 44-0154
31 INFORMATION FOR SEQ ID NO: 173:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 5 amino acids
34 TYPE: AMINO ACID
35 STRANDEDNESS: single

```

```

1 TOPOLOGY: linear
2 FEATURE:
3 NAME/KEY: Modified site
4 LOCATION: 5
5 OTHER INFORMATION: Note "this position is R NBZ."
6 US-07-789-184-173

```

```

Query Match      81.8%  Score 9;  DB 1;  Length 5;
Best Local Similarity 66.7%  Pred. No. 1.9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Gaps 0;

```

```

QY 1 LXR 3
1 1
DB 3 LAR 5

```

```

RESULT 13
US-08-406-192-12
1 Sequence 12, Application US/08406192
2 Patent No. 5749287
3 GENERAL INFORMATION:
4 APPLICANT: Wilbur, D. Scott
5 APPLICANT: Prathare, Pradip M
6 TITLE OF INVENTION: Biotinylated Cobalamins
7 NUMBER OF SEQUENCES: 47
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
10 STREET: 1420 Fifth Avenue, Suite 2800
11 CITY: Seattle
12 STATE: Washington
13 COUNTRY: U.S.A.
14 ZIP: WA 98101-2333
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.40
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08406,192
22 FILING DATE: 16-MAR-1995
23 CLASSIFICATION: 530
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/224,841
26 FILING DATE: 08-APR-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Kozoni, George E.
29 REGISTRATION NUMBER: 47,919
30 REFERENCE CITATION NUMBER: RE018947
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (206) 682 8100
33 TELEFAX: (206) 224 0779
34 TELEX: 4948023
35 INFORMATION FOR SEQ ID NO: 12:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 5 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: peptide
42 US-08-406-192-12

```

```

Query Match      81.8%  Score 9;  DB 1;  Length 5;
Best Local Similarity 66.7%  Pred. No. 1.9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Gaps 0;

```

```

QY 1 LXR 3
1 1
DB 3 LAR 5

```

```

RESULT 14
US-08-460-443B-37
1 Sequence 47, Application US/0840443B

```

Patent No. 5741664
 GENERAL INFORMATION:
 APPLICANT: Marcus D. Ballinger and James A. Wells
 TITLE OF INVENTION: SUBSTITUTED VARIANTS CATABOLIC OF CHLAVING
 TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08,460,343B
 FILING DATE: 01-Jun-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/398028
 FILING DATE: 03-mar-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 46,575
 REFERENCE/DOCKET NUMBER: 00946C1
 TELEPHONE: 650/425-8228
 TELEFAX: 650/425-9881
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-460-343B-37

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 DB 1 LTR 3

RESULT 15
 US-08-460-343B-38
 Sequence 38, Application US/0846043B
 Patent No. 5741664
 GENERAL INFORMATION:
 APPLICANT: Marcus D. Ballinger and James A. Wells
 TITLE OF INVENTION: SUBSTITUTED VARIANTS CATABOLIC OF CHLAVING
 TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,343B
 FILING DATE: 01-Jun-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/398028
 FILING DATE: 03-mar-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 46,575
 REFERENCE/DOCKET NUMBER: 00946C1
 TELEPHONE: 650/425-8228
 TELEFAX: 650/425-9881
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-460-443B-38

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 DB 2 LSR 4

RESULT 16
 US-08-475-263-174
 Sequence 173, Application US/08475263
 Patent No. 5756994
 GENERAL INFORMATION:
 APPLICANT: COACHING, SHAIN K.
 APPLICANT: SCARFOPOL, ROBERT M.
 TITLE OF INVENTION: RECOMBINANT TROPHOBlastic RECEPTOR AND
 TITLE OF INVENTION: RELATED PHARMACEUTICALS
 NUMBER OF SEQUENCES: 223
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 2000 Pennsylvania Ave., NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475,263
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,459
 REFERENCE/DOCKET NUMBER: 22000 20502.03
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0764
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 174:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 5
 OTHER INFORMATION: /note "This position is R N02."
 US-08-475-263-173

Query Match 81.8%; Score 9; DB 1; Length 5;

Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2: Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
1 1
1b 3 LXR 5

RESULT 17

US-08-498-028B-47
Sequence 47, Application US/08/498028B
Patent No. 5789295

GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WinEdit (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 4.45

ATTORNEY/AGENT INFORMATION:
NAME: Kubinco, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DECK NUMBER: 19946

TELEPHONE: 650/225-9229
TELEFAX: 650/225-9229

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-498-028B-47

Query Match 81.8%; Score 9; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2: Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
1 1
1b 1 LXR 3

RESULT 18

US-08-498-028B-48
Sequence 48, Application US/08/498028B
Patent No. 5789295

GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WinEdit (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 4.45

ATTORNEY/AGENT INFORMATION:
NAME: Kubinco, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DECK NUMBER: 19946

TELEPHONE: 650/225-9229
TELEFAX: 650/225-9229

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-498-028B-38

Query Match 81.8%; Score 9; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2: Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
1 1
1b 2 LXR 4

RESULT 19

US-08-266-407A-48
Sequence 48, Application US/08/266407A
Patent No. 5786156

GENERAL INFORMATION:
APPLICANT: Laddol-Peters, W. C.
REFERENCE/DECK NUMBER: 19946

TITLE OF INVENTION: IMPROVED ACTIVE PEPTIDES OF Apo(a)
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:

ADDRESSEE: ARZO NO. 5786156d
STREET: 1340 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,407A
FILING DATE: 27-JUN-1994
CLASSIFICATION: 4.45

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:

NAME: Gormley, Mary F.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-258-9200
TELEFAX: 301-977-0847

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: Linear

MOLECULE TYPE: protein
US-08-266-407A-38

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3
 | |
 Db 1 LSR 3

RESULT 20

US-08-485-886-173
 : Sequence 173 Application US-0804prog
 : Patent No. 5788248
 : GENERAL INFORMATION:
 : APPLICANT: COUGHLIN, SHAUN R.
 : APPLICANT: SCARBOROUGH, ROBERT M.
 : TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 : TITLE OF INVENTION: RELATED PHARMACEUTICALS
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MOPPINSON & POEPPER
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304-1018
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/485,886
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/789,184
 : FILING DATE: 07-NOV-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: MUKASHIGE, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/AGENT NUMBER: 22009-20502.20
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 813-5600
 : TELEFAX: (415) 494-0792
 : TELEX: 34-0154
 : INFORMATION FOR SEQ ID NO: 173.
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: Modified-site
 : LOCATION: 5
 : OTHER INFORMATION: /note= "this position is R NH2."
 US-08-485-886-173

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3
 | |
 Db 3 LSR 5

RESULT 21

US-08-504-265B-37
 : Sequence 37 Application US/080504265B
 : Patent No. 5837516
 : GENERAL INFORMATION:
 : APPLICANT: Marcus D. Ballinger and James A. Wells

: TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
 : TITLE OF INVENTION: SUBSTITUTES CONTAINING BASIC RESIDUES
 : NUMBER OF SEQUENCES: 90
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 M floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatIn (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: 08/087,504/265B
 : FILING DATE: 19-Jul-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/398,928
 : FILING DATE: 03-MAR-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kubiacek, Jeffrey S.
 : REGISTRATION NUMBER: 36,575
 : REFERENCE/AGENT NUMBER: 10936PJ
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650/225-8228
 : TELEFAX: 650/952-9881
 : INFORMATION FOR SEQ ID NO: 37:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: Amino Acid
 : TOPOLOGY: Linear
 : US-08-504-265B-37

Query Match 81.8%; Score 9; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3
 | |
 Db 1 LTR 3

RESULT 22

US-08-504-265B-38
 : Sequence 38 Application 08/087516
 : Patent No. 5837516
 : GENERAL INFORMATION:
 : APPLICANT: Marcus D. Ballinger and James A. Wells
 : TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
 : TITLE OF INVENTION: SUBSTITUTES CONTAINING BASIC RESIDUES
 : NUMBER OF SEQUENCES: 90
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 M floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatIn (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: 08/087,504/265B
 : FILING DATE: 19-Jul-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/398,928
 : FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Kubinek, Jeffrey S.
 REGISTRATION NUMBER: 30,675
 REFERENCE/DECKET NUMBER: P0946P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-8229
 TELEFAX: 650/952-0881
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08 504-265B-38

Query Match 81.8% Score 9; DB 2; Length 5;
 Best Local Similarity 66.7% Prod. No. 1.9c-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 DB 2 LSR 4

RESULT 24
 US-08 545-151-12
 : Sequence 12, Application US/08545151
 : Patent No. 5840712
 : GENERAL INFORMATION:
 : APPLICANT: Mordan Jr, A. Charles
 : APPLICANT: Whitby, D. Scott
 : APPLICANT: Pruthi, Pradip M
 : TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
 : TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
 : NUMBER OF SEQUENCES: 47
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Christensen & Connor, Johnson & Kindness PLLC
 : STREET 1120 Fifth Avenue, Suite 2400
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: U.S.A.
 : ZIP: WA 98101 2400
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/545,151
 : FILING DATE: 19-OCT-1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCI/US95/04404
 : FILING DATE: 07-APR-1995
 : APPLICATION NUMBER: US 08/406,192
 : FILING DATE: 16-MAR-1995
 : APPLICATION NUMBER: US 08/406,194
 : FILING DATE: 16-MAR-1995
 : APPLICATION NUMBER: US 08/406,191
 : FILING DATE: 16-MAR-1995
 : APPLICATION NUMBER: US 08/224,831
 : FILING DATE: 08-APR-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Renzoni, George E.
 : REGISTRATION NUMBER: 37,919
 : REFERENCE/DECKET NUMBER: P0C119478
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (206) 682 8100
 : TELEFAX: (206) 224 0779
 : TELEX: 4948023
 : INFORMATION FOR SEQ ID NO: 12:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: amino acid

STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 US-08-545-151-12

Query Match 81.8% Score 9; DB 2; Length 5;
 Best Local Similarity 66.7% Prod. No. 1.9c-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 DB 3 LSR 5

RESULT 24
 US-08-392-973A-7
 : Sequence 7, Application US/08092974A
 : Patent No. 5844453
 : GENERAL INFORMATION:
 : APPLICANT: Holder, Andrew T.
 : APPLICANT: Reathie, James
 : TITLE OF INVENTION: GROWTH HORMONE POTENTIATING MOLECULES
 : NUMBER OF SEQUENCES: 37
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: HALE AND DERR LLP
 : STREET 60 State Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: United States of America
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.40
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/092,974A
 : FILING DATE: 25-APR-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BAKER, Hollie L.
 : REGISTRATION NUMBER: 31,321
 : REFERENCE/DECKET NUMBER: 102286,301
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-526-6000
 : TELEFAX: 617-526-5000
 : INFORMATION FOR SEQ ID NO: 7:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: amino acid
 : TOPOLOGY: Linear
 : MOLECULE TYPE: peptide
 : FRAGMENT TYPE: internal
 : FEATURE:
 : NAME/KEY: Peptide
 : LOCATION: 1-5
 : OTHER INFORMATION: Z-score "91 95 RESIDU OF OVINE
 : OTHER INFORMATION: "B-OSSE"

Query Match 81.8% Score 9; DB 2; Length 5;
 Best Local Similarity 66.7% Prod. No. 1.9c-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 DB 3 LSR 5

RESULT 25
 US-08-392-973A-8
 : Sequence 8, Application US/08092974A
 : Patent No. 5844453

```

1  GENERAL INFORMATION:
2  APPLICANT: BEATTIE, James
3  TITLE OF INVENTION: GROWTH HORMONE POTENTIATING MOLECULES
4  NUMBER OF SEQUENCES: 37
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: HALE AND DORR LLP
7  STREET: 60 State Street
8  CITY: Boston
9  STATE: MA
10 COUNTRY: United States of America
11 ZIP: 02109
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US 09/498,556
19 FILING DATE: 25-APR-1995
20 CLASSIFICATION: 424
21 ATTORNEY/AGENT INFORMATION:
22 NAME: BAKER, Hollie L.
23 REGISTRATION NUMBER: 31,321
24 REFERENCE TO PCT NUMBER: 199286 301
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 617-526-6000
27 TELEFAX: 617-526-6000
28 INFORMATION FOR SEQ ID NO: 8:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 5 amino acids
31 TYPE: amino acid
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 FRAGMENT TYPE: internal
35 FEATURE:
36 NAME/KEY: Peptide
37 LOCATION: 1..5
38 OTHER INFORMATION: "92 95 RESIDUE OF AVINE"
39 OTHER INFORMATION: HORMONE"
40 US-09-362-973A-8
41 Query Match 91.8% Score 9: 98 2: Length 5:
42 Best Local Similarity 66.7% Pred. No. 1.9e+05;
43 Matches 2: Conservative 0; Mismatches 1; Indels 0, Gaps 0.
44 QY 1 LXR 4
45 DB 2 LSR 4
46 RESULT 26
47 US-08-492-973A-9
48 Sequence 9, Application US/09492973A
49 Patent No. 5843453
50 GENERAL INFORMATION:
51 APPLICANT: BEATTIE, James
52 TITLE OF INVENTION: GROWTH HORMONE POTENTIATING MOLECULES
53 NUMBER OF SEQUENCES: 37
54 CORRESPONDENCE ADDRESS:
55 ADDRESSEE: HALE AND DORR LLP
56 STREET: 60 State Street
57 CITY: Boston
58 STATE: MA
59 COUNTRY: United States of America
60 ZIP: 02109
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Floppy disk
63 COMPUTER: IBM PC compatible
64 OPERATING SYSTEM: PC-DOS/MS-DOS
65 SOFTWARE: PatentIn Release #1.0, Version #1.30
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US 08/492,973
68 FILING DATE: 25-APR-1995
69 CLASSIFICATION: 424
70 ATTORNEY/AGENT INFORMATION:
71 NAME: BAKER, Hollie L.
72 REGISTRATION NUMBER: 31,321
73 REFERENCE TO PCT NUMBER: 199286 301
74 TELECOMMUNICATION INFORMATION:
75 TELEPHONE: 617-526-6000
76 TELEFAX: 617-526-6000
77 INFORMATION FOR SEQ ID NO: 9:
78 SEQUENCE CHARACTERISTICS:
79 LENGTH: 5 amino acids
80 TYPE: amino acid
81 TOPOLOGY: linear
82 MOLECULE TYPE: peptide
83 FRAGMENT TYPE: internal
84 FEATURE:
85 NAME/KEY: Peptide
86 LOCATION: 1..5
87 OTHER INFORMATION: "94 97 RESIDUE OF AVINE"
88 OTHER INFORMATION: HORMONE"
89 US-08-492-973A-9
90 Query Match 91.8% Score 9: 98 2: Length 5:
91 Best Local Similarity 66.7% Pred. No. 1.9e+05;
92 Matches 2: Conservative 0; Mismatches 1; Indels 0, Gaps 0.
93 QY 1 LXR 4
94 DB 2 LSR 4
95 RESULT 27
96 US-08-477-362-173
97 Sequence 174, Application US/08477462
98 Patent No. 5849507
99 GENERAL INFORMATION:
100 APPLICANT: STABOWICZ, ROBERT M.
101 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
102 TITLE OF INVENTION: RECOMBINANT PHARMACEUTICALS
103 NUMBER OF SEQUENCES: 223
104 CORRESPONDENCE ADDRESS:
105 ADDRESSEE: MORGAN & FAULKNER
106 STREET: 755 Page Mill Road
107 CITY: Palo Alto
108 STATE: California
109 COUNTRY: USA
110 ZIP: 94304-1018
111 COMPUTER READABLE FORM:
112 MEDIUM TYPE: Floppy disk
113 COMPUTER: IBM PC compatible
114 FILING DATE: 07-JUN-1995
115 SOFTWARE: PatentIn Release #1.0, Version #1.25
116 CURRENT APPLICATION DATA:
117 APPLICATION NUMBER: US/98/177,362
118 FILING DATE: 07-JUN-1995
119 CLASSIFICATION: 435
120 PRIOR APPLICATION DATA:
121 APPLICATION NUMBER: US 07/789,184
122 FILING DATE: 07-NOV-1991
123 ATTORNEY/AGENT INFORMATION:
124 NAME: MURASHIGE, KATE H.
125 REGISTRATION NUMBER: 29,959
126 REFERENCE TO PCT NUMBER: 1990 0050420
127 TELECOMMUNICATION INFORMATION:
128 TELEPHONE: (415) 814-5600
129 TELEFAX: (415) 494-0792
130 TELETYPE: 34-0154
131 INFORMATION FOR SEQ ID NO: 174:
132 SEQUENCE CHARACTERISTICS:
133 LENGTH: 5 amino acids

```

```

1  APPLICATION NUMBER: US/98/052,973A
2  FILING DATE: 25-APR-1995
3  CLASSIFICATION: 424
4  ATTORNEY/AGENT INFORMATION:
5  NAME: BAKER, Hollie L.
6  REGISTRATION NUMBER: 31,321
7  REFERENCE TO PCT NUMBER: 199286 301
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 617-526-6000
10 TELEFAX: 617-526-6000
11 INFORMATION FOR SEQ ID NO: 9:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 5 amino acids
14 TYPE: amino acid
15 TOPOLOGY: linear
16 MOLECULE TYPE: peptide
17 FRAGMENT TYPE: internal
18 FEATURE:
19 NAME/KEY: Peptide
20 LOCATION: 1..5
21 OTHER INFORMATION: "94 97 RESIDUE OF AVINE"
22 OTHER INFORMATION: HORMONE"
23 US-08-492-973A-9
24 Query Match 91.8% Score 9: 98 2: Length 5:
25 Best Local Similarity 66.7% Pred. No. 1.9e+05;
26 Matches 2: Conservative 0; Mismatches 1; Indels 0, Gaps 0.
27 QY 1 LXR 4
28 DB 1 LSR 3
29 RESULT 27
30 US-08-477-362-173
31 Sequence 174, Application US/08477462
32 Patent No. 5849507
33 GENERAL INFORMATION:
34 APPLICANT: STABOWICZ, ROBERT M.
35 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
36 TITLE OF INVENTION: RECOMBINANT PHARMACEUTICALS
37 NUMBER OF SEQUENCES: 223
38 CORRESPONDENCE ADDRESS:
39 ADDRESSEE: MORGAN & FAULKNER
40 STREET: 755 Page Mill Road
41 CITY: Palo Alto
42 STATE: California
43 COUNTRY: USA
44 ZIP: 94304-1018
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: Floppy disk
47 COMPUTER: IBM PC compatible
48 FILING DATE: 07-JUN-1995
49 SOFTWARE: PatentIn Release #1.0, Version #1.25
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER: US/98/177,362
52 FILING DATE: 07-JUN-1995
53 CLASSIFICATION: 435
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 07/789,184
56 FILING DATE: 07-NOV-1991
57 ATTORNEY/AGENT INFORMATION:
58 NAME: MURASHIGE, KATE H.
59 REGISTRATION NUMBER: 29,959
60 REFERENCE TO PCT NUMBER: 1990 0050420
61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE: (415) 814-5600
63 TELEFAX: (415) 494-0792
64 TELETYPE: 34-0154
65 INFORMATION FOR SEQ ID NO: 174:
66 SEQUENCE CHARACTERISTICS:
67 LENGTH: 5 amino acids

```

1 TYPE: amino acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 FEATURE:
5 NAME/KEY: Modified-site
6 LOCATION: 5
7 OTHER INFORMATION: /note: "This position is R NH2."
8 US 08-477-362-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 3 LXR 5

RESULT 28
US 08-477-134-173
1 Sequence 173, Application US/08/173134
2 Patent No. 5856448
3 GENERAL INFORMATION:
4 APPLICANT: SCARBERG, ROBERT M.
5 TITLE OF INVENTION: EPY-METHAM: THE OPIUM SPECTRUM AND
6 NUMBER OF SEQUENCES: 224
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: MERRISON & PFEISTER
9 STREET: 755 Page Mill Road
10 CITY: Palo Alto
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94304-1018
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: 08/047,473-173
20 FILING DATE: 07-JUN-1995
21 CLASSIFICATION: 546
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/789,184
24 FILING DATE: 07-NOV-1991
25 ATTORNEY/AGENT INFORMATION:
26 NAME: MURASHIGE, KATE H.
27 REGISTRATION NUMBER: 29,959
28 REFERENCE/JACKET NUMBER: 22000-20502.20
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (415) 814-5600
31 TELEFAX: (415) 494-0792
32 TELEX: 44-0154
33 INFORMATION FOR SEQ ID NO: 173:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 5 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 FEATURE:
40 NAME/KEY: Modified-site
41 LOCATION: 5
42 OTHER INFORMATION: /note: "This position is R NH2."
43 US 08-477-134-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1

1 TYPE: amino acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 FEATURE:
5 NAME/KEY: Modified-site
6 LOCATION: 5
7 OTHER INFORMATION: /note: "This position is R NH2."
8 US 08-477-362-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 3 LXR 5

RESULT 28
US 08-477-134-173
1 Sequence 173, Application US/08/173134
2 Patent No. 5856448
3 GENERAL INFORMATION:
4 APPLICANT: SCARBERG, ROBERT M.
5 TITLE OF INVENTION: EPY-METHAM: THE OPIUM SPECTRUM AND
6 NUMBER OF SEQUENCES: 224
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: MERRISON & PFEISTER
9 STREET: 755 Page Mill Road
10 CITY: Palo Alto
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94304-1018
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: 08/047,473-173
20 FILING DATE: 07-JUN-1995
21 CLASSIFICATION: 546
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/789,184
24 FILING DATE: 07-NOV-1991
25 ATTORNEY/AGENT INFORMATION:
26 NAME: MURASHIGE, KATE H.
27 REGISTRATION NUMBER: 29,959
28 REFERENCE/JACKET NUMBER: 22000-20502.20
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (415) 814-5600
31 TELEFAX: (415) 494-0792
32 TELEX: 44-0154
33 INFORMATION FOR SEQ ID NO: 173:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 5 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 FEATURE:
40 NAME/KEY: Modified-site
41 LOCATION: 5
42 OTHER INFORMATION: /note: "This position is R NH2."
43 US 08-477-134-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1

1 TYPE: amino acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 FEATURE:
5 NAME/KEY: Modified-site
6 LOCATION: 5
7 OTHER INFORMATION: /note: "This position is R NH2."
8 US 08-477-362-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 3 LXR 5

RESULT 29
US 08-892-544-48
1 Sequence 48, Application US/08/054448
2 Patent No. 5874544
3 GENERAL INFORMATION:
4 APPLICANT: Laddell Peters, W. C.
5 TITLE OF INVENTION: Immunoactive Peptides of Apo(a)
6 NUMBER OF SEQUENCES: 48
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: AKZO No. 5874544-1
9 STREET: 1430 Piccard Drive
10 CITY: Rockville
11 STATE: Maryland
12 COUNTRY: US
13 ZIP: 20850
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: 08/054,448-48
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US/08/266,407
24 FILING DATE: 27-JUN-1994
25 APPLICATION NUMBER: US 08/172,461
26 FILING DATE: 21-DEC-1993
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Gormley, Mary E.
29 REGISTRATION NUMBER: 44,409
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 301-288-5200
32 TELEFAX: 301-977-0847
33 INFORMATION FOR SEQ ID NO: 48:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 4 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38 FEATURE:
39 NAME/KEY: Modified-site
40 LOCATION: 5
41 OTHER INFORMATION: /note: "This position is R NH2."
42 US 08-892-544-48

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 3 LXR 5

RESULT 30
US 08-473-469A-174
1 Sequence 173, Application US/08/473469A
2 Patent No. 6024936
3 GENERAL INFORMATION:
4 APPLICANT: COUGHIN, SHAUN R.
5 TITLE OF INVENTION: RECOMBINANT THROMBIN ESTERASE AND
6 NUMBER OF SEQUENCES: 224
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: MERRISON & PFEISTER
9 STREET: 755 Page Mill Road
10 CITY: Palo Alto
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94304-1018

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 3 LXR 5


```

: COMPUTER PEAKABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/475,489A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/789,184
: FILING DATE: 1991-11-07
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 173:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R 882."
:
: Query Match 81.8%; Score 9; DB 3; Length 5;
: Best Local Similarity 66.7%; Pred. No. 1,96-05;
: Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 LXR 3
: Db 3 LAR 5
:
: RESULT 31
: US-08-485-695-173
: Sequence 173, Application US/08485695
: Patent No. 6124191
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FORSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER PEAKABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,695
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 173:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R 882."

```

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: REFERENCE/SEQUENCE NUMBER: 29,959, 29,959, 29,959, 29,959
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 173:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R 882."
:
: Query Match 81.8%; Score 9; DB 3; Length 5;
: Best Local Similarity 66.7%; Pred. No. 1,96-05;
: Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 LXR 3
: Db 3 LAR 5
:
: RESULT 42
: US-08-018-760-174
: Sequence 174, Application US/08018760
: Patent No. 6197541
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FORSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER PEAKABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/018,760
: FILING DATE: 17-FEB-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 174:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R 882."

```

US-09-018-760-174

Query Match 81.8%; Score 9; DB 4; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1,960,05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 4 LXR 5

RESULT 44

US-09-246-500B-17
 : Sequence 17, Application US/09246500B
 : Patent No. 6,245,494
 : GENERAL INFORMATION:
 : APPLICANT: Hojii, Tony E.
 : TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
 : TITLE OF INVENTION: Protein Associated Serine Protease Activity and Methods
 : TITLE OF INVENTION: Using the Substrates
 : FILE REFERENCE: 24730-2204
 : CURRENT APPLICATION NUMBER: US/09/246,500B
 : CURRENT FILING DATE: 1999-02-08
 : NUMBER OF SEQ ID NOS: 19
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 17
 : LENGTH: 5
 : TYPE: PRT
 : ORGANISM: MASP substrate
 US-09-246-500B-17

Query Match 81.8%; Score 9; DB 4; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1,960,05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 4 LXR 5

RESULT 45

US-09-018-760-174
 : Patent No. 5,169,933
 : APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG,
 : JALAN R.; NICHOLS, EVERETT I.
 : TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS
 : FOR ENHANCED CYTOTOXICITY AND IMAGING
 : NUMBER OF SEQUENCES: 45
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/97/990,241
 : FILING DATE: 07-AUG-1989
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 242,347
 : FILING DATE: 15-AUG-1988
 : SEQ ID NO: 16;
 : LENGTH: 5
 : TYPE: PRT
 : ORGANISM: MASP substrate
 US-09-018-760-174

Query Match 81.8%; Score 9; DB 6; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1,960,05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 4 LXR 5

RESULT 46

US-09-246-500B-17
 : Patent No. 5,464,756
 : APPLICANT: HENNIG, PIERRE L.; VANDER, ROCHER L.; WILKINS,
 : JAMES A.; YANISURA, DANIEL G.
 : TITLE OF INVENTION: PEPTIDES AND COMPOSITIONS FOR THE

ISOLATION HUMAN RELAXIN

NUMBER OF SEQUENCES: 42
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/97/990,266
 : FILING DATE: 01-JUL-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 447,550
 : FILING DATE: 04-MAY-1989
 : SEQ ID NO: 42;
 : LENGTH: 5
 : TYPE: PRT
 : ORGANISM: HUMAN
 US-09-246-500B-17

Query Match 81.8%; Score 9; DB 6; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1,960,05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 1 LXR 4

RESULT 46

US-08-246-427-11
 : Sequence 11, Application US/08246427
 : Patent No. 5,641,310
 : GENERAL INFORMATION:
 : APPLICANT: Ward, Eric
 : APPLICANT: Votruba, Sandra
 : APPLICANT: Koizumi, Sain-Ichi
 : APPLICANT: Tada, Sachio
 : APPLICANT: Mori, Ichiro
 : APPLICANT: Iwasaki, Gojii
 : TITLE OF INVENTION: Herbicide Resistant Plants
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CITRAGEIC Corporation
 : STREET: 7 Skyline Drive
 : CITY: Hawthorne
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10532

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/98/246,427
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/96/1,644
 : FILING DATE: 13 MAY 1993

ATTORNEY/AGENT INFORMATION:
 NAME: Spruill, W. Murray
 REGISTRATION NUMBER: 32,943
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8615
 TELEFAX: (919) 541-8689
 : INFORMATION PER SEQ ID NO: 11:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 6 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : HYPOTHEetical: No
 : FRAGMENT TYPE: internal
 : FEATURE:
 : NAME/KEY: Peptide
 : LOCATION: 1-6
 : OTHER INFORMATION: Zcode "Sequence for Internal

Patent No. 5541310
OTHER INFORMATION: peptide #2 of purified IGDP"

Query Match 81.8% Score 9; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
DB 3 LSR 5

RESULT 47

US-07-923-724-35
Sequence 35, Application US/07022724
Patent No. 698292
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fahrström, Richard B.
TITLE OF INVENTION: Production of Phylase Degraded Enzymes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbatu, Michele A.
REGISTRATION NUMBER: 31,851
REFERENCE/DOCKET NUMBER: 1050,0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: both

US-07-923-724-35

Query Match 81.8% Score 9; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 4
DB 4 LSR 6

RESULT 48

US-08-641-427A-2
Sequence 3, Application US/08/64142A
Patent No. 5811094
GENERAL INFORMATION:
APPLICANT: MERRILL, Carl R.
APPLICANT: CAMERON, Richard M.
APPLICANT: ADHYA, Sankar L.
TITLE OF INVENTION: ANTIBACTERIAL LIBRARY WITH BACTERIOPHAGE
TITLE OF INVENTION: GENETICALLY MODIFIED TO DELAY INACTIVATION BY THE HOST
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Gram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005 5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,427A
FILING DATE: 12 APR 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,956
FILING DATE: 05-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/593,269
FILING DATE: 29 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: KILLS, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 10026-6002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 81.8% Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 4
DB 1 LAR 4

RESULT 49

US-08-806-203-2
Sequence 2, Application US/08/806203
Patent No. 5830434
GENERAL INFORMATION:
APPLICANT: TAYLOR, IAN L.
APPLICANT: GUTTS, THOMAS
TITLE OF INVENTION: METHODS OF TREATING DM1 INSULIN
REPERTOIR DIABETES MELLITUS WITH PANCREATIC POLYPEPTIDE

1 NUMBER OF SEQUENCES: 5
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 4 STREET: Suite 1200, 127 Peachtree Street
 5 CITY: Atlanta
 6 STATE: Georgia
 7 COUNTRY: USA
 8 ZIP: 30303
 9
 10 COMPUTER READABLE FORM:
 11 MEDIUM TYPE: floppy disk
 12 COMPUTER: IBM PC compatible
 13 OPERATING SYSTEM: PC-DOS/MS-DOS
 14 SOFTWARE: Patent In Release #1.0, Version #1.40
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US/08/806,204
 17 FILING DATE:
 18 CLASSIFICATION: 514
 19 ATTORNEY/AGENT INFORMATION:
 20 NAME: Spratt, Gwendolyn D.
 21 REGISTRATION NUMBER: 36,016
 22 REFERENCE/CHECK NUMBER: 19070,0028
 23 TELECOMMUNICATION INFORMATION:
 24 TELEPHONE: 404/688-0770
 25 TELEFAX: 404/688-9880
 26 INFORMATION FOR SEQ ID NO: 2:
 27 SEQUENCE CHARACTERISTICS:
 28 LENGTH: 6 amino acids
 29 TYPE: amino acid
 30 STRANDEDNESS: not relevant
 31 TOPOLOGY: linear
 32 MOLECULE TYPE: peptide
 33 US-08-806-204-2

Query Match 81.8%; Score 9; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 3
 1 1
 DB 1 LTR 3

1 RESULT 40
 2 US-08-806-204-3
 3 Sequence 4, Application US/08806203
 4 Patent No. 583044
 5 GENERAL INFORMATION:
 6 APPLICANT: TAYLOR, IAN L.
 7 APPLICANT: GETTYS, THOMAS
 8 TITLE OF INVENTION: METHODS OF TREATING NON-INSULIN
 9 TYPE OF INVENTION: DEPENDENT DIABETES MELLITUS WITH PANCREATIC POLYPEPTIDE
 10 NUMBER OF SEQUENCES: 5
 11 CORRESPONDENT ADDRESS:
 12 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 13 STREET: Suite 1200, 127 Peachtree Street
 14 CITY: Atlanta
 15 STATE: Georgia
 16 COUNTRY: USA
 17 ZIP: 30303
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: floppy disk
 20 COMPUTER: IBM PC compatible
 21 OPERATING SYSTEM: PC-DOS/MS-DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.40
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/806,204
 25 FILING DATE:
 26 CLASSIFICATION: 514
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: Spratt, Gwendolyn D.
 29 REGISTRATION NUMBER: 36,016
 30 REFERENCE/CHECK NUMBER: 19070,0028
 31 TELECOMMUNICATION INFORMATION:

1 TELEPHONE: 404/688-0770
 2 TELEFAX: 404/688-9880
 3 INFORMATION FOR SEQ ID NO: 4:
 4 SEQUENCE CHARACTERISTICS:
 5 LENGTH: 6 amino acids
 6 TYPE: amino acid
 7 STRANDEDNESS: not relevant
 8 TOPOLOGY: linear
 9 MOLECULE TYPE: peptide
 10 US-08-806-204-4

Query Match 81.8%; Score 9; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 4
 1 1
 DB 1 LTR 4

1 RESULT 41
 2 US-08-806-204-4
 3 Sequence 4, Application US/08806204
 4 Patent No. 583044
 5 GENERAL INFORMATION:
 6 APPLICANT: TAYLOR, IAN L.
 7 APPLICANT: GETTYS, THOMAS
 8 TITLE OF INVENTION: METHODS OF TREATING NON-INSULIN
 9 TYPE OF INVENTION: DEPENDENT DIABETES MELLITUS WITH PANCREATIC POLYPEPTIDE
 10 NUMBER OF SEQUENCES: 5
 11 CORRESPONDENT ADDRESS:
 12 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 13 STREET: Suite 1200, 127 Peachtree Street
 14 CITY: Atlanta
 15 STATE: Georgia
 16 COUNTRY: USA
 17 ZIP: 30303
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: floppy disk
 20 COMPUTER: IBM PC compatible
 21 OPERATING SYSTEM: PC-DOS/MS-DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.40
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/806,204
 25 FILING DATE:
 26 CLASSIFICATION: 514
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: Spratt, Gwendolyn D.
 29 REGISTRATION NUMBER: 36,016
 30 REFERENCE/CHECK NUMBER: 19070,0028
 31 TELECOMMUNICATION INFORMATION:
 32 TELEPHONE: 404/688-0770
 33 TELEFAX: 404/688-9880
 34 INFORMATION FOR SEQ ID NO: 4:
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 6 amino acids
 37 TYPE: amino acid
 38 STRANDEDNESS: not relevant
 39 TOPOLOGY: linear
 40 MOLECULE TYPE: peptide
 41 US-08-806-204-4

Query Match 81.8%; Score 9; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 LXR 4
 1 1
 DB 1 LTR 4

1 RESULT 42
 2 US-08-806-204-5

```

: Sequence 5, Application US/08806203
: Patent No. 5830434
: GENERAL INFORMATION:
: APPLICANT: TAYLOR, IAN L.
: APPLICANT: GETTYS, THOMAS
: TITLE OF INVENTION: METHODS OF TREATING NON INSULIN
: DEPENDENT DIABETIS MELLITUS WITH PANCREATIC POLYPEPTIDE
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NEEDLE & ROSENBERG, P.C.
: STREET: Suite 1200, 127 Peachtree Street
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08-498-556c
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Spratt, Wendolyn D.
: REGISTRATION NUMBER: 36,016
: REFERENCE/CKET NUMBER: 14676 0029
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 404/688-0770
: TELEFAX: 404/688-4444
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-806-203-5

```

```

Query Match 81.8% Score 9: DB 2: Length 6;
Best Local Similarity 66.7% Pred. No. 1.9e+05;
Matches 2: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

```

```

QY 1 LXR 3
   1 1
Db 1 LIR 3

```

```

RESULT 43
US-08-609-426A-35
: Sequence 25, Application US/08669126
: Patent No. 5830733
: GENERAL INFORMATION:
: APPLICANT: Nevalainen, Helena K.M.
: APPLICANT: Paloheimo, Marja T.
: APPLICANT: Miettinen-Oinonen, Arja S.K.
: APPLICANT: Terkkeli, Tuula K.
: APPLICANT: Cantrell, Michael
: APPLICANT: Piddington, Christopher S.
: APPLICANT: Pambossek, John A.
: APPLICANT: Turunen, Marja K.
: APPLICANT: Fagerström, Richard B.
: APPLICANT: Houston, Christine S.
: TITLE OF INVENTION: Production of Phytase Degrading Enzymes
: TITLE OF INVENTION: in Trichoderma
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.

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: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08-498-556c
: FILING DATE: 01-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/923,724
: FILING DATE: 31-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/496,155
: FILING DATE: 19-MAR-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/044,677
: FILING DATE: 29-APR-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 8610600
: CLASSIFICATION: 3: APW-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Grant E.
: REGISTRATION NUMBER: F 41,264
: REFERENCE/CKET NUMBER: 1050,0080001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 433-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: TOPOLOGY: both
: US-08-609-426A-35

```

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Query Match 81.8% Score 9: DB 2: Length 6;
Best Local Similarity 66.7% Pred. No. 1.9e+05;
Matches 2: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

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QY 1 LXR 3
   1 1
Db 4 LIR 6

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RESULT 44
US-08-374-6520-25
: Sequence 25, Application US/084746520
: Patent No. 5834286
: GENERAL INFORMATION:
: APPLICANT: Nevalainen, Helena K.M.
: APPLICANT: Paloheimo, Marja T.
: APPLICANT: Pambossek, Richard B.
: APPLICANT: Miettinen-Oinonen, Arja S.
: APPLICANT: Terrier, Marja K.
: APPLICANT: Pambossek, John A.
: APPLICANT: Piddington, Christopher S.
: APPLICANT: Cantrell, Michael A.
: TITLE OF INVENTION: RECOMBINANT CELLS, INA CONSTRUCTS,
: TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
: TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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1 OPERATING SYSTEM: PC-IPUS/MS-DOS
2 SOFTWARE: Patent In Release #1.0, Version #1.40
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/474,652C
5 FILING DATE: 24 MAY-1995
6 CLASSIFICATION: 435
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: PCT/US93/07058
9 FILING DATE: 27 JUL-1993
10 CLASSIFICATION: 435
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/925,401
13 FILING DATE: 31-JUL-1992
14 CLASSIFICATION: 435
15 ATTORNEY/AGENT INFORMATION:
16 NAME: REED, GRANT E.
17 REGISTRATION NUMBER: 41,264
18 REFERENCE NUMBER: 1050-071001
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 202-371-2600
21 TELEFAX: 202-371-2540
22 INFORMATION FOR SEQ ID NO: 25:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 6 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: single
27 TOPOLOGY: not relevant
28 MOLECULE TYPE: peptide
29 US-08-474-652C-25

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Query Match      81.8%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;
27 1 LXR 4
DB 4 LTR 6

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RESULT 45
US-08-492-973A-15
1 Sequence 15, Application US/08392973A
2 Patent No. 5843453
3 GENERAL INFORMATION:
4 APPLICANT: HOLDER, Andrew T.
5 TITLE OF INVENTION: GROWTH HORMONE POTENTIATING MOLECULES
6 NUMBER OF SEQUENCES: 37
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: HALE AND DORR LLP
9 STREET: 60 State Street
10 CITY: Boston
11 STATE: MA
12 COUNTRY: United States of America
13 ZIP: 02109
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-IPUS/MS-DOS
18 SOFTWARE: Patent In Release #1.0, Version #1.40
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/492,973A
21 FILING DATE: 25 APR-1995
22 CLASSIFICATION: 424
23 ATTORNEY/AGENT INFORMATION:
24 NAME: BAKER, Hollie L.
25 REGISTRATION NUMBER: 41,421
26 REFERENCE NUMBER: 102286,301
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 617-526-6000
29 TELEFAX: 617-526-5000
30 INFORMATION FOR SEQ ID NO: 15:
31 SEQUENCE CHARACTERISTICS:

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1 LENGTH: 6 amino acids
2 TYPE: amino acid
3 TOPOLOGY: linear
4 MOLECULE TYPE: peptide
5 FRAGMENT TYPE: internal
6 FEATURE:
7 NAME/KEY: Peptide
8 LOCATION: 1-6
9 OTHER INFORMATION: Zide "91-96 RINDER OF PINE
10 OTHER INFORMATION: GROWTH HORMONE"
11 US-08-492-973A-15
12 Query Match      81.8%; Score 9; DB 2; Length 6;
13 Best Local Similarity 66.7%; Pred. No. 1.5e+05;
14 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
15 QY 1 LXR 4
16 DB 3 LXR 6
17 Search completed: April 30, 2003, 1:47:28
18 Job time : 19.7273 secs

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genCore version 5.1.4.p5_4578
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1M protein - protein search, using sw model

Run on: April 30, 2003, 13:37:03 : Search time 20.7272 seconds
(without alignments)
16.652 Million cell updates/sec

Title: US-09-498-556C-357

Perfect score: 11

Sequence: 1 LXPX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 96286695 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 9%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

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- 2: /usr22/prod/aa/1/for pub/seqs/new_pap.pap
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- 13: /usr22/prod/aa/1/pub/pap/seqs/new_pap.pap
- 14: /usr22/prod/aa/1/pub/pap/seqs/new_pap.pap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	9	81.8	6	9	US-09-498-556C-357
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9	9	81.8	6	9	US-09-498-556C-357
10	9	81.8	7	9	US-09-498-556C-357
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16	9	81.8	7	9	US-09-498-556C-357
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19	9	81.8	7	9	US-09-498-556C-357

93	9	81.8	7	9	US-10-006-069A-150	Sequence 150, App	156	9	81.8	7	9	US-09-846-0348-71	Sequence 71, App
94	9	81.8	7	9	US-10-006-069A-153	Sequence 153, App	167	9	81.8	7	9	US-09-846-0348-78	Sequence 78, App
95	9	81.8	7	9	US-10-006-069A-154	Sequence 154, App	168	9	81.8	7	9	US-09-846-0348-79	Sequence 79, App
96	9	81.8	7	9	US-10-006-069A-155	Sequence 155, App	169	9	81.8	7	9	US-09-846-0348-80	Sequence 80, App
97	9	81.8	7	9	US-10-006-069A-157	Sequence 157, App	170	9	81.8	7	9	US-09-846-0348-82	Sequence 82, App
98	9	81.8	7	9	US-10-006-069A-163	Sequence 163, App	171	9	81.8	7	9	US-09-846-0348-84	Sequence 84, App
99	9	81.8	7	9	US-10-006-069A-164	Sequence 164, App	172	9	81.8	7	9	US-09-846-0348-84	Sequence 84, App
100	9	81.8	7	9	US-10-006-069A-165	Sequence 165, App	173	9	81.8	7	9	US-09-846-0348-87	Sequence 87, App
101	9	81.8	7	9	US-10-006-069A-166	Sequence 166, App	174	9	81.8	7	9	US-09-846-0348-90	Sequence 90, App
102	9	81.8	7	9	US-10-006-069A-167	Sequence 167, App	175	9	81.8	7	9	US-09-846-0348-91	Sequence 91, App
103	9	81.8	7	9	US-10-006-069A-168	Sequence 168, App	176	9	81.8	7	9	US-09-846-0348-92	Sequence 92, App
104	9	81.8	7	9	US-10-006-069A-170	Sequence 170, App	177	9	81.8	7	9	US-09-846-0348-97	Sequence 97, App
105	9	81.8	7	9	US-10-006-069A-171	Sequence 171, App	178	9	81.8	7	9	US-09-846-0348-98	Sequence 98, App
106	9	81.8	7	9	US-10-006-069A-172	Sequence 172, App	179	9	81.8	7	9	US-09-846-0348-100	Sequence 100, App
107	9	81.8	7	9	US-10-006-069A-173	Sequence 173, App	180	9	81.8	7	9	US-09-846-0348-101	Sequence 101, App
108	9	81.8	7	9	US-10-006-069A-174	Sequence 174, App	181	9	81.8	7	9	US-09-846-0348-102	Sequence 102, App
109	9	81.8	7	9	US-10-006-069A-176	Sequence 176, App	182	9	81.8	7	9	US-09-846-0348-104	Sequence 104, App
110	9	81.8	7	9	US-10-006-069A-177	Sequence 177, App	183	9	81.8	7	9	US-09-846-0348-104	Sequence 104, App
111	9	81.8	7	9	US-10-006-069A-178	Sequence 178, App	184	9	81.8	7	9	US-09-846-0348-105	Sequence 105, App
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114	9	81.8	7	9	US-10-006-069A-182	Sequence 182, App	187	9	81.8	7	9	US-09-846-0348-109	Sequence 109, App
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248	9	81.8	7	9	US-09-846-034B-203	Sequence 203, Aff	321	9	81.8	7	9	US-09-990-186-153	Sequence 153, Aff
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254	9	81.8	7	9	US-09-846-034B-209	Sequence 209, Aff	327	9	81.8	7	9	US-09-990-186-159	Sequence 159, Aff
255	9	81.8	7	9	US-09-846-034B-210	Sequence 210, Aff	328	9	81.8	7	9	US-09-990-186-160	Sequence 160, Aff
256	9	81.8	7	9	US-09-846-034B-211	Sequence 211, Aff	329	9	81.8	7	9	US-09-990-186-161	Sequence 161, Aff
257	9	81.8	7	9	US-09-846-034B-212	Sequence 212, Aff	330	9	81.8	7	9	US-09-990-186-162	Sequence 162, Aff
258	9	81.8	7	9	US-09-846-034B-213	Sequence 213, Aff	331	9	81.8	7	9	US-09-990-186-163	Sequence 163, Aff
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261	9	81.8	7	9	US-09-846-034B-216	Sequence 216, Aff	334	9	81.8	7	9	US-09-990-186-166	Sequence 166, Aff
262	9	81.8	7	9	US-09-846-034B-217	Sequence 217, Aff	335	9	81.8	7	9	US-09-990-186-167	Sequence 167, Aff
263	9	81.8	7	9	US-09-846-034B-218	Sequence 218, Aff	336	9	81.8	7	9	US-09-990-186-168	Sequence 168, Aff
264	9	81.8	7	9	US-09-846-034B-219	Sequence 219, Aff	337	9	81.8	7	9	US-09-990-186-169	Sequence 169, Aff
265	9	81.8	7	9	US-09-846-034B-220	Sequence 220, Aff	338	9	81.8	7	9	US-09-990-186-170	Sequence 170, Aff
266	9	81.8	7	9	US-09-846-034B-221	Sequence 221, Aff	339	9	81.8	7	9	US-09-990-186-171	Sequence 171, Aff
267	9	81.8	7	9	US-09-846-034B-222	Sequence 222, Aff	340	9	81.8	7	9	US-09-990-186-172	Sequence 172, Aff
268	9	81.8	7	9	US-09-846-034B-223	Sequence 223, Aff	341	9	81.8	7	9	US-09-990-186-173	Sequence 173, Aff
269	9	81.8	7	9	US-09-846-034B-224	Sequence 224, Aff	342	9	81.8	7	9	US-09-990-186-174	Sequence 174, Aff
270	9	81.8	7	9	US-09-846-034B-225	Sequence 225, Aff	343	9	81.8	7	9	US-09-990-186-175	Sequence 175, Aff
271	9	81.8	7	9	US-09-846-034B-226	Sequence 226, Aff	344	9	81.8	7	9	US-09-990-186-176	Sequence 176, Aff
272	9	81.8	7	9	US-09-846-034B-227	Sequence 227, Aff	345	9	81.8	7	9	US-09-990-186-177	Sequence 177, Aff
273	9	81.8	7	9	US-09-846-034B-228	Sequence 228, Aff	346	9	81.8	7	9	US-09-990-186-178	Sequence 178, Aff
274	9	81.8	7	9	US-09-846-034B-229	Sequence 229, Aff	347	9	81.8	7	9	US-09-990-186-179	Sequence 179, Aff
275	9	81.8	7	9	US-09-846-034B-230	Sequence 230, Aff	348	9	81.8	7	9	US-09-990-186-180	Sequence 180, Aff
276	9	81.8	7	9	US-09-846-034B-231	Sequence 231, Aff	349	9	81.8	7	9	US-09-990-186-181	Sequence 181, Aff
277	9	81.8	7	9	US-09-846-034B-232	Sequence 232, Aff	350	9	81.8	7	9	US-09-990-186-182	Sequence 182, Aff
278	9	81.8	7	9	US-09-846-034B-233	Sequence 233, Aff	351	9	81.8	7	9	US-09-990-186-183	Sequence 183, Aff
279	9	81.8	7	9	US-09-846-034B-234	Sequence 234, Aff	352	9	81.8	7	9	US-09-990-186-184	Sequence 184, Aff
280	9	81.8	7	9	US-09-846-034B-235	Sequence 235, Aff	353	9	81.8	7	9	US-09-990-186-185	Sequence 185, Aff
281	9	81.8	7	9	US-09-846-034B-236	Sequence 236, Aff	354	9	81.8	7	9	US-09-990-186-186	Sequence 186, Aff
282	9	81.8	7	9	US-09-846-034B-237	Sequence 237, Aff	355	9	81.8	7	9	US-09-990-186-187	Sequence 187, Aff
283	9	81.8	7	9	US-09-846-034B-238	Sequence 238, Aff	356	9	81.8	7	9	US-09-990-186-188	Sequence 188, Aff
284	9	81.8	7	9	US-09-846-034B-239	Sequence 239, Aff	357	9	81.8	7	9	US-09-990-186-189	Sequence 189, Aff
285	9	81.8	7	9	US-09-846-034B-240	Sequence 240, Aff	358	9	81.8	7	9	US-09-990-186-190	Sequence 190, Aff
286	9	81.8	7	9	US-09-846-034B-241	Sequence 241, Aff	359	9	81.8	7	9	US-09-990-186-191	Sequence 191, Aff
287	9	81.8	7	9	US-09-846-034B-242	Sequence 242, Aff	360	9	81.8	7	9	US-09-990-186-192	Sequence 192, Aff
288	9	81.8	7	9	US-09-846-034B-243	Sequence 243, Aff	361	9	81.8	7	9	US-09-990-186-193	Sequence 193, Aff
289	9	81.8	7	9	US-09-846-034B-244	Sequence 244, Aff	362	9	81.8	7	9	US-09-990-186-194	Sequence 194, Aff
290	9	81.8	7	9	US-09-846-034B-245	Sequence 245, Aff	363	9	81.8	7	9	US-09-990-186-195	Sequence 195, Aff
291	9	81.8	7	9	US-09-846-034B-246	Sequence 246, Aff	364	9	81.8	7	9	US-09-990-186-196	Sequence 196, Aff
292	9	81.8	7	9	US-09-846-034B-247	Sequence 247, Aff	365	9	81.8	7	9	US-09-990-186-197	Sequence 197, Aff
293	9	81.8	7	9	US-09-846-034B-248	Sequence 248, Aff	366	9	81.8	7	9	US-09-990-186-198	Sequence 198, Aff
294	9	81.8	7	9	US-09-846-034B-249	Sequence 249, Aff	367	9	81.8	7	9	US-09-990-186-199	Sequence 199, Aff
295	9	81.8	7	9	US-09-846-034B-250	Sequence 250, Aff	368	9	81.8	7	9	US-09-990-186-200	Sequence 200, Aff
296	9	81.8	7	9	US-09-846-034B-251	Sequence 251, Aff	369	9	81.8	7	9	US-09-990-186-201	Sequence 201, Aff
297	9	81.8	7	9	US-09-846-034B-252	Sequence 252, Aff	370	9	81.8	7	9	US-09-990-186-202	Sequence 202, Aff
298	9	81.8	7	9	US-09-846-034B-253	Sequence 253, Aff	371	9	81.8	7	9	US-09-990-186-203	Sequence 203, Aff
299	9	81.8	7	9	US-09-846-034B-254	Sequence 254, Aff	372	9	81.8	7	9	US-09-990-186-204	Sequence 204, Aff
300	9	81.8	7	9	US-09-846-034B-255	Sequence 255, Aff	373	9	81.8	7	9	US-09-990-186-205	Sequence 205, Aff
301	9	81.8	7	9	US-09-846-034B-256	Sequence 256, Aff	374	9	81.8	7	9	US-09-990-186-206	Sequence 206, Aff
302	9	81.8	7	9	US-09-846-034B-257	Sequence 257, Aff	375	9	81.8	7	9	US-09-990-186-207	Sequence 207, Aff
303	9	81.8	7	9	US-09-846-034B-258	Sequence 258, Aff	376	9	81.8	7	9	US-09-990-186-208	Sequence 208, Aff
304	9	81.8	7	9	US-09-846-034B-259	Sequence 259, Aff	377	9	81.8	7	9	US-09-990-186-209	Sequence 209, Aff
305	9	81.8	7	9	US-09-846-034B-260	Sequence 260, Aff	378	9	81.8	7	9	US-09-990-186-210	Sequence 210, Aff
306	9	81.8	7	9	US-09-846-034B-261	Sequence 261, Aff	379	9	81.8	7	9	US-09-990-186-211	Sequence 211, Aff
307	9	81.8	7	9	US-09-846-034B-262	Sequence 262, Aff	380	9	81.8	7	9	US-09-990-186-212	Sequence 212, Aff
308	9	81.8	7	9	US-09-846-034B-263	Sequence 263, Aff	381	9	81.8	7	9	US-09-990-186-213	Sequence 213, Aff
309	9	81.8	7	9	US-09-846-034B-264	Sequence 264, Aff	382	9	81.8	7	9	US-09-990-186-214	Sequence 214, Aff
310	9	81.8	7	9	US-09-846-034B-265	Sequence 265, Aff	383	9	81.8	7	9	US-09-990-186-215	Sequence 215, Aff
311	9	81.8	7	9	US-09-846-034B-266	Sequence 266, Aff	384	9	81.8	7	9	US-09-990-186-216	Sequence 216, Aff

385	9	81.8	7	9	US-09-990-186-266	Sequence 266, App	458	9	81.8	7	9	US-09-990-186-103	Sequence 403, App
386	9	81.8	7	9	US-09-990-186-267	Sequence 267, App	459	9	81.8	7	9	US-09-990-186-104	Sequence 404, App
387	9	81.8	7	9	US-09-990-186-268	Sequence 268, App	460	9	81.8	7	9	US-09-990-186-105	Sequence 405, App
388	9	81.8	7	9	US-09-990-186-269	Sequence 269, App	461	9	81.8	7	9	US-09-990-186-106	Sequence 406, App
389	9	81.8	7	9	US-09-990-186-270	Sequence 270, App	462	9	81.8	7	9	US-09-990-186-107	Sequence 407, App
390	9	81.8	7	9	US-09-990-186-271	Sequence 271, App	463	9	81.8	7	9	US-09-990-186-108	Sequence 408, App
391	9	81.8	7	9	US-09-990-186-272	Sequence 272, App	464	9	81.8	7	9	US-09-990-186-109	Sequence 409, App
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393	9	81.8	7	9	US-09-990-186-274	Sequence 274, App	466	9	81.8	7	9	US-09-990-186-111	Sequence 411, App
394	9	81.8	7	9	US-09-990-186-275	Sequence 275, App	467	9	81.8	7	9	US-09-990-186-112	Sequence 412, App
395	9	81.8	7	9	US-09-990-186-276	Sequence 276, App	468	9	81.8	7	9	US-09-990-186-113	Sequence 413, App
396	9	81.8	7	9	US-09-990-186-277	Sequence 277, App	469	9	81.8	7	9	US-09-990-186-114	Sequence 414, App
397	9	81.8	7	9	US-09-990-186-278	Sequence 278, App	470	9	81.8	7	9	US-09-990-186-115	Sequence 415, App
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400	9	81.8	7	9	US-09-990-186-281	Sequence 281, App	473	9	81.8	7	9	US-09-990-186-118	Sequence 418, App
401	9	81.8	7	9	US-09-990-186-282	Sequence 282, App	474	9	81.8	7	9	US-09-990-186-119	Sequence 419, App
402	9	81.8	7	9	US-09-990-186-283	Sequence 283, App	475	9	81.8	7	9	US-09-990-186-120	Sequence 420, App
403	9	81.8	7	9	US-09-990-186-284	Sequence 284, App	476	9	81.8	7	9	US-09-990-186-121	Sequence 421, App
404	9	81.8	7	9	US-09-990-186-285	Sequence 285, App	477	9	81.8	7	9	US-09-990-186-122	Sequence 422, App
405	9	81.8	7	9	US-09-990-186-286	Sequence 286, App	478	9	81.8	7	9	US-09-990-186-123	Sequence 423, App
406	9	81.8	7	9	US-09-990-186-300	Sequence 300, App	479	9	81.8	7	9	US-09-990-186-124	Sequence 424, App
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414	9	81.8	7	9	US-09-990-186-313	Sequence 313, App	487	9	81.8	7	9	US-09-990-186-132	Sequence 432, App
415	9	81.8	7	9	US-09-990-186-326	Sequence 326, App	488	9	81.8	7	9	US-09-990-186-133	Sequence 433, App
416	9	81.8	7	9	US-09-990-186-332	Sequence 332, App	489	9	81.8	7	9	US-09-990-186-134	Sequence 434, App
417	9	81.8	7	9	US-09-990-186-334	Sequence 334, App	490	9	81.8	7	9	US-09-990-186-135	Sequence 435, App
418	9	81.8	7	9	US-09-990-186-339	Sequence 339, App	491	9	81.8	7	9	US-09-990-186-136	Sequence 436, App
419	9	81.8	7	9	US-09-990-186-349	Sequence 349, App	492	9	81.8	7	9	US-09-990-186-137	Sequence 437, App
420	9	81.8	7	9	US-09-990-186-343	Sequence 343, App	493	9	81.8	7	9	US-09-990-186-138	Sequence 438, App
421	9	81.8	7	9	US-09-990-186-345	Sequence 346, App	494	9	81.8	7	9	US-09-990-186-139	Sequence 439, App
422	9	81.8	7	9	US-09-990-186-347	Sequence 347, App	495	9	81.8	7	9	US-09-990-186-140	Sequence 440, App
423	9	81.8	7	9	US-09-990-186-348	Sequence 348, App	496	9	81.8	7	9	US-09-990-186-141	Sequence 441, App
424	9	81.8	7	9	US-09-990-186-349	Sequence 349, App	497	9	81.8	7	9	US-09-990-186-142	Sequence 442, App
425	9	81.8	7	9	US-09-990-186-350	Sequence 350, App	498	9	81.8	7	9	US-09-990-186-143	Sequence 443, App
426	9	81.8	7	9	US-09-990-186-364	Sequence 364, App	499	9	81.8	7	9	US-09-990-186-144	Sequence 444, App
427	9	81.8	7	9	US-09-990-186-365	Sequence 365, App	500	9	81.8	7	9	US-09-990-186-145	Sequence 445, App
428	9	81.8	7	9	US-09-990-186-366	Sequence 366, App	501	9	81.8	7	9	US-09-990-186-146	Sequence 446, App
429	9	81.8	7	9	US-09-990-186-367	Sequence 367, App	502	9	81.8	7	9	US-09-990-186-147	Sequence 447, App
430	9	81.8	7	9	US-09-990-186-368	Sequence 368, App	503	9	81.8	7	9	US-09-990-186-148	Sequence 448, App
431	9	81.8	7	9	US-09-990-186-369	Sequence 369, App	504	9	81.8	7	9	US-09-990-186-149	Sequence 449, App
432	9	81.8	7	9	US-09-990-186-371	Sequence 371, App	505	9	81.8	7	9	US-09-990-186-150	Sequence 450, App
433	9	81.8	7	9	US-09-990-186-372	Sequence 372, App	506	9	81.8	7	9	US-09-990-186-151	Sequence 451, App
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435	9	81.8	7	9	US-09-990-186-374	Sequence 374, App	508	9	81.8	7	9	US-09-990-186-153	Sequence 453, App
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437	9	81.8	7	9	US-09-990-186-376	Sequence 376, App	510	9	81.8	7	9	US-09-990-186-155	Sequence 455, App
438	9	81.8	7	9	US-09-990-186-377	Sequence 377, App	511	9	81.8	7	9	US-09-990-186-156	Sequence 456, App
439	9	81.8	7	9	US-09-990-186-378	Sequence 378, App	512	9	81.8	7	9	US-09-990-186-157	Sequence 457, App
440	9	81.8	7	9	US-09-990-186-379	Sequence 379, App	513	9	81.8	7	9	US-09-990-186-158	Sequence 458, App
441	9	81.8	7	9	US-09-990-186-383	Sequence 383, App	514	9	81.8	7	9	US-09-990-186-159	Sequence 459, App
442	9	81.8	7	9	US-09-990-186-384	Sequence 384, App	515	9	81.8	7	9	US-09-990-186-160	Sequence 460, App
443	9	81.8	7	9	US-09-990-186-385	Sequence 385, App	516	9	81.8	7	9	US-09-990-186-161	Sequence 461, App
444	9	81.8	7	9	US-09-990-186-386	Sequence 386, App	517	9	81.8	7	9	US-09-990-186-162	Sequence 462, App
445	9	81.8	7	9	US-09-990-186-395	Sequence 395, App	518	9	81.8	7	9	US-09-990-186-163	Sequence 463, App
446	9	81.8	7	9	US-09-990-186-396	Sequence 396, App	519	9	81.8	7	9	US-09-990-186-164	Sequence 464, App
447	9	81.8	7	9	US-09-990-186-399	Sequence 399, App	520	9	81.8	7	9	US-09-990-186-165	Sequence 465, App
448	9	81.8	7	9	US-09-990-186-390	Sequence 390, App	521	9	81.8	7	9	US-09-990-186-166	Sequence 466, App
449	9	81.8	7	9	US-09-990-186-391	Sequence 391, App	522	9	81.8	7	9	US-09-990-186-167	Sequence 467, App
450	9	81.8	7	9	US-09-990-186-392	Sequence 392, App	523	9	81.8	7	9	US-09-990-186-168	Sequence 468, App
451	9	81.8	7	9	US-09-990-186-393	Sequence 393, App	524	9	81.8	7	9	US-09-990-186-169	Sequence 469, App
452	9	81.8	7	9	US-09-990-186-394	Sequence 394, App	525	9	81.8	7	9	US-09-990-186-170	Sequence 470, App
453	9	81.8	7	9	US-09-990-186-395	Sequence 395, App	526	9	81.8	7	9	US-09-990-186-171	Sequence 471, App
454	9	81.8	7	9	US-09-990-186-396	Sequence 396, App	527	9	81.8	7	9	US-09-990-186-172	Sequence 472, App
455	9	81.8	7	9	US-09-990-186-397	Sequence 397, App	528	9	81.8	7	9	US-09-990-186-173	Sequence 473, App
456	9	81.8	7	9	US-09-990-186-398	Sequence 398, App	529	9	81.8	7	9	US-09-990-186-174	Sequence 474, App
457	9	81.8	7	9	US-09-990-186-399	Sequence 399, App	530	9	81.8	7	9	US-09-990-186-175	Sequence 475, App

531	9	81.8	7	9	US-09-990-186-712	Sequence 712, App	604	9	91.8	7	9	US-09-990-186-822	Sequence 822, App
532	9	81.8	7	9	US-09-990-186-713	Sequence 713, App	605	9	81.8	7	9	US-09-990-186-823	Sequence 823, App
533	9	81.8	7	9	US-09-990-186-714	Sequence 714, App	606	9	81.8	7	9	US-09-990-186-824	Sequence 824, App
534	9	81.8	7	9	US-09-990-186-715	Sequence 715, App	607	9	81.8	7	9	US-09-990-186-825	Sequence 825, App
535	9	81.8	7	9	US-09-990-186-716	Sequence 716, App	608	9	81.8	7	9	US-09-990-186-840	Sequence 840, App
536	9	81.8	7	9	US-09-990-186-720	Sequence 720, App	609	9	81.8	7	9	US-09-990-186-841	Sequence 841, App
537	9	81.8	7	9	US-09-990-186-721	Sequence 721, App	610	9	81.8	7	9	US-09-990-186-842	Sequence 842, App
538	9	81.8	7	9	US-09-990-186-722	Sequence 722, App	611	9	81.8	7	9	US-09-990-186-843	Sequence 843, App
539	9	81.8	7	9	US-09-990-186-723	Sequence 723, App	612	9	81.8	7	9	US-09-990-186-844	Sequence 844, App
540	9	81.8	7	9	US-09-990-186-724	Sequence 724, App	613	9	81.8	7	9	US-09-990-186-845	Sequence 845, App
541	9	81.8	7	9	US-09-990-186-725	Sequence 725, App	614	9	81.8	7	9	US-09-990-186-855	Sequence 855, App
542	9	81.8	7	9	US-09-990-186-726	Sequence 726, App	615	9	81.8	7	9	US-09-990-186-856	Sequence 856, App
543	9	81.8	7	9	US-09-990-186-729	Sequence 729, App	616	9	81.8	7	9	US-09-990-186-858	Sequence 858, App
544	9	81.8	7	9	US-09-990-186-733	Sequence 733, App	617	9	81.8	7	9	US-09-990-186-840	Sequence 840, App
545	9	81.8	7	9	US-09-990-186-734	Sequence 734, App	618	9	81.8	7	9	US-09-990-186-842	Sequence 842, App
546	9	81.8	7	9	US-09-990-186-735	Sequence 735, App	619	9	81.8	7	9	US-09-990-186-844	Sequence 844, App
547	9	81.8	7	9	US-09-990-186-736	Sequence 736, App	620	9	81.8	7	9	US-09-990-186-845	Sequence 845, App
548	9	81.8	7	9	US-09-990-186-737	Sequence 737, App	621	9	81.8	7	9	US-09-990-186-847	Sequence 847, App
549	9	81.8	7	9	US-09-990-186-739	Sequence 739, App	622	9	81.8	7	9	US-09-990-186-848	Sequence 848, App
550	9	81.8	7	9	US-09-990-186-740	Sequence 740, App	623	9	81.8	7	9	US-09-990-186-849	Sequence 849, App
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994      9  81.8  7  9  US-09-990-186-1530      Sequence 1530, Ap
995      9  81.8  7  9  US-09-990-186-1531      Sequence 1531, Ap
996      9  81.8  7  9  US-09-990-186-1547      Sequence 1547, Ap
997      9  81.8  7  9  US-09-990-186-1541      Sequence 1541, Ap
998      9  81.8  7  9  US-09-990-186-1544      Sequence 1544, Ap
999      9  81.8  7  9  US-09-990-186-1546      Sequence 1546, Ap
1000     9  81.8  7  10 US-09-845-226-25      Sequence 26, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-249-159-2
: Sequence 2, Applicant: us-09-2002416r
: Patent No. US2002015478A1
: GENERAL INFORMATION:
: APPLICANT: Yuan, Zhenyu
: TITLE OF INVENTION: Direct Adsorption Scintillation Assay
: TITLE OF INVENTOR: for Measuring Enzyme Activity and Assaying Biochemical
: TITLE OF INVENTOR: Processes
: FILE REFERENCE: 342412000600
: CURRENT APPLICATION NUMBER: US-09-249-159-2
: PRIOR FILING DATE: 1999-02-09
: PRIOR FILING DATE: 1999-02-10
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Synthetic peptide
US-09-249-159-2

```

```

Query Match      81.8%  Score 9,  DB 10,  Length 4,
Best Local Similarity 66.7%  Prod. No. 2,90-05,
Matches 2; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 4
   1 1
Db 2 LXR 4

```

```

RESULT 2
US-09-818-656A-8

```

```

: Sequence 8, Applicant: US/09818656A
: Patent No. US20020142381A1

```

```

: GENERAL INFORMATION:
: APPLICANT: GONG, Fancheng et al.
: TITLE OF INVENTOR: ISOLATED HUMAN TRANSCRIPTER PROTEINS,
: TITLE OF INVENTOR: NOVELLY ACID DERIVATIVES ENCODING HUMAN TRANSCRIPTER PROTEINS,
: TITLE OF INVENTOR, AND USES THEREOF
: FILE REFERENCE: CLO01191

```

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: CURRENT APPLICATION NUMBER: US/09818656A

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: CURRENT FILING DATE: 2000-04-28

```

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: NUMBER OF SEQ ID NOS: 104

```

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: SOFTWARE: FASTSEQ for Windows Version 4.0

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: SEQ ID NO 8

```

```

: LENGTH: 4

```

```

: TYPE: PRT

```

```

: ORGANISM: Homo sapiens

```

```

US-09-818-656A-8

```

```

Query Match      81.8%  Score 9,  DB 10,  Length 4,

```

```

Best Local Similarity 66.7%  Prod. No. 2,90-05,

```

```

Matches 2; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 4

```

```

Db 2 LXR 4

```

RESULT 4

```

US-10-006-557-7

```

```

: Sequence 7, Applicant: US/10006557

```

```

: Patent No. US2002017464A1

```

```

: GENERAL INFORMATION:

```

```

: APPLICANT: Kind, Avonco, L.

```

```

: APPLICANT: Abrahamson, Susan

```

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: APPLICANT: Ptasley, Michael

```

```

: TITLE OF INVENTION: Modulation of Pericyte Proliferation

```

```

: FILE REFERENCE: 2712936789A

```

```

: CURRENT APPLICATION NUMBER: US/10006557

```

```

: CURRENT FILING DATE: 2001-12-04

```

```

: PRIOR APPLICATION NUMBER: 09/250,942

```

```

: PRIOR FILING DATE: 2000-12-01

```

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: NUMBER OF SEQ ID NOS: 15

```

```

: SOFTWARE: PatentIn version 4.1

```

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: SEQ ID NO 7

```

```

: LENGTH: 5

```

```

: TYPE: PRT

```

```

: ORGANISM: Homo sapiens

```

```

: FEATURE:

```

```

: NAME/KEY: WSC_FEATURE

```

```

: OTHER INFORMATION: XMP.711

```

```

: NAME/KEY: SITE

```

```

: LOCATION: (1)..(1)

```

```

: OTHER INFORMATION: Position 1 is derivatized at the alpha-amino group with

```

```

: NAME/KEY: SITE

```

```

: LOCATION: (5)..(5)

```

```

: OTHER INFORMATION: Position 4 is substituted with 4 biphenyl ala

```

```

: NAME/KEY: SITE

```

```

: LOCATION: (1)..(2)

```

```

: OTHER INFORMATION: Positions 1-2 are D amino acids

```

```

: NAME/KEY: SITE

```

```

: LOCATION: (1)..(3)

```

```

: OTHER INFORMATION: Position 3 is L amino acid

```

```

: NAME/KEY: SITE

```

```

: LOCATION: (4)..(5)

```

```

: OTHER INFORMATION: Positions 4-5 are D amino acids

```

```

: NAME/KEY: SITE

```

```

: LOCATION: (5)..(5)

```

```

: OTHER INFORMATION: AMINATION-The C-terminus is Amidated

```

```

US-10-006-557-7

```

```

Query Match      81.8%  Score 9,  DB 9,  Length 6,

```

```

Best Local Similarity 66.7%  Prod. No. 2,90-05,

```

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
| |
Db 2 LAR 4

RESULT 4

US-09-486-734A-17
; Sequence 17, Application US/09486734A
; Patent No. US20020154732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to L-Tyrosine
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 33339/16048
; CURRENT APPLICATION NUMBER: US/09486734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR99/01877
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BsdM submit
US-09-486-734A-17

Query Match 81.8% Score 9; DB 9; Length 6;
Best Local Similarity 66.7% Pred. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
| |
Db 3 LAR 5

RESULT 5

US-09-486-734A-27
; Sequence 27, Application US/09486734A
; Patent No. US20020154732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to L-Tyrosine
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 33339/16048
; CURRENT APPLICATION NUMBER: US/09486734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR99/01877
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: BsdM submit
US-09-486-734A-27

Query Match 81.8% Score 9; DB 9; Length 6;
Best Local Similarity 66.7% Pred. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 4
| |
Db 1 LAR 4

RESULT 6

US-09-770-102A-17
; Sequence 17, Application US/99770102A
; Publication No. US20020197606A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel
; TITLE OF INVENTION: Compositions and Methods for Modifying the Modification of M
; TITLE OF INVENTION: Independent Binding Partner Polypeptides
; FILE REFERENCE: 1999/01862
; CURRENT APPLICATION NUMBER: US/99770102A
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: EP 97/173284
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent n version 3.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; NAME/KEY: DOMAIN
; LOCATION: (1)...(6)
; OTHER INFORMATION: Consensus sequence
US-09-770-102A-17

Query Match 81.8% Score 9; DB 9; Length 6;
Best Local Similarity 66.7% Pred. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 4
| |
Db 3 LSR 5

RESULT 7

US-09-866-512A-9
; Sequence 9, Application US/99866512A
; Publication No. US2003005494A1
; GENERAL INFORMATION:
; APPLICANT: Meade, Thomas J
; TITLE OF INVENTION: Magnetic Resonance Imaging Agents for the Detection of Physiol
; TITLE OF INVENTION: Agents
; FILE REFERENCE: A 58634 7
; CURRENT APPLICATION NUMBER: US/99866512A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EP/297,619
; PRIOR FILING DATE: 2001-05-26
; PRIOR APPLICATION NUMBER: EP 460,511
; PRIOR FILING DATE: 1997-06-02
; PRIOR APPLICATION NUMBER: EP 297,619
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: EP 471,855
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: EP 1,14,372
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: EP 1,14,372
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/405,046
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: EP 1,14,372

? PRIOR FILING DATE: 1997-10-27
 ? NUMBER OF SEQ ID NOS: 17
 ? SOFTWARE: Patent in version 3.1
 ? SEQ ID NO 9
 ? LENGTH: 6
 ? TYPE: PRI
 ? ORGANISM: Unknown
 ? FEATURE:
 ? OTHER INFORMATION: could be from any mammal.
 US-09-666-512A 9

Query Match 81.8%; Score 9; DB 9; Length 6;
 Best local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 6; Gaps 0;

QY 1 LXR 3
 11
 Db 4 LXR 6

RESULT 8
 US-09-600-700 73
 ? Sequence 73, Application US/09500700
 ? Publication No. US20030059767A1
 ? GENERAL INFORMATION:
 ? APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
 ? APPLICANT: BARBAS III, Carlos F.
 ? APPLICANT: GOTTESFELD, Joel M.
 ? APPLICANT: WRIGHT, Peter F.
 ? TITLE OF INVENTION: 222S PEPTIDE PEPTIDE DERIVATIVES AND METHODS THEREFOR
 ? FILE REFERENCE: SCRIPT160-4
 ? CURRENT APPLICATION NUMBER: US/09500700
 ? PRIOR FILING DATE: 2003-01-10
 ? PRIOR APPLICATION NUMBER: US 08/863,813
 ? PRIOR FILING DATE: 1997-05-27
 ? PRIOR APPLICATION NUMBER: US 08/676,318
 ? PRIOR FILING DATE: 1996-12-30
 ? PRIOR APPLICATION NUMBER: PCT/US95/09829
 ? PRIOR FILING DATE: 1995-01-18
 ? PRIOR APPLICATION NUMBER: US 08/112,604
 ? PRIOR FILING DATE: 1994-09-26
 ? PRIOR APPLICATION NUMBER: US 08/183,119
 ? PRIOR FILING DATE: 1994-01-18
 ? NUMBER OF SEQ ID NOS: 127
 ? SOFTWARE: Patent in version 3.1
 ? SEQ ID NO 73
 ? LENGTH: 6
 ? TYPE: PRI
 ? ORGANISM: Artificial sequence
 ? FEATURE:
 ? OTHER INFORMATION: Modified sequence of finger 1 of 711248

Query Match 81.8%; Score 9; DB 9; Length 6;
 Best local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 6; Gaps 0;

QY 1 LXR 3
 11
 Db 4 LXR 6

RESULT 9
 US-09-795-903A 26
 ? Sequence 26, Application US/09795903A
 ? Patent No. US20020164760A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Lin, Jordan J.N.
 ? APPLICANT: Lin, Xindi
 ? APPLICANT: Kopsch, Gerald
 ? TITLE OF INVENTION: Catalytically Active Procombipin Metapetin and Methods
 ? FILE REFERENCE: CMBF 179

? CURRENT APPLICATION NUMBER: US/09795903A
 ? CURRENT FILING DATE: 2001-02-28
 ? PRIOR APPLICATION NUMBER: 09/604,608
 ? PRIOR FILING DATE: 2000-06-27
 ? PRIOR APPLICATION NUMBER: 60/166,060
 ? PRIOR FILING DATE: 1999-11-30
 ? PRIOR APPLICATION NUMBER: 60/177,836
 ? PRIOR FILING DATE: 2000-01-26
 ? PRIOR APPLICATION NUMBER: 60/178,368
 ? PRIOR FILING DATE: 2000-01-27
 ? PRIOR APPLICATION NUMBER: 60/210,292
 ? PRIOR FILING DATE: 2000-06-08
 ? NUMBER OF SEQ ID NOS: 31
 ? SOFTWARE: Patent in Ver. 2.1
 ? SEQ ID NO 26
 ? LENGTH: 7
 ? TYPE: PRI
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ? OTHER INFORMATION: Peptide
 US-09-795-903A 26

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 11
 Db 4 LXR 6

RESULT 10
 US-09-826-290-370
 ? Sequence 370, Application US/09826290
 ? Patent No. US2002016498A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Barham, L. Kathryn
 ? APPLICANT: Friedman, David L.
 ? APPLICANT: Herath, Herath Mudiyansilage Athula Chandrasiri
 ? APPLICANT: Kimmel, Linda R.
 ? APPLICANT: Parokh, Rajesh Bhikhu
 ? APPLICANT: Potter, David M.
 ? APPLICANT: Rohlf, Christian
 ? APPLICANT: Silber, R. Michael
 ? APPLICANT: Stieger, Thomas R.
 ? APPLICANT: Sunderland, P. Troy
 ? APPLICANT: Townsend, Robert David
 ? APPLICANT: White, Frost
 ? APPLICANT: Williams, Stephen A.
 ? TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
 ? TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
 ? FILE REFERENCE: 2572-1-001 N2
 ? CURRENT APPLICATION NUMBER: US/09826290
 ? CURRENT FILING DATE: 2001-04-06
 ? PRIOR APPLICATION NUMBER: US 60/194,504
 ? PRIOR FILING DATE: 2000-04-03
 ? PRIOR APPLICATION NUMBER: US 60/253,647
 ? PRIOR FILING DATE: 2000-11-28
 ? NUMBER OF SEQ ID NOS: 492
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 370
 ? LENGTH: 7
 ? TYPE: PRI
 ? ORGANISM: homo sapien
 US-09-826-290-370

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 5 LSR 7

RESULT 11

US-09-468-561A-273
 : Sequence 50, Application US/09468561A
 : Patent No. US20020164642A1
 : GENERAL INFORMATION:
 : APPLICANT: Tomlinson, Ian M
 : TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
 : FILE REFERENCE: 8039/1073B
 : CURRENT APPLICATION NUMBER: US/09468561A
 : CURRENT FILING DATE: 2001-10-01
 : PRIOR APPLICATION NUMBER: GB 9722131.1
 : PRIOR FILING DATE: 1997-10-20
 : PRIOR APPLICATION NUMBER: US 60/065,248
 : PRIOR FILING DATE: 1997-11-13
 : PRIOR APPLICATION NUMBER: US 60/066,729
 : PRIOR FILING DATE: 1997-11-21
 : PRIOR APPLICATION NUMBER: PCT/98/03135
 : PRIOR FILING DATE: 1998-10-20
 : PRIOR APPLICATION NUMBER: US 09/511,939
 : PRIOR FILING DATE: 2000-02-24
 : NUMBER OF SEQ ID NOS: 350
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 273
 : LENGTH: 7
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-468-561A-273

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 2
 1 1
 Db 2 LSR 4

RESULT 12

US-09-498-909-7
 : Sequence 7, Application US/09498909
 : Patent No. US2002016464A1
 : GENERAL INFORMATION:
 : APPLICANT: Briggman, Joseph
 : TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
 : FILE REFERENCE: MTP-027
 : CURRENT APPLICATION NUMBER: US/09498909
 : CURRENT FILING DATE: 2001-11-30
 : PRIOR APPLICATION NUMBER: US 60/250,284
 : PRIOR FILING DATE: 2000-11-30
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 7
 : LENGTH: 7
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-498-909-7

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 Db 5 LSR 7

RESULT 13

US-10-080-100-50
 : Sequence 50, Application US/10080100
 : Patent No. US20020165356A1
 : GENERAL INFORMATION:
 : APPLICANT: Barbas, Carlos
 : TITLE OF INVENTION: Zinc Finger Binding Domains for
 : TITLE OF INVENTION: Nucleotide Sequence AMR
 : FILE REFERENCE: ISR1 760.0
 : CURRENT APPLICATION NUMBER: US/10080100
 : CURRENT FILING DATE: 2002-02-21
 : PRIOR APPLICATION NUMBER: 92/57791.106
 : PRIOR FILING DATE: 2001-02-21
 : NUMBER OF SEQ ID NOS: 114
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 50
 : LENGTH: 7
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: synthesized
 : US-10-080-100-50

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 Db 5 LSR 7

RESULT 14

US-10-080-100-51
 : Sequence 51, Application US/10080100
 : Patent No. US20020165356A1
 : GENERAL INFORMATION:
 : APPLICANT: Barbas, Carlos
 : TITLE OF INVENTION: Zinc Finger Binding Domains for
 : TITLE OF INVENTION: Nucleotide Sequence AMR
 : FILE REFERENCE: ISR1 760.0
 : CURRENT APPLICATION NUMBER: US/10080100
 : CURRENT FILING DATE: 2002-02-21
 : PRIOR APPLICATION NUMBER: 92/57791.106
 : PRIOR FILING DATE: 2001-02-21
 : NUMBER OF SEQ ID NOS: 114
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 51
 : LENGTH: 7
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: synthesized
 : US-10-080-100-51

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 Db 5 LSR 7

RESULT 15

US-10-080-100-82
 : Sequence 82, Application US/10080100
 : Patent No. US20020165356A1
 : GENERAL INFORMATION:
 : APPLICANT: Barbas, Carlos
 : TITLE OF INVENTION: Zinc Finger Binding Domains for

? TITLE OF INVENTION: Nucleotide Sequence ANN
 ? FILE REFERENCE: US84 760.0
 ? CURRENT APPLICATION NUMBER: US2002/016596A1
 ? CURRENT FILING DATE: 2002-02-21
 ? PRIOR APPLICATION NUMBER: US09/799,106
 ? PRIOR FILING DATE: 2001-02-21
 ? NUMBER OF SEQ ID NOS: 113
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO 82
 ? LENGTH: 7
 ? TYPE: PR1
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Synthesized
 US-10-080-100-82

Query Match 81.8% Score 9; DB 9; Length 7;
 Best Local Similarity 66.7% Pred. No. 2,90+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 DB 5 LXR 7

RESULT 16
 US-10-080-100-97
 ? Sequence 97 Application: us-09-498-556c-357
 ? Patent No. US2002/016596A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Barbas, Carlos
 ? APPLICANT: Broder, Birgit
 ? TITLE OF INVENTION: Zinc Finger Binding Domains for
 ? FILE REFERENCE: US84 760.0
 ? CURRENT APPLICATION NUMBER: US2002/016596A1
 ? CURRENT FILING DATE: 2002-02-21
 ? PRIOR APPLICATION NUMBER: US09/799,106
 ? PRIOR FILING DATE: 2001-02-21
 ? NUMBER OF SEQ ID NOS: 113
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO 97
 ? LENGTH: 7
 ? TYPE: PR1
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Synthesized
 US-10-080-100-97

Query Match 81.8% Score 9; DB 9; Length 7;
 Best Local Similarity 66.7% Pred. No. 2,90+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 DB 5 LXR 7

RESULT 17
 US-10-080-100-112
 ? Sequence 112 Application: us-09-498-556c-357
 ? Patent No. US2002/016596A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Barbas, Carlos
 ? APPLICANT: Broder, Birgit
 ? TITLE OF INVENTION: Zinc Finger Binding Domains for
 ? FILE REFERENCE: US84 760.0
 ? CURRENT APPLICATION NUMBER: US2002/016596A1
 ? CURRENT FILING DATE: 2002-02-21
 ? PRIOR APPLICATION NUMBER: US09/799,106
 ? PRIOR FILING DATE: 2001-02-21
 ? NUMBER OF SEQ ID NOS: 113

? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO 112
 ? LENGTH: 7
 ? TYPE: PR1
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Synthesized
 US-10-080-100-112

Query Match 81.8% Score 9; DB 9; Length 7;
 Best Local Similarity 66.7% Pred. No. 2,90+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 DB 5 LXR 7

RESULT 18
 US-09-995-973-16
 ? Sequence 16 Application US/0995973
 ? Publication No. US20030024006A1
 ? GENERAL INFORMATION:
 ? APPLICANT: CHOO, Yoon
 ? APPLICANT: ULLMAN, Christopher G.
 ? TITLE OF INVENTION: GENE SWITCHES
 ? FILE REFERENCE: 8425-2004 / 67 US1
 ? CURRENT FILING DATE: 2002-04-19
 ? NUMBER OF SEQ ID NOS: 59
 ? SOFTWARE: Patent In Ver. 2.0
 ? SEQ ID NO 16
 ? LENGTH: 7
 ? TYPE: PR1
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Description of Artificial Sequence; Zinc Finger
 US-09-995-973-16

Query Match 81.8% Score 9; DB 9; Length 7;
 Best Local Similarity 66.7% Pred. No. 2,90+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 DB 5 LXR 7

RESULT 19
 US-09-995-973-50
 ? Sequence 50 Application US/0995973
 ? Publication No. US20030024006A1
 ? GENERAL INFORMATION:
 ? APPLICANT: CHOO, Yoon
 ? APPLICANT: ULLMAN, Christopher G.
 ? TITLE OF INVENTION: GENE SWITCHES
 ? FILE REFERENCE: 8425-2004 / 67 US1
 ? CURRENT APPLICATION NUMBER: US/09/995,973
 ? CURRENT FILING DATE: 2002-04-19
 ? NUMBER OF SEQ ID NOS: 59
 ? SOFTWARE: Patent In Ver. 2.0
 ? SEQ ID NO 50
 ? LENGTH: 7
 ? TYPE: PR1
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Description of Artificial Sequence; Zinc Finger
 US-09-995-973-50

Query Match 81.8% Score 9; DB 9; Length 7;
 Best Local Similarity 66.7% Pred. No. 2,90+05;

Matches 2: Conservative 0: Mismatches 1: Indels 2: Gaps 3:

QY 1 LXR 3
1 1
DB 5 LSR 7

RESULT 20

US-10-006-069A-30

: Sequence 30, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolffe, Alan

: APPLICANT: Eisenberg, Stephen P.

: APPLICANT: Jarvis, Eric

: APPLICANT: Sandamo Biosciences, Inc.

: TITLE OF INVENTION: Regulation of Apoptogenesis With Zinc

: FILE REFERENCE: 019496-0058300S

: CURRENT APPLICATION NUMBER: US/1000069A

: PRIOR FILING DATE: 2001-12-17

: PRIOR APPLICATION NUMBER: US 09/733,604

: PRIOR FILING DATE: 2000-12-07

: PRIOR APPLICATION NUMBER: US 09/736,083

: PRIOR FILING DATE: 2000-12-12

: PRIOR APPLICATION NUMBER: US 09/846,033

: PRIOR FILING DATE: 2001-04-30

: NUMBER OF SEQ ID NOS: 252

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 30

: LENGTH: 7

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: finger

US-10-006-069A-30

Query Match

Best Local Similarity 81.8%; Score 9; DB 9; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.9e+05;

Matches 2: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 LXR 3
1 1
DB 5 LSR 7

RESULT 21

US-10-006-069A-34

: Sequence 34, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolffe, Alan

: APPLICANT: Eisenberg, Stephen P.

: APPLICANT: Jarvis, Eric

: APPLICANT: Sandamo Biosciences, Inc.

: TITLE OF INVENTION: Regulation of Apoptogenesis With Zinc

: FILE REFERENCE: 019496-0058300S

: CURRENT APPLICATION NUMBER: US/1000069A

: PRIOR FILING DATE: 2001-12-17

: PRIOR APPLICATION NUMBER: US 09/733,604

: PRIOR FILING DATE: 2000-12-07

: PRIOR APPLICATION NUMBER: US 09/736,083

: PRIOR FILING DATE: 2000-12-12

: PRIOR APPLICATION NUMBER: US 09/846,033

: SEQ FILE: FASTSEQ for Windows Version 3.0

: NUMBER OF SEQ ID NOS: 252

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 44

: LENGTH: 7

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: finger

US-10-006-069A-44

Query Match 81.8%; Score 9; DB 9; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.9e+05;

Matches 2: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 LXR 3
1 1
DB 5 LSR 7

RESULT 22

US-10-006-069A-45

: Sequence 35, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolffe, Alan

: APPLICANT: Eisenberg, Stephen P.

: APPLICANT: Jarvis, Eric

: APPLICANT: Sandamo Biosciences, Inc.

: TITLE OF INVENTION: Regulation of Apoptogenesis With Zinc

: FILE REFERENCE: 019496-0058300S

: CURRENT APPLICATION NUMBER: US/1000069A

: PRIOR FILING DATE: 2001-12-17

: PRIOR APPLICATION NUMBER: US 09/733,604

: PRIOR FILING DATE: 2000-12-07

: PRIOR APPLICATION NUMBER: US 09/736,083

: PRIOR FILING DATE: 2000-12-12

: PRIOR APPLICATION NUMBER: US 09/846,033

: NUMBER OF SEQ ID NOS: 252

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 45

: LENGTH: 7

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: finger

US-10-006-069A-45

Query Match

Best Local Similarity 81.8%; Score 9; DB 9; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.9e+05;

Matches 2: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 LXR 3
1 1
DB 5 LSR 7

RESULT 23

US-10-006-069A-46

: Sequence 36, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolffe, Alan

```

1 APPLICANT: Eisenberg, Stephen P.
2 APPLICANT: Jarvis, Eric
3 APPLICANT: Sangamo Biosciences, Inc.
4 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
5 FILE REFERENCE: 019496-0058400S
6 CURRENT APPLICATION NUMBER: US/10/006,069A
7 PRIOR FILING DATE: 2001-12-17
8 PRIOR APPLICATION NUMBER: US 09/744,604
9 PRIOR FILING DATE: 2000-12-07
10 PRIOR APPLICATION NUMBER: US 09/746,084
11 PRIOR FILING DATE: 2000-12-12
12 PRIOR APPLICATION NUMBER: US 09/846,034
13 PRIOR FILING DATE: 2001-04-30
14 NUMBER OF SEQ ID NOS: 252
15 SOFTWARE: FastSeq for Windows Version 4.0
16 SEQ ID NO 46
17 LENGTH: 7
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Finger
22 US-10-006,069A-46

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 66.7%  Prod. No. 2,9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;

```

```

QY 1 LXR 4
1 1
DB 5 LIR 7

```

```

RESULT 24
US-10-006,069A-48
1 Sequence 38, Application US/10006069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolfre, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
13 FILE REFERENCE: 019496-0058400S
14 CURRENT APPLICATION NUMBER: US/10/006,069A
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/744,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/746,084
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,034
21 PRIOR FILING DATE: 2001-04-30
22 NUMBER OF SEQ ID NOS: 252
23 SOFTWARE: FastSeq for Windows Version 4.0
24 SEQ ID NO 48
25 LENGTH: 7
26 TYPE: PRT
27 ORGANISM: Artificial Sequence
28 FEATURE:
29 OTHER INFORMATION: Finger
30 US-10-006,069A-48

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 66.7%  Prod. No. 2,9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;

```

```

QY 1 LXR 4
1 1

```

```

Db 5 LXR 7

RESULT 25
US-10-006-069A-49
1 Sequence 39, Application US/10006069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolfre, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
13 FILE REFERENCE: 019496-0058400S
14 CURRENT APPLICATION NUMBER: US/10/006,069A
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/744,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/746,084
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,034
21 PRIOR FILING DATE: 2001-04-30
22 NUMBER OF SEQ ID NOS: 252
23 SOFTWARE: FastSeq for Windows Version 4.0
24 SEQ ID NO 49
25 LENGTH: 7
26 TYPE: PRT
27 ORGANISM: Artificial Sequence
28 FEATURE:
29 OTHER INFORMATION: Finger
30 US-10-006-069A-49

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 66.7%  Prod. No. 2,9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;

```

```

QY 1 LXR 3
1 1
DB 5 LIR 7

```

```

RESULT 26
US-10-006-069A-40
1 Sequence 40, Application US/10006069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolfre, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
13 FILE REFERENCE: 019496-0058400S
14 CURRENT APPLICATION NUMBER: US/10/006,069A
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/744,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/746,084
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,034
21 PRIOR FILING DATE: 2001-04-30
22 NUMBER OF SEQ ID NOS: 252
23 SOFTWARE: FastSeq for Windows Version 4.0
24 SEQ ID NO 40

```

```

: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-40

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   1 1
Db 5 LAR 7

```

RESULT 27

```

: Sequence 41, Application US/1000069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo BioSciences, Inc.

```

```

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: Finger Proteins

```

```

: CURRENT APPLICATION NUMBER: US 09/733,604
: PRIOR APPLICATION NUMBER: US 09/733,604

```

```

: PRIOR FILING DATE: 2001-12-07
: PRIOR FILING DATE: 2000-12-07

```

```

: PRIOR FILING DATE: 2000-12-12
: PRIOR FILING DATE: 2000-12-12

```

```

: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 352

```

```

: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 41

```

```

: LENGTH: 7
: TYPE: PRT

```

```

: ORGANISM: Artificial Sequence
: FEATURE:

```

```

: OTHER INFORMATION: finger
US-10-006-069A-41

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   1 1
Db 5 LAR 7

```

RESULT 28

```

: Sequence 42, Application US/1000069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo BioSciences, Inc.

```

```

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc

```

```

: TITLE OF INVENTION: Finger Proteins
: FILE REFERENCE: 019496-0058300S
: CURRENT APPLICATION NUMBER: US/1000069A

```

```

: PRIOR FILING DATE: 2001-12-17
: PRIOR FILING DATE: 2000-12-07

```

```

: PRIOR FILING DATE: 2000-12-12
: PRIOR FILING DATE: 2000-12-12

```

```

: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 352

```

```

: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 42

```

```

: LENGTH: 7
: TYPE: PRT

```

```

: ORGANISM: Artificial Sequence
: FEATURE:

```

```

: OTHER INFORMATION: finger
US-10-006-069A-42

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   1 1
Db 5 LAR 7

```

RESULT 29

```

: Sequence 43, Application US/1000069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew

```

```

: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi

```

```

: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.

```

```

: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo BioSciences, Inc.

```

```

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: Finger Proteins

```

```

: CURRENT APPLICATION NUMBER: US 09/733,604
: PRIOR APPLICATION NUMBER: US 09/733,604

```

```

: PRIOR FILING DATE: 2001-12-07
: PRIOR FILING DATE: 2000-12-07

```

```

: PRIOR FILING DATE: 2000-12-12
: PRIOR FILING DATE: 2000-12-12

```

```

: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 352

```

```

: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 43

```

```

: LENGTH: 7
: TYPE: PRT

```

```

: ORGANISM: Artificial Sequence
: FEATURE:

```

```

: OTHER INFORMATION: finger
US-10-006-069A-43

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   1 1
Db 5 LAR 7

```

RESULT 30

```

US-10-006-069A-47
: Sequence 47, Application US/10006069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Kobar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Qiang
: APPLICANT: Wollie, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sandamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Androgenesis with Zinc
: TITLE OF INVENTION: Finger Proteins
: FILE REFERENCE: 019496-0058400S
: CURRENT APPLICATION NUMBER: US 09/736,084
: PRIOR FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,084
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,034
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 47
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-47

```

```

Query Match      81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 41
US-10-006-069A-49
: Sequence 49, Application US/10006069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Kobar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Qiang
: APPLICANT: Wollie, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sandamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Androgenesis with Zinc
: TITLE OF INVENTION: Finger Proteins
: FILE REFERENCE: 019496-0058400S
: CURRENT APPLICATION NUMBER: US 09/736,084
: PRIOR FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,084
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,034
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 49
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:

```

```

: OTHER INFORMATION: finger
US-10-006-069A-49
Query Match      81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Query Match      81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 44
US-10-006-069A-52
: Sequence 52, Application US/10006069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Kobar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Qiang
: APPLICANT: Wollie, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sandamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Androgenesis with Zinc
: TITLE OF INVENTION: Finger Proteins
: FILE REFERENCE: 019496-0058400S
: CURRENT APPLICATION NUMBER: US 09/736,084
: PRIOR FILING DATE: 2001-12-17

```

```

: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 52
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-52

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 56.7%  Pct. Id. 2.9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;

```

```

QY 1 LXR 3
   | |
Db 5 LTR 7

```

RESULT 34

```

US-10-006-069A-54
: Sequence 54, Application US/10006069A
: Publication No. US20010021776A1
: GENERAL INFORMATION:
: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolffe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005840S
: CURRENT APPLICATION NUMBER: US 10/006069A
: PRIOR FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/732,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 54
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-54

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 56.7%  Pct. Id. 2.9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;

```

```

QY 1 LXR 3
   | |
Db 5 LTR 7

```

RESULT 35

```

US-10-006-069A-55
: Sequence 55, Application US/10006069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolffe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005840S
: CURRENT APPLICATION NUMBER: US/10/006,069A
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 55
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-55

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 56.7%  Pct. Id. 2.9e+05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;

```

```

QY 1 LXR 3
   | |
Db 5 LTR 7

```

RESULT 36

```

US-10-006-069A-56
: Sequence 56, Application US/10006069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolffe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005840S
: CURRENT APPLICATION NUMBER: US/10/006,069A
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 56
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-56

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;

```

Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 37

US-10-006-069A-57
Sequence 57, Application US/10006069A
Publication No. US20030021776A1
GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Androgenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/10-006-069A
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 57
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: finger
US-10-006-069A-57

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 38

US-10-006-069A-59
Sequence 59, Application US/10006069A
Publication No. US20030021776A1
GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Androgenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/10-006-069A
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: finger
US-10-006-069A-59

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 40

US-10-006-069A-61
Sequence 61, Application US/10006069A
Publication No. US20030021776A1
GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Androgenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/10-006-069A
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: finger
US-10-006-069A-60

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

PRIOR APPLICATION NUMBER: US 09/846,044
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: finger
US-10-006-069A-59

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 39

US-10-006-069A-60
Sequence 60, Application US/10006069A
Publication No. US20030021776A1
GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Androgenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/10-006-069A
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,044
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: finger
US-10-006-069A-60

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7


```

1 APPLICANT: Wolffe, Alan
2 APPLICANT: Eisenberg, Stephen P.
3 APPLICANT: Jarvis, Eric
4 APPLICANT: Sangamo Biosciences, Inc.
5 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
6 FILE REFERENCE: 019496-0058300S
7 CURRENT APPLICATION NUMBER: US 09/774,604
8 PRIOR FILING DATE: 2001-12-17
9 PRIOR APPLICATION NUMBER: US 09/774,604
10 PRIOR FILING DATE: 2000-12-07
11 PRIOR APPLICATION NUMBER: US 09/774,623
12 PRIOR FILING DATE: 2000-12-12
13 PRIOR APPLICATION NUMBER: US 09/846,033
14 PRIOR FILING DATE: 2001-04-30
15 NUMBER OF SEQ ID NOS: 252
16 SOFTWARE: FastSeq for Windows Version 3.0
17 SEQ ID NO 61
18 LENGTH: 7
19 TYPE: PRT
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: Finger
US-10-006-069A-61

```

```

Query Match      81.8%   Score 9;   DB 9;   Length 7;
Best Local Similarity 66.7%;   Pred. No. 2.9e+05;
Matches 2;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

```

```

QY 1 LXR 3
   | |
DB 5 LXR 7

```

```

RESULT 41
US-10-006-069A-64
1 Sequence 64, Application US/1006069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolffe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
13 FILE REFERENCE: 019496-0058300S
14 CURRENT APPLICATION NUMBER: US/10,006,064A
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/774,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/774,623
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,033
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 3.0
23 SEQ ID NO 64
24 LENGTH: 7
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Finger
US-10-006-069A-64

```

```

Query Match      91.8%   Score 9;   DB 9;   Length 7;
Best Local Similarity 66.7%;   Pred. No. 2.9e+05;
Matches 2;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

```

```

QY 1 LXR 3

```

```

Db 5 LXR 7
RESULT 42
US-10-006-069A-65
1 Sequence 65, Application US/1006069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolffe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
13 FILE REFERENCE: 019496-0058300S
14 CURRENT APPLICATION NUMBER: US/10,006,064A
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/774,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/774,623
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,033
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 3.0
23 SEQ ID NO 65
24 LENGTH: 7
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Finger
US-10-006-069A-65

```

```

Query Match      81.8%   Score 9;   DB 9;   Length 7;
Best Local Similarity 66.7%;   Pred. No. 2.9e+05;
Matches 2;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

```

```

QY 1 LXR 3
   | |
DB 5 LXR 7

```

```

RESULT 43
US-10-006-069A-66
1 Sequence 66, Application US/1006069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolffe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
13 FILE REFERENCE: 019496-0058300S
14 CURRENT APPLICATION NUMBER: US/10,006,064A
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/774,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/774,623
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,033
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 3.0

```

; SEQ ID NO 66
 ; LENGTH: 7
 ; TYPE: PRI
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: finger
 US 10-006-069A-66

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 DB 5 LTR 7

RESULT 44

US-10-006-069A-67
 ; Sequence 67; Application US/10006069A
 ; Publication No. US20030921776A1

; GENERAL INFORMATION:
 ; APPLICANT: Rebar, Edward
 ; APPLICANT: Jamieson, Andrew
 ; APPLICANT: Liu, Qiang
 ; APPLICANT: Liu, Pei-Qi
 ; APPLICANT: Welfre, Alan
 ; APPLICANT: Eisenberg, Stephen P.
 ; APPLICANT: Jarvis, Eric

; APPLICANT: Sanquamo Biosciences, Inc.

; TITLE OF INVENTION: Regulation of Androgenesis With Zinc

; FILE REFERENCE: 019496-005830DS

; CURRENT APPLICATION NUMBER: US/10/006,069A

; CURRENT FILING DATE: 2001-12-17

; PRIOR FILING DATE: 2000-12-07

; PRIOR FILING DATE: 2000-12-07

; PRIOR FILING DATE: 2000-12-12

; PRIOR FILING DATE: 2000-12-12

; PRIOR FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 252

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 67
 ; LENGTH: 7
 ; TYPE: PRI
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: finger
 US 10-006-069A-67

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 DB 5 LTR 7

RESULT 45

US-10-006-069A-68
 ; Sequence 68; Application US/10006069A
 ; Publication No. US20030921776A1

; GENERAL INFORMATION:

; APPLICANT: Rebar, Edward

; APPLICANT: Jamieson, Andrew

; APPLICANT: Liu, Qiang

; APPLICANT: Liu, Pei-Qi

; APPLICANT: Welfre, Alan

; APPLICANT: Eisenberg, Stephen P.

; APPLICANT: Jarvis, Eric

; APPLICANT: Sanquamo Biosciences, Inc.

; TITLE OF INVENTION: Regulation of Androgenesis With Zinc

; FILE REFERENCE: 019496-005830DS

; CURRENT APPLICATION NUMBER: US/10/006,069A

; CURRENT FILING DATE: 2001-12-17

; PRIOR FILING DATE: 2000-12-07

; PRIOR FILING DATE: 2000-12-07

; PRIOR FILING DATE: 2000-12-12

; PRIOR FILING DATE: 2000-12-12

; PRIOR FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 252

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 68

; LENGTH: 7

; TYPE: PRI

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: finger

US-10-006-069A-68

Query Match 81.8%; Score 9; DB 9; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.9e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

| |

DB 5 LTR 7

Search completed: April 30, 2004, 14:45:01
 Job time : 22.7273 secs

GenCore version 5.1.4.15.4529
Copyright (c) 1993 - 2000 Campden Ltd.

OM protein: protein search, using sw model

Run on: April 30, 2003, 13:21:58 : Search time 39.4545 seconds
(without alignments)
23,641 Million cell updates/yr

Title: US-09-498-556c-79
Period score: 32
Sequence: 1 XGSPYFN 7

Scoring table: BLASTSUM62

Gapf 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum HP seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database	A_Genseq_1000p
1: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15293	FAT
2: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15307	FAT
3: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15325	FAT
4: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15343	FAT
5: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15361	FAT
6: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15379	FAT
7: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15397	FAT
8: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15415	FAT
9: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15433	FAT
10: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15451	FAT
11: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15469	FAT
12: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15487	FAT
13: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15505	FAT
14: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15523	FAT
15: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15541	FAT
16: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15559	FAT
17: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15577	FAT
18: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15595	FAT
19: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15613	FAT
20: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15631	FAT
21: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15649	FAT
22: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15667	FAT
23: /S1052/seqdata/genomes/Homo sapiens/Homo sapiens/AA15685	FAT

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	93.8	5	17	AA091721
2	30	93.8	5	20	AA090440
3	30	93.8	5	21	AA091325
4	30	93.8	7	17	AA091730
5	30	93.8	7	20	AA090449
6	30	93.8	7	21	AA091334
7	30	93.8	7	20	AA090450
8	30	93.8	7	21	AA091335
9	30	93.8	8	20	AA090451
10	30	93.8	8	20	AA090452

11	30	93.8	82	21	AA0915293
12	30	93.8	82	21	AA0915307
13	30	93.8	82	20	AA090425
14	30	93.8	84	20	AA090424
15	30	93.8	84	20	AA090424
16	30	93.8	84	20	AA090424
17	30	93.8	84	21	AA0915317
18	30	93.8	86	22	AA091998
19	30	93.8	86	20	AA090421
20	30	93.8	86	21	AA0915301
21	30	93.8	91	20	AA090393
22	30	93.8	91	20	AA090393
23	30	93.8	91	21	AA0915345
24	30	93.8	91	21	AA0915345
25	30	93.8	97	17	AA0917309
26	30	93.8	97	20	AA090437
27	30	93.8	97	20	AA0915386
28	30	93.8	102	21	AA0915295
29	30	93.8	108	20	AA090398
30	30	93.8	108	20	AA0915292
31	30	93.8	124	21	AA090540
32	30	93.8	138	22	AA090987
33	30	93.8	161	20	AA090438
34	30	93.8	162	20	AA090437
35	30	93.8	162	20	AA090437
36	30	93.8	162	21	AA0915321
37	30	93.8	162	21	AA0915322
38	30	93.8	171	20	AA090435
39	30	93.8	180	17	AA091713
40	30	93.8	180	17	AA091713
41	30	93.8	181	17	AA091711
42	30	93.8	181	17	AA091711
43	30	93.8	181	17	AA091711
44	30	93.8	181	17	AA091711
45	30	93.8	181	17	AA091711
46	30	93.8	181	17	AA091711
47	30	93.8	181	17	AA091711
48	30	93.8	181	17	AA091711
49	30	93.8	181	17	AA091711
50	30	93.8	181	17	AA091711
51	30	93.8	181	17	AA091711
52	30	93.8	181	17	AA091711
53	30	93.8	181	17	AA091711
54	30	93.8	181	17	AA091711
55	30	93.8	181	17	AA091711
56	30	93.8	181	17	AA091711
57	30	93.8	181	17	AA091711
58	30	93.8	181	17	AA091711
59	30	93.8	181	17	AA091711
60	30	93.8	181	17	AA091711
61	30	93.8	181	17	AA091711
62	30	93.8	181	17	AA091711
63	30	93.8	181	17	AA091711
64	30	93.8	181	17	AA091711
65	30	93.8	181	17	AA091711
66	30	93.8	181	17	AA091711
67	30	93.8	181	17	AA091711
68	30	93.8	181	17	AA091711
69	30	93.8	181	17	AA091711
70	30	93.8	181	17	AA091711
71	30	93.8	181	17	AA091711
72	30	93.8	181	17	AA091711
73	30	93.8	181	17	AA091711
74	30	93.8	181	17	AA091711
75	30	93.8	181	17	AA091711
76	30	93.8	181	17	AA091711
77	30	93.8	181	17	AA091711
78	30	93.8	181	17	AA091711
79	30	93.8	181	17	AA091711
80	30	93.8	181	17	AA091711
81	30	93.8	181	17	AA091711
82	30	93.8	181	17	AA091711
83	30	93.8	181	17	AA091711
84	30	93.8	181	17	AA091711
85	30	93.8	181	17	AA091711
86	30	93.8	181	17	AA091711
87	30	93.8	181	17	AA091711
88	30	93.8	181	17	AA091711
89	30	93.8	181	17	AA091711
90	30	93.8	181	17	AA091711
91	30	93.8	181	17	AA091711
92	30	93.8	181	17	AA091711
93	30	93.8	181	17	AA091711

84	27	84.4	105	17	AAH51797	Ac, dAMP2f, Ancylos
85	27	84.4	105	17	AAH51798	Ac, dAMP2f, Ancylos
86	27	84.4	105	20	AAH51799	Nematode extracted
87	27	84.4	105	20	AAH51800	Nematode extracted
88	27	84.4	105	17	AAH51801	Ac, dAMP2f, Ancylos
89	27	84.4	105	17	AAH51802	Nematode extracted
90	27	84.4	105	17	AAH51803	Ac, dAMP2f, Ancylos
91	27	84.4	105	17	AAH51804	Ac, dAMP2f, Ancylos
92	27	84.4	105	17	AAH51805	Nematode extracted
93	27	84.4	105	17	AAH51806	Human polypeptide
94	27	84.4	105	17	AAH51807	Human polypeptide
95	27	84.4	105	17	AAH51808	Human polypeptide
96	27	84.4	105	17	AAH51809	Human polypeptide
97	27	84.4	105	17	AAH51810	Human polypeptide
98	27	84.4	105	17	AAH51811	Human polypeptide
99	27	84.4	105	17	AAH51812	Human polypeptide
100	27	84.4	105	17	AAH51813	Human polypeptide
101	27	84.4	105	17	AAH51814	Human polypeptide
102	27	84.4	105	17	AAH51815	Human polypeptide
103	27	84.4	105	17	AAH51816	Human polypeptide
104	27	84.4	105	17	AAH51817	Human polypeptide
105	27	84.4	105	17	AAH51818	Human polypeptide
106	27	84.4	105	17	AAH51819	Human polypeptide
107	27	84.4	105	17	AAH51820	Human polypeptide
108	27	84.4	105	17	AAH51821	Human polypeptide
109	27	84.4	105	17	AAH51822	Human polypeptide
110	27	84.4	105	17	AAH51823	Human polypeptide
111	27	84.4	105	17	AAH51824	Human polypeptide
112	27	84.4	105	17	AAH51825	Human polypeptide
113	27	84.4	105	17	AAH51826	Human polypeptide
114	27	84.4	105	17	AAH51827	Human polypeptide
115	27	84.4	105	17	AAH51828	Human polypeptide
116	27	84.4	105	17	AAH51829	Human polypeptide
117	27	84.4	105	17	AAH51830	Human polypeptide
118	27	84.4	105	17	AAH51831	Human polypeptide
119	27	84.4	105	17	AAH51832	Human polypeptide
120	27	84.4	105	17	AAH51833	Human polypeptide
121	27	84.4	105	17	AAH51834	Human polypeptide
122	27	84.4	105	17	AAH51835	Human polypeptide
123	27	84.4	105	17	AAH51836	Human polypeptide
124	27	84.4	105	17	AAH51837	Human polypeptide
125	27	84.4	105	17	AAH51838	Human polypeptide
126	27	84.4	105	17	AAH51839	Human polypeptide
127	27	84.4	105	17	AAH51840	Human polypeptide
128	27	84.4	105	17	AAH51841	Human polypeptide
129	27	84.4	105	17	AAH51842	Human polypeptide
130	27	84.4	105	17	AAH51843	Human polypeptide
131	27	84.4	105	17	AAH51844	Human polypeptide
132	27	84.4	105	17	AAH51845	Human polypeptide
133	27	84.4	105	17	AAH51846	Human polypeptide
134	27	84.4	105	17	AAH51847	Human polypeptide
135	27	84.4	105	17	AAH51848	Human polypeptide
136	27	84.4	105	17	AAH51849	Human polypeptide
137	27	84.4	105	17	AAH51850	Human polypeptide
138	27	84.4	105	17	AAH51851	Human polypeptide
139	27	84.4	105	17	AAH51852	Human polypeptide
140	27	84.4	105	17	AAH51853	Human polypeptide
141	27	84.4	105	17	AAH51854	Human polypeptide
142	27	84.4	105	17	AAH51855	Human polypeptide
143	27	84.4	105	17	AAH51856	Human polypeptide
144	27	84.4	105	17	AAH51857	Human polypeptide
145	27	84.4	105	17	AAH51858	Human polypeptide
146	27	84.4	105	17	AAH51859	Human polypeptide
147	27	84.4	105	17	AAH51860	Human polypeptide
148	27	84.4	105	17	AAH51861	Human polypeptide
149	27	84.4	105	17	AAH51862	Human polypeptide
150	27	84.4	105	17	AAH51863	Human polypeptide
151	27	84.4	105	17	AAH51864	Human polypeptide
152	27	84.4	105	17	AAH51865	Human polypeptide
153	27	84.4	105	17	AAH51866	Human polypeptide
154	27	84.4	105	17	AAH51867	Human polypeptide
155	27	84.4	105	17	AAH51868	Human polypeptide
156	27	84.4	105	17	AAH51869	Human polypeptide

230	25	78.1	166	19	AAW67469	E. coli mutant per	302	78.1	514	23	AAW49134	Human specific pro
231	25	78.1	166	19	AAW67465	E. coli periplasm	304	78.1	515	26	AAW41761	Human P-70m prote
232	25	78.1	166	19	AAW67466	E. coli mutant per	305	78.1	516	21	AAW444257	Human P6708 (P60)
233	25	78.1	166	19	AAW67467	E. coli mutant per	306	78.1	516	21	AAW57462	Arabidopsis thalia
234	25	78.1	166	22	AAW01676	Human gene 5 enco	307	78.1	515	21	AAW61132	Arabidopsis thalia
235	25	78.1	166	22	AAW01707	Human gene 5 enco	308	78.1	515	22	AAW29061	Human pro polypept
236	25	78.1	166	23	AAW63949	Human albumin fus	309	78.1	515	22	AAW07598	glycoprotein 5 llo
237	25	78.1	166	23	AAW63950	Human albumin fus	310	78.1	516	22	AAW75947	glycoprotein 5 llo
238	25	78.1	168	22	AAW69478	Protophila melano	311	78.1	516	22	AAW94799	Human P-70m prote
239	25	78.1	171	21	AAW94721	Cytochrome P450 #	312	78.1	516	23	AAW14737	Human P-70m prote
240	25	78.1	191	21	AAW63227	Protophila melano	313	78.1	516	23	AAW14737	Human P-70m prote
241	25	78.1	197	20	AAW59671	Secreted protein	314	78.1	516	23	AAW14737	Human P-70m prote
242	25	78.1	191	21	AAW59596	HIV-1 non subtyp	315	78.1	516	23	AAW59596	Human secreted pro
243	25	78.1	214	23	AAW59596	Lactobacillus lactis	316	78.1	516	23	AAW59596	Human secreted pro
244	25	78.1	215	23	AAW59596	Revel human thali	317	78.1	516	23	AAW59596	Arabidopsis thalia
245	25	78.1	216	23	AAW59596	Protophila melano	318	78.1	516	23	AAW59596	Arabidopsis thalia
246	25	78.1	227	19	AAW59596	S. pneumoniae det	319	78.1	516	23	AAW59596	Arabidopsis thalia
247	25	78.1	227	21	AAW59596	Yeast polypeptide	320	78.1	516	23	AAW59596	Arabidopsis thalia
248	25	78.1	239	22	AAW59596	Staphylococcus aur	321	78.1	516	23	AAW59596	Arabidopsis thalia
249	25	78.1	249	24	AAW59596	S. aureus adhesion	322	78.1	516	23	AAW59596	Maltotetraose, ps
250	25	78.1	249	24	AAW59596	Human GRP95	323	78.1	516	23	AAW59596	Revel human protei
251	25	78.1	244	21	AAW59596	Arabidopsis thalia	324	78.1	516	23	AAW59596	Human vesicle asso
252	25	78.1	244	21	AAW59596	Arabidopsis thalia	325	78.1	516	23	AAW59596	Arabidopsis thalia
253	25	78.1	246	22	AAW59596	Revel human thali	326	78.1	516	23	AAW59596	Human testis det
254	25	78.1	251	21	AAW59596	Arabidopsis thalia	327	78.1	516	23	AAW59596	Arabidopsis thalia
255	25	78.1	251	21	AAW59596	Arabidopsis thalia	328	78.1	516	23	AAW59596	Arabidopsis thalia
256	25	78.1	251	21	AAW59596	Human MCDI SEI	329	78.1	516	23	AAW59596	Arabidopsis thalia
257	25	78.1	256	23	AAW59596	Staphylococcus aur	330	78.1	516	23	AAW59596	Arabidopsis thalia
258	25	78.1	256	23	AAW59596	Lactobacillus lactis	331	78.1	516	23	AAW59596	Human 25278 surfat
259	25	78.1	256	23	AAW59596	Human TMAP11 pro	332	78.1	516	23	AAW59596	Arabidopsis thalia
260	25	78.1	256	23	AAW59596	Human alpha 2 plas	333	78.1	516	23	AAW59596	E. coli cellular p
261	25	78.1	256	23	AAW59596	Arabidopsis thalia	334	78.1	516	23	AAW59596	Salmonella typhi c
262	25	78.1	256	23	AAW59596	Arabidopsis thalia	335	78.1	516	23	AAW59596	Arabidopsis thalia
263	25	78.1	256	23	AAW59596	Arabidopsis thalia	336	78.1	516	23	AAW59596	Arabidopsis thalia
264	25	78.1	256	23	AAW59596	S. epidermidis spe	337	78.1	516	23	AAW59596	Arabidopsis thalia
265	25	78.1	256	23	AAW59596	S. epidermidis spe	338	78.1	516	23	AAW59596	Arabidopsis thalia
266	25	78.1	256	23	AAW59596	Human secreted pro	339	78.1	516	23	AAW59596	Arabidopsis thalia
267	25	78.1	256	23	AAW59596	Human lactin beta	340	78.1	516	23	AAW59596	Arabidopsis thalia
268	25	78.1	256	23	AAW59596	Human secreted pro	341	78.1	516	23	AAW59596	Arabidopsis thalia
269	25	78.1	256	23	AAW59596	MAF Kinase Phosha	342	78.1	516	23	AAW59596	Arabidopsis thalia
270	25	78.1	256	23	AAW59596	Human lactate de	343	78.1	516	23	AAW59596	Arabidopsis thalia
271	25	78.1	256	23	AAW59596	Protophila melano	344	78.1	516	23	AAW59596	Arabidopsis thalia
272	25	78.1	256	23	AAW59596	Arabidopsis thalia	345	78.1	516	23	AAW59596	Arabidopsis thalia
273	25	78.1	256	23	AAW59596	Arabidopsis thalia	346	78.1	516	23	AAW59596	Arabidopsis thalia
274	25	78.1	256	23	AAW59596	Herbicidally activ	347	78.1	516	23	AAW59596	Arabidopsis thalia
275	25	78.1	256	23	AAW59596	Human alpha 2 plas	348	78.1	516	23	AAW59596	Arabidopsis thalia
276	25	78.1	256	23	AAW59596	Staphylococcus spe	349	78.1	516	23	AAW59596	Arabidopsis thalia
277	25	78.1	256	23	AAW59596	Protein protein #1	350	78.1	516	23	AAW59596	Arabidopsis thalia
278	25	78.1	256	23	AAW59596	Protein protein #2	351	78.1	516	23	AAW59596	Arabidopsis thalia
279	25	78.1	256	23	AAW59596	Coffee theobromine	352	78.1	516	23	AAW59596	Arabidopsis thalia
280	25	78.1	256	23	AAW59596	Listeria monocytosa	353	78.1	516	23	AAW59596	Arabidopsis thalia
281	25	78.1	256	23	AAW59596	Human lactin beta	354	78.1	516	23	AAW59596	Arabidopsis thalia
282	25	78.1	256	23	AAW59596	Coffee theobromine	355	78.1	516	23	AAW59596	Arabidopsis thalia
283	25	78.1	256	23	AAW59596	Coffee theobromine	356	78.1	516	23	AAW59596	Arabidopsis thalia
284	25	78.1	256	23	AAW59596	Human SEPS protein	357	78.1	516	23	AAW59596	Arabidopsis thalia
285	25	78.1	256	23	AAW59596	Arabidopsis thalia	358	78.1	516	23	AAW59596	Arabidopsis thalia
286	25	78.1	256	23	AAW59596	Arabidopsis thalia	359	78.1	516	23	AAW59596	Arabidopsis thalia
287	25	78.1	256	23	AAW59596	Arabidopsis thalia	360	78.1	516	23	AAW59596	Arabidopsis thalia
288	25	78.1	256	23	AAW59596	Arabidopsis thalia	361	78.1	516	23	AAW59596	Arabidopsis thalia
289	25	78.1	256	23	AAW59596	Arabidopsis thalia	362	78.1	516	23	AAW59596	Arabidopsis thalia
290	25	78.1	256	23	AAW59596	Arabidopsis thalia	363	78.1	516	23	AAW59596	Arabidopsis thalia
291	25	78.1	256	23	AAW59596	Arabidopsis thalia	364	78.1	516	23	AAW59596	Arabidopsis thalia
292	25	78.1	256	23	AAW59596	Arabidopsis thalia	365	78.1	516	23	AAW59596	Arabidopsis thalia
293	25	78.1	256	23	AAW59596	Arabidopsis thalia	366	78.1	516	23	AAW59596	Arabidopsis thalia
294	25	78.1	256	23	AAW59596	Arabidopsis thalia	367	78.1	516	23	AAW59596	Arabidopsis thalia
295	25	78.1	256	23	AAW59596	Arabidopsis thalia	368	78.1	516	23	AAW59596	Arabidopsis thalia
296	25	78.1	256	23	AAW59596	Arabidopsis thalia	369	78.1	516	23	AAW59596	Arabidopsis thalia
297	25	78.1	256	23	AAW59596	Arabidopsis thalia	370	78.1	516	23	AAW59596	Arabidopsis thalia
298	25	78.1	256	23	AAW59596	Arabidopsis thalia	371	78.1	516	23	AAW59596	Arabidopsis thalia
299	25	78.1	256	23	AAW59596	Arabidopsis thalia	372	78.1	516	23	AAW59596	Arabidopsis thalia
300	25	78.1	256	23	AAW59596	Arabidopsis thalia	373	78.1	516	23	AAW59596	Arabidopsis thalia
301	25	78.1	256	23	AAW59596	Arabidopsis thalia	374	78.1	516	23	AAW59596	Arabidopsis thalia
302	25	78.1	256	23	AAW59596	Arabidopsis thalia	375	78.1	516	23	AAW59596	Arabidopsis thalia

476	79.1	792	24	APP61415	Brain/idiopathic atrophic	44	75.0	17	24	AA099901	Insulin/insulin li
477	79.1	802	21	Human GRP78 chaperone	Human GRP78 chaperone	450	75.0	17	24	AA099923	Insulin/insulin li
478	79.1	802	21	Human PRO polypeptide	Human PRO polypeptide	451	75.0	17	24	AA099925	Insulin/insulin li
479	79.1	825	18	Human furin-like protease	Human furin-like protease	452	75.0	17	24	AA099937	Insulin/insulin li
480	79.1	861	23	Human laminin gamma 2	Human laminin gamma 2	453	75.0	17	24	AA099938	Insulin/insulin li
481	79.1	861	23	Human laminin gamma 3	Human laminin gamma 3	454	75.0	17	24	AA099940	Insulin/insulin li
482	79.1	866	23	Human laminin gamma 4	Human laminin gamma 4	455	75.0	17	24	AA099942	Insulin/insulin li
483	79.1	875	16	Human laminin gamma 5	Human laminin gamma 5	456	75.0	17	24	AA099944	Insulin/insulin li
484	79.1	875	16	Human laminin gamma 6	Human laminin gamma 6	457	75.0	17	24	AA099946	Insulin/insulin li
485	79.1	919	23	Human laminin gamma 7	Human laminin gamma 7	458	75.0	17	24	AA099948	Insulin/insulin li
486	79.1	920	18	Human laminin gamma 8	Human laminin gamma 8	459	75.0	17	24	AA099950	Insulin/insulin li
487	79.1	924	22	Human laminin gamma 9	Human laminin gamma 9	460	75.0	17	24	AA099952	Insulin/insulin li
488	79.1	925	17	Human laminin gamma 10	Human laminin gamma 10	461	75.0	17	24	AA099954	Insulin/insulin li
489	79.1	935	22	Human laminin gamma 11	Human laminin gamma 11	462	75.0	17	24	AA099956	Insulin/insulin li
490	79.1	935	22	Human laminin gamma 12	Human laminin gamma 12	463	75.0	17	24	AA099958	Insulin/insulin li
491	79.1	967	23	Human laminin gamma 13	Human laminin gamma 13	464	75.0	17	24	AA099960	Insulin/insulin li
492	79.1	967	23	Human laminin gamma 14	Human laminin gamma 14	465	75.0	17	24	AA099962	Insulin/insulin li
493	79.1	977	21	Human laminin gamma 15	Human laminin gamma 15	466	75.0	17	24	AA099964	Insulin/insulin li
494	79.1	1001	22	Human laminin gamma 16	Human laminin gamma 16	467	75.0	17	24	AA099966	Insulin/insulin li
495	79.1	1017	22	Human laminin gamma 17	Human laminin gamma 17	468	75.0	17	24	AA099968	Insulin/insulin li
496	79.1	1020	22	Human laminin gamma 18	Human laminin gamma 18	469	75.0	17	24	AA099970	Insulin/insulin li
497	79.1	1027	22	Human laminin gamma 19	Human laminin gamma 19	470	75.0	17	24	AA099972	Insulin/insulin li
498	79.1	1037	22	Human laminin gamma 20	Human laminin gamma 20	471	75.0	17	24	AA099974	Insulin/insulin li
499	79.1	1068	21	Human laminin gamma 21	Human laminin gamma 21	472	75.0	17	24	AA099976	Insulin/insulin li
500	79.1	1095	22	Human laminin gamma 22	Human laminin gamma 22	473	75.0	17	24	AA099978	Insulin/insulin li
501	79.1	1111	17	Human laminin gamma 23	Human laminin gamma 23	474	75.0	17	24	AA099980	Insulin/insulin li
502	79.1	1111	17	Human laminin gamma 24	Human laminin gamma 24	475	75.0	17	24	AA099982	Insulin/insulin li
503	79.1	1131	24	Human laminin gamma 25	Human laminin gamma 25	476	75.0	17	24	AA099984	Insulin/insulin li
504	79.1	1131	24	Human laminin gamma 26	Human laminin gamma 26	477	75.0	17	24	AA099986	Insulin/insulin li
505	79.1	1132	22	Human laminin gamma 27	Human laminin gamma 27	478	75.0	17	24	AA099988	Insulin/insulin li
506	79.1	1155	22	Human laminin gamma 28	Human laminin gamma 28	479	75.0	17	24	AA099990	Insulin/insulin li
507	79.1	1172	21	Human laminin gamma 29	Human laminin gamma 29	480	75.0	17	24	AA099992	Insulin/insulin li
508	79.1	1172	21	Human laminin gamma 30	Human laminin gamma 30	481	75.0	17	24	AA099994	Insulin/insulin li
509	79.1	1193	17	Human laminin gamma 31	Human laminin gamma 31	482	75.0	17	24	AA099996	Insulin/insulin li
510	79.1	1193	17	Human laminin gamma 32	Human laminin gamma 32	483	75.0	17	24	AA099998	Insulin/insulin li
511	79.1	1193	17	Human laminin gamma 33	Human laminin gamma 33	484	75.0	17	24	AA099999	Insulin/insulin li
512	79.1	1193	17	Human laminin gamma 34	Human laminin gamma 34	485	75.0	17	24	AA099999	Insulin/insulin li
513	79.1	1193	17	Human laminin gamma 35	Human laminin gamma 35	486	75.0	17	24	AA099999	Insulin/insulin li
514	79.1	1247	22	Human laminin gamma 36	Human laminin gamma 36	487	75.0	17	24	AA099999	Insulin/insulin li
515	79.1	1382	20	Human laminin gamma 37	Human laminin gamma 37	488	75.0	17	24	AA099999	Insulin/insulin li
516	79.1	1382	20	Human laminin gamma 38	Human laminin gamma 38	489	75.0	17	24	AA099999	Insulin/insulin li
517	79.1	1487	21	Human laminin gamma 39	Human laminin gamma 39	490	75.0	17	24	AA099999	Insulin/insulin li
518	79.1	1487	21	Human laminin gamma 40	Human laminin gamma 40	491	75.0	17	24	AA099999	Insulin/insulin li
519	79.1	1511	22	Human laminin gamma 41	Human laminin gamma 41	492	75.0	17	24	AA099999	Insulin/insulin li
520	79.1	1511	22	Human laminin gamma 42	Human laminin gamma 42	493	75.0	17	24	AA099999	Insulin/insulin li
521	79.1	1511	22	Human laminin gamma 43	Human laminin gamma 43	494	75.0	17	24	AA099999	Insulin/insulin li
522	79.1	1511	22	Human laminin gamma 44	Human laminin gamma 44	495	75.0	17	24	AA099999	Insulin/insulin li
523	79.1	1511	22	Human laminin gamma 45	Human laminin gamma 45	496	75.0	17	24	AA099999	Insulin/insulin li
524	79.1	1511	22	Human laminin gamma 46	Human laminin gamma 46	497	75.0	17	24	AA099999	Insulin/insulin li
525	79.1	1511	22	Human laminin gamma 47	Human laminin gamma 47	498	75.0	17	24	AA099999	Insulin/insulin li
526	79.1	1511	22	Human laminin gamma 48	Human laminin gamma 48	499	75.0	17	24	AA099999	Insulin/insulin li
527	79.1	1511	22	Human laminin gamma 49	Human laminin gamma 49	500	75.0	17	24	AA099999	Insulin/insulin li
528	79.1	1511	22	Human laminin gamma 50	Human laminin gamma 50	501	75.0	17	24	AA099999	Insulin/insulin li
529	79.1	1511	22	Human laminin gamma 51	Human laminin gamma 51	502	75.0	17	24	AA099999	Insulin/insulin li
530	79.1	1511	22	Human laminin gamma 52	Human laminin gamma 52	503	75.0	17	24	AA099999	Insulin/insulin li
531	79.1	1511	22	Human laminin gamma 53	Human laminin gamma 53	504	75.0	17	24	AA099999	Insulin/insulin li
532	79.1	1511	22	Human laminin gamma 54	Human laminin gamma 54	505	75.0	17	24	AA099999	Insulin/insulin li
533	79.1	1511	22	Human laminin gamma 55	Human laminin gamma 55	506	75.0	17	24	AA099999	Insulin/insulin li
534	79.1	1511	22	Human laminin gamma 56	Human laminin gamma 56	507	75.0	17	24	AA099999	Insulin/insulin li
535	79.1	1511	22	Human laminin gamma 57	Human laminin gamma 57	508	75.0	17	24	AA099999	Insulin/insulin li
536	79.1	1511	22	Human laminin gamma 58	Human laminin gamma 58	509	75.0	17	24	AA099999	Insulin/insulin li
537	79.1	1511	22	Human laminin gamma 59	Human laminin gamma 59	510	75.0	17	24	AA099999	Insulin/insulin li
538	79.1	1511	22	Human laminin gamma 60	Human laminin gamma 60	511	75.0	17	24	AA099999	Insulin/insulin li
539	79.1	1511	22	Human laminin gamma 61	Human laminin gamma 61	512	75.0	17	24	AA099999	Insulin/insulin li
540	79.1	1511	22	Human laminin gamma 62	Human laminin gamma 62	513	75.0	17	24	AA099999	Insulin/insulin li
541	79.1	1511	22	Human laminin gamma 63	Human laminin gamma 63	514	75.0	17	24	AA099999	Insulin/insulin li
542	79.1	1511	22	Human laminin gamma 64	Human laminin gamma 64	515	75.0	17	24	AA099999	Insulin/insulin li
543	79.1	1511	22	Human laminin gamma 65	Human laminin gamma 65	516	75.0	17	24	AA099999	Insulin/insulin li
544	79.1	1511	22	Human laminin gamma 66	Human laminin gamma 66	517	75.0	17	24	AA099999	Insulin/insulin li
545	79.1	1511	22	Human laminin gamma 67	Human laminin gamma 67	518	75.0	17	24	AA099999	Insulin/insulin li
546	79.1	1511	22	Human laminin gamma 68	Human laminin gamma 68	519	75.0	17	24	AA099999	Insulin/insulin li
547	79.1	1511	22	Human laminin gamma 69	Human laminin gamma 69	520	75.0	17	24	AA099999	Insulin/insulin li
548	79.1	1511	22	Human laminin gamma 70	Human laminin gamma 70	521	75.0	17	24	AA099999	Insulin/insulin li

522	24	75.0	58	18	RAN28441	Staphylococcus ant	595	164	22	AAW12226	Human fibroblast
523	24	75.0	58	21	AAW57011	Arabidopsis thalia	596	165	21	AAW14387	Arabidopsis thalia
524	24	75.0	58	23	AAW06251	Human CRF protein	597	166	22	AAW14442	Human CRF protein
525	24	75.0	59	22	AAW08877	Human excretory re	598	167	22	AAW14442	Human excretory re
526	24	75.0	59	23	AAW13676	Human bladder anti	599	168	22	AAW13676	Human bladder anti
527	24	75.0	59	23	AAW13676	Human bladder anti	600	169	22	AAW13676	Human bladder anti
528	24	75.0	60	22	AAW06647	Human CRF protein	601	170	22	AAW06647	Human CRF protein
529	24	75.0	61	22	AAW15289	Human CRF protein	602	171	22	AAW15289	Human CRF protein
530	24	75.0	61	22	AAW15289	Human CRF protein	603	172	22	AAW15289	Human CRF protein
531	24	75.0	61	22	AAW15289	Human CRF protein	604	173	22	AAW15289	Human CRF protein
532	24	75.0	62	22	AAW09545	Human CRF protein	605	174	22	AAW09545	Human CRF protein
533	24	75.0	62	23	AAW38487	Staphylococcus epi	606	175	21	AAW15641	Human CRF protein
534	24	75.0	63	20	AAW36130	Human CRF protein	607	176	21	AAW36130	Human CRF protein
535	24	75.0	64	22	AAW09167	Propionibacterium	608	177	22	AAW09167	Propionibacterium
536	24	75.0	64	22	AAW09167	Propionibacterium	609	178	22	AAW09167	Propionibacterium
537	24	75.0	65	21	AAW12127	Arabidopsis thalia	610	179	22	AAW12127	Arabidopsis thalia
538	24	75.0	65	22	AAW12127	Arabidopsis thalia	611	180	22	AAW12127	Arabidopsis thalia
539	24	75.0	65	22	AAW09700	Human CRF protein	612	181	22	AAW09700	Human CRF protein
540	24	75.0	66	22	AAW17639	Human CRF protein	613	182	22	AAW17639	Human CRF protein
541	24	75.0	66	22	AAW17639	Human CRF protein	614	183	22	AAW17639	Human CRF protein
542	24	75.0	68	21	AAW13676	Human CRF protein	615	184	22	AAW13676	Human CRF protein
543	24	75.0	68	21	AAW13676	Human CRF protein	616	185	22	AAW13676	Human CRF protein
544	24	75.0	68	22	AAW08630	Human CRF protein	617	186	22	AAW08630	Human CRF protein
545	24	75.0	69	22	AAW15289	Human CRF protein	618	187	22	AAW15289	Human CRF protein
546	24	75.0	70	22	AAW06647	Human CRF protein	619	188	22	AAW06647	Human CRF protein
547	24	75.0	70	22	AAW06647	Human CRF protein	620	189	22	AAW06647	Human CRF protein
548	24	75.0	71	19	AAW39743	S. pneumoniae rep	621	190	22	AAW39743	S. pneumoniae rep
549	24	75.0	72	21	AAW15641	Arabidopsis thalia	622	191	22	AAW15641	Arabidopsis thalia
550	24	75.0	72	21	AAW15641	Arabidopsis thalia	623	192	22	AAW15641	Arabidopsis thalia
551	24	75.0	72	21	AAW15641	Arabidopsis thalia	624	193	22	AAW15641	Arabidopsis thalia
552	24	75.0	72	22	AAW08630	Human CRF protein	625	194	22	AAW08630	Human CRF protein
553	24	75.0	72	23	AAW09700	Human CRF protein	626	195	22	AAW09700	Human CRF protein
554	24	75.0	76	21	AAW15641	Arabidopsis thalia	627	196	22	AAW15641	Arabidopsis thalia
555	24	75.0	76	21	AAW15641	Arabidopsis thalia	628	197	22	AAW15641	Arabidopsis thalia
556	24	75.0	78	16	AAW17257	SSAL2 Synchro	629	198	22	AAW17257	SSAL2 Synchro
557	24	75.0	78	16	AAW17257	SSAL2 Synchro	630	199	22	AAW17257	SSAL2 Synchro
558	24	75.0	78	19	AAW50011	Human hyaluronan s	631	200	22	AAW50011	Human hyaluronan s
559	24	75.0	78	19	AAW50011	Human hyaluronan s	632	201	22	AAW50011	Human hyaluronan s
560	24	75.0	78	22	AAW05913	Human hyaluronan s	633	202	22	AAW05913	Human hyaluronan s
561	24	75.0	79	9	AAW04468	Human CRF protein	634	203	22	AAW04468	Human CRF protein
562	24	75.0	80	9	AAW04468	Human CRF protein	635	204	22	AAW04468	Human CRF protein
563	24	75.0	80	9	AAW04468	Human CRF protein	636	205	22	AAW04468	Human CRF protein
564	24	75.0	81	22	AAW13676	Human CRF protein	637	206	22	AAW13676	Human CRF protein
565	24	75.0	82	22	AAW06647	Human CRF protein	638	207	22	AAW06647	Human CRF protein
566	24	75.0	83	22	AAW13676	Human CRF protein	639	208	22	AAW13676	Human CRF protein
567	24	75.0	85	22	AAW06647	Human CRF protein	640	209	22	AAW06647	Human CRF protein
568	24	75.0	85	22	AAW06647	Human CRF protein	641	210	22	AAW06647	Human CRF protein
569	24	75.0	85	22	AAW06647	Human CRF protein	642	211	22	AAW06647	Human CRF protein
570	24	75.0	85	22	AAW06647	Human CRF protein	643	212	22	AAW06647	Human CRF protein
571	24	75.0	85	22	AAW06647	Human CRF protein	644	213	22	AAW06647	Human CRF protein
572	24	75.0	85	22	AAW06647	Human CRF protein	645	214	22	AAW06647	Human CRF protein
573	24	75.0	85	23	AAW17257	Human CRF protein	646	215	22	AAW17257	Human CRF protein
574	24	75.0	88	23	AAW06647	Human CRF protein	647	216	22	AAW06647	Human CRF protein
575	24	75.0	88	23	AAW06647	Human CRF protein	648	217	22	AAW06647	Human CRF protein
576	24	75.0	88	23	AAW06647	Human CRF protein	649	218	22	AAW06647	Human CRF protein
577	24	75.0	89	21	AAW13676	Human CRF protein	650	219	22	AAW13676	Human CRF protein
578	24	75.0	90	21	AAW13676	Human CRF protein	651	220	22	AAW13676	Human CRF protein
579	24	75.0	91	19	AAW13676	Human CRF protein	652	221	22	AAW13676	Human CRF protein
580	24	75.0	92	22	AAW06647	Human CRF protein	653	222	22	AAW06647	Human CRF protein
581	24	75.0	93	21	AAW06647	Human CRF protein	654	223	22	AAW06647	Human CRF protein
582	24	75.0	93	21	AAW06647	Human CRF protein	655	224	22	AAW06647	Human CRF protein
583	24	75.0	94	19	AAW13676	Human CRF protein	656	225	22	AAW13676	Human CRF protein
584	24	75.0	94	20	AAW13676	Human CRF protein	657	226	22	AAW13676	Human CRF protein
585	24	75.0	95	21	AAW13676	Human CRF protein	658	227	22	AAW13676	Human CRF protein
586	24	75.0	98	20	AAW13676	Human CRF protein	659	228	22	AAW13676	Human CRF protein
587	24	75.0	99	22	AAW06647	Human CRF protein	660	229	22	AAW06647	Human CRF protein
588	24	75.0	101	22	AAW06647	Human CRF protein	661	230	22	AAW06647	Human CRF protein
589	24	75.0	101	23	AAW06647	Human CRF protein	662	231	22	AAW06647	Human CRF protein
590	24	75.0	102	19	AAW06647	Human CRF protein	663	232	22	AAW06647	Human CRF protein
591	24	75.0	102	21	AAW13676	Human CRF protein	664	233	22	AAW13676	Human CRF protein
592	24	75.0	103	21	AAW13676	Human CRF protein	665	234	22	AAW13676	Human CRF protein
593	24	75.0	103	21	AAW13676	Human CRF protein	666	235	22	AAW13676	Human CRF protein
594	24	75.0	103	21	AAW13676	Human CRF protein	667	236	22	AAW13676	Human CRF protein

668	24	75.0	143	24	741	163	22	Arb93384	Nevel human diamo
669	24	76.0	143	24	742	163	22	Arb96122	Putative isoprop
670	24	76.0	143	24	743	164	21	AA325006	Arabidopsis thalia
671	24	76.0	143	24	744	164	21	AA347068	Arabidopsis thalia
672	24	76.0	143	24	745	164	22	AA356359	Putative isoprop
673	24	76.0	143	24	746	165	22	AA356359	Human EST encoded
674	24	76.0	143	24	747	167	21	AA347068	E. coli proliferat
675	24	76.0	143	24	748	167	21	AA347068	E. coli proliferat
676	24	76.0	143	24	749	167	21	AA347068	Human polypeptide
677	24	76.0	143	24	750	169	23	AA347068	Arabidopsis thalia
678	24	76.0	143	24	751	170	22	AA347068	Nevel human diamo
679	24	76.0	143	24	752	170	22	AA347068	Arabidopsis thalia
680	24	76.0	143	24	753	172	21	AA347068	Arabidopsis thalia
681	24	76.0	143	24	754	172	21	AA347068	Arabidopsis thalia
682	24	76.0	143	24	755	173	21	AA347068	Zea mays protein 1
683	24	76.0	143	24	756	173	21	AA347068	Arabidopsis thalia
684	24	76.0	143	24	757	173	22	AA347068	Nevel human diamo
685	24	76.0	143	24	758	173	22	AA347068	Nevel human diamo
686	24	76.0	143	24	759	173	22	AA347068	Nevel human diamo
687	24	76.0	143	24	760	173	22	AA347068	Human ovalin anti
688	24	76.0	143	24	761	173	22	AA347068	Arabidopsis thalia
689	24	76.0	143	24	762	173	22	AA347068	Arabidopsis thalia
690	24	76.0	143	24	763	173	22	AA347068	Arabidopsis thalia
691	24	76.0	143	24	764	173	22	AA347068	Arabidopsis thalia
692	24	76.0	143	24	765	173	22	AA347068	Arabidopsis thalia
693	24	76.0	143	24	766	173	22	AA347068	Arabidopsis thalia
694	24	76.0	143	24	767	173	22	AA347068	Arabidopsis thalia
695	24	76.0	143	24	768	173	22	AA347068	Arabidopsis thalia
696	24	76.0	143	24	769	173	22	AA347068	Arabidopsis thalia
697	24	76.0	143	24	770	173	22	AA347068	Arabidopsis thalia
698	24	76.0	143	24	771	173	22	AA347068	Arabidopsis thalia
699	24	76.0	143	24	772	173	22	AA347068	Arabidopsis thalia
700	24	76.0	143	24	773	173	22	AA347068	Arabidopsis thalia
701	24	76.0	143	24	774	173	22	AA347068	Arabidopsis thalia
702	24	76.0	143	24	775	173	22	AA347068	Arabidopsis thalia
703	24	76.0	143	24	776	173	22	AA347068	Arabidopsis thalia
704	24	76.0	143	24	777	173	22	AA347068	Arabidopsis thalia
705	24	76.0	143	24	778	173	22	AA347068	Arabidopsis thalia
706	24	76.0	143	24	779	173	22	AA347068	Arabidopsis thalia
707	24	76.0	143	24	780	173	22	AA347068	Arabidopsis thalia
708	24	76.0	143	24	781	173	22	AA347068	Arabidopsis thalia
709	24	76.0	143	24	782	173	22	AA347068	Arabidopsis thalia
710	24	76.0	143	24	783	173	22	AA347068	Arabidopsis thalia
711	24	76.0	143	24	784	173	22	AA347068	Arabidopsis thalia
712	24	76.0	143	24	785	173	22	AA347068	Arabidopsis thalia
713	24	76.0	143	24	786	173	22	AA347068	Arabidopsis thalia
714	24	76.0	143	24	787	173	22	AA347068	Arabidopsis thalia
715	24	76.0	143	24	788	173	22	AA347068	Arabidopsis thalia
716	24	76.0	143	24	789	173	22	AA347068	Arabidopsis thalia
717	24	76.0	143	24	790	173	22	AA347068	Arabidopsis thalia
718	24	76.0	143	24	791	173	22	AA347068	Arabidopsis thalia
719	24	76.0	143	24	792	173	22	AA347068	Arabidopsis thalia
720	24	76.0	143	24	793	173	22	AA347068	Arabidopsis thalia
721	24	76.0	143	24	794	173	22	AA347068	Arabidopsis thalia
722	24	76.0	143	24	795	173	22	AA347068	Arabidopsis thalia
723	24	76.0	143	24	796	173	22	AA347068	Arabidopsis thalia
724	24	76.0	143	24	797	173	22	AA347068	Arabidopsis thalia
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730	24	76.0	143	24	803	173	22	AA347068	Arabidopsis thalia
731	24	76.0	143	24	804	173	22	AA347068	Arabidopsis thalia
732	24	76.0	143	24	805	173	22	AA347068	Arabidopsis thalia
733	24	76.0	143	24	806	173	22	AA347068	Arabidopsis thalia
734	24	76.0	143	24	807	173	22	AA347068	Arabidopsis thalia
735	24	76.0	143	24	808	173	22	AA347068	Arabidopsis thalia
736	24	76.0	143	24	809	173	22	AA347068	Arabidopsis thalia
737	24	76.0	143	24	810	173	22	AA347068	Arabidopsis thalia
738	24	76.0	143	24	811	173	22	AA347068	Arabidopsis thalia
739	24	76.0	143	24	812	173	22	AA347068	Arabidopsis thalia
740	24	76.0	143	24	813	173	22	AA347068	Arabidopsis thalia

960 24 75.0 314 21 AAN90783
 961 24 75.0 314 22 AAN93465
 962 24 75.0 314 22 AAM93824
 963 24 75.0 315 22 AAB76736
 964 24 75.0 316 23 AAF60912
 965 24 75.0 316 23 AAF60913
 966 24 75.0 317 15 AAR54718
 967 24 75.0 317 21 AAG47542
 968 24 75.0 318 15 AAR47069
 969 24 75.0 319 15 AAG47071
 970 24 75.0 318 21 AAG50955
 971 24 75.0 318 23 AAB60860
 972 24 75.0 318 23 AAB60943
 973 24 75.0 319 21 AAN20487
 974 24 75.0 319 21 AAG47277
 975 24 75.0 319 21 AAY52255
 976 24 75.0 320 14 AAR43279
 977 24 75.0 320 18 AAM48217
 978 24 75.0 320 23 AAB60878
 979 24 75.0 320 23 ABB41459
 980 24 75.0 321 21 AAB29257
 981 24 75.0 321 21 AAB34747
 982 24 75.0 321 23 AAY52341
 983 24 75.0 321 23 ABB60699
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 991 24 75.0 324 12 AAB21247
 992 24 75.0 324 12 AAR13275
 993 24 75.0 324 13 AAF21833
 994 24 75.0 324 18 AAN31297
 995 24 75.0 324 18 AAN31407
 996 24 75.0 324 20 AAK77731
 997 24 75.0 324 20 AAN21493
 998 24 75.0 324 21 AAB60733
 999 24 75.0 324 23 ABB92876
 1000 24 75.0 325 21 AAG10313

ALIGNMENT

RESULT 1
 AAR91721
 ID AAR91721 standard; Protein; 5 AA.
 XX
 AC AAR91721;
 XX
 DE 17-NOV 1996 (first entry)
 DE
 DE NAP subsequence.
 DE
 XX AC-AAR91, Hs-AAR91, NaAR91, Aa-AAR91, Ad-AAR91, anti-coagulant,
 KW nematode-extracted anti-coagulant protein; serine protease;
 KW nematode; thrombosis; parasitic worm.
 XX
 OS Synthetic.
 XX
 XX W09612021-A2.
 PN
 XX 25-APR-1996.
 PD
 XX 17-OCT-1995; 9505-0514241.
 PF
 XX 05-JUN-1995; 9505-0486399.
 PR
 PR 14-OCT-1994; 9505-0326110.
 PR 05-JUN-1995; 9505-0463965.
 PR 05-JUN-1995; 9505-0465380.
 PR 05-JUN-1995; 9505-0486397.

XX
 PA (CORV-) CORVAS INT INC.
 XX
 FI Berquim PW, Ganssems YOLJ, Jaspers LS, Larochie YR;
 FI Lauwereys MJ, Messens JHJ, Mayle M, Staussens PPH;
 XX Vlasak GP;
 XX WFL, 1996, 222367/22.
 DE
 DE Proteins with anticoagulant activity: serine protease inhibitory
 activity - isolated from nematodes and useful to inhibit blood
 coagulation
 XX
 PS Claim 10; Page 144; 243pp; English.
 XX
 CC Proteins with anticoagulant activity: serine protease inhibitory
 activity, isolated from nematodes, are useful to inhibit blood
 coagulation. The proteins can be added to blood collection tubes
 defining the collection of mammalian plasma. They are also useful
 CC to prevent or inhibit thrombosis, and may be given alone or in
 CC combination with other therapeutic or in vivo diagnostic agents.
 CC The proteins can serve as immunogens to raise antibodies for use in
 CC the diagnosis and identification of NAP concn. levels in biological
 CC fluids, e.g. to detect mammalian infection with a parasitic worm.
 CC They can also be used as immunogens in prophylactic and therapeutic
 CC vaccines against parasitic worm infection. The proteins may
 CC double the clotting time of human plasma in thrombin time assays
 CC when present at 10-50 nMol, and double the clotting time of human
 CC plasma in activated partial thrombin time assays when present
 CC at 10-100 nMol.
 CC The anticoagulant proteins are pref. derived from
 CC Anelasma vancouver, A. cylindricum, A. duodenale, Necator
 CC americanus or Helicoverma polygyrus.
 CC The proteins pref. have 2 NAP domains and specifically inhibit
 CC the catalytic activity of the factor VIIa/TF complex in the
 CC presence of factor Xa or a catalytically inactive factor Xa derivative.
 CC do not specifically inhibit the activation of factor VIII in the
 CC absence of TF and do not specifically inhibit prothrombinase.
 CC Proteins derived in AAR91720 E91732 are preferred sub-sequences
 CC of a genetic NAP sequence.
 XX
 XX Sequence 5 AA:
 DE
 DE Query Match 93.8%; Score 40; Bk 17; Length 5;
 DE Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 DE Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GFYRN 7

Db 1 GFYRN 5

RESULT 2

AAV30440
 ID AAV30440 standard; Peptide; 5 AA.
 XX
 AC AAV30440;
 XX
 DE 15-NOV-1999 (first entry)
 DE
 DE Nematode extracted anticoagulant protein fragment.
 DE
 XX Nematode extracted anticoagulant protein; NAP, anti-coagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.
 XX
 OS Unidentified.
 XX
 XX US9505294-A.
 PN
 XX 21-SEP-1999.
 PD
 XX 19 APR-1996; 9605-0634641.
 PF
 XX

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PR 19-APR-1996; 960S-0634641.
PR 18-OCT-1994; 940S-0326110.
PR 05-JUN-1995; 950S-0461965.
PR 05-JUN-1995; 950S-0463880.
PR 05-JUN-1995; 950S-0486397.
PR 05-JUN-1995; 950S-0486399.
PR 17-OCT-1995; 950S-0513231.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Berquins PW, Ganssens PEH, Jespers LS, Laroché YR, Moyle M;
XX Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
XX Vlasuk GP;
XX
XX WPI: 1999-530669/45
XX
XX Screening an isolated protein for Nematode-extracted Anticoagulant
XX Protein domains
XX
XX Disclosure, Column 151; 197pp; English.
XX
XX The present sequence represents a nematode-extracted anticoagulant
XX protein (NAP) fragment. The protein has activity as an anticoagulant
XX and/or serine protease inhibitor. The protein contains at least one
XX NAP domain which has selective inhibitory activity for factor VIIa/TF.
XX The specification describes a method for screening an isolated protein
XX at least one domain for factor VIIa/TF selective inhibitory activity.
XX The method comprises determining the time to clotting effected by a
XX concentration of the isolated protein in an ex vivo prothrombin time
XX (PT) assay, and an ex vivo activated partial thromboplastin time (aPTT)
XX assay, calculating prolongation of clotting effected by the isolated
XX protein in each of the PT and aPTT assay, with respect to a baseline
XX clotting value for each assay, where prolongation of clotting is
XX calculated as fold elevation of clotting time relative to a baseline
XX clotting value, where a doubling of clotting time is deemed a two-fold
XX elevation, and calculating a PT to aPTT prolongation ratio, where a
XX ratio at least one is indicative of factor VIIa/TF inhibitory activity.
XX The method is useful for determining if a protein has factor VIIa/TF
XX inhibitory activity
XX
XX Sequence 5 AA:
XX
XX Query Match 93.8%; Score 30; DB 20; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 GYVRN 7
XX Db | | | | |
XX 1 GYVRN 5
XX
XX RESULT 3
XX AAB15325
XX ID AAB15325 standard; Peptide: 5 AA.
XX
XX AC AAB15325;
XX
XX DT 19-DEC-2000 (first entry)
XX
XX DE NAP domain fragment #2.
XX
XX KW Nematode-extracted anticoagulant protein. NAP domain; blood clotting;
XX canine hookworm; thrombosis; vaccine.
XX
XX OS Unidentified
XX
XX PN US6087487-A.
XX
XX PD 11-JUL-2000.
XX
XX PF 12-FEB-1999; 990S-0245451.
XX
XX PN 17-OCT-1995; 950S-0513231.
XX

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PR 17-APR-1997; 970S-0809455.
PR 19-OCT-1994; 940S-0326110.
PR 05-JUN-1995; 950S-0461965.
PR 05-JUN-1995; 950S-0463880.
PR 05-JUN-1995; 950S-0486397.
PR 05-JUN-1995; 950S-0486399.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Lauwereys MJ, Stanssens PEH, Jespers LS, Ganssens YGL, Moyle M;
XX Berquins PW, Messens JHL, Laroché YR, Vlasuk GP;
XX WPI: 2000-531359/48.
XX
XX X-ray crystallographic analysis of a protein having factor Xa inhibitory
XX activity for preventing and treating blood clotting disorders.
XX comprises nematode-extracted anticoagulant protein domains
XX
XX Claim 3; Column 285; 197pp; English.
XX
XX The present sequence is a fragment of the NAP domain (see AAB15347),
XX which is found in all nematode extracted anticoagulant proteins (NAPS).
XX Proteins of this kind have been shown to be effective at preventing
XX blood clotting without causing excessive bleeding. They can be used in
XX blood collection tubes to aid the isolation of plasma from the blood, to
XX prevent thrombosis which may be linked to the rupture of an
XX atherosclerotic plaque, acute myocardial infarction, angina,
XX thrombotic therapy, percutaneous transluminal coronary angioplasty,
XX disseminated intravascular coagulopathy, infection, cancer and septic
XX shock, and to produce antibodies. In the latter instance, the antibodies
XX can be raised in order to detect infection by nematodes (the coding
XX sequence can also be used for this) or as diagnostic tests. The proteins
XX can also be used as vaccines against nematode parasites.
XX
XX Sequence 5 AA:
XX
XX Query Match 92.8%; Score 20; DB 21; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 GYVRN 7
XX Db | | | | |
XX 1 GYVRN 5
XX
XX RESULT 4
XX AAR91740
XX ID AAR91740 standard; Protein: 7 AA.
XX
XX AC AAR91740.
XX
XX DT 17-NOV-1995 (first entry)
XX
XX DE NAP subsequence.
XX
XX KW A. AATF, Bp. AATF, Bp. AATF, A. AATF, A. AATF; anticoagulant;
XX nematode-extracted anticoagulant protein; serine protease;
XX thrombosis; parasitic worm.
XX
XX OS Synthetic.
XX
XX PF /Label - difference 1
XX /Label - Glu, Asp, OTHER
XX /Note: "at least one of residue 1 or residue 2
XX is Glu or Asp"
XX
XX PF /Label - difference 2
XX /Label - Glu, Asp, OTHER
XX /Note: "at least one of residue 1 or residue 2
XX is Glu or Asp"
XX
XX PN WC0612021-A2.
XX

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PD 25 APR 1996.
 XX
 PF 17-OCT-1995; 95WO-0513231.
 XX
 PR 05-JUN-1995; 95OS-0486399.
 PR 18-OCT-1994; 94OS-0326110.
 PR 05-JUN-1995; 95OS-0461965.
 PR 05-JUN-1995; 95OS-0455380.
 PR 05-JUN-1995; 95OS-0486397.
 XX
 XX (ORV-) CORVAS INT INC.
 PA Bertram PM, Ganssmans YGJ, Jaspers LS, Laroché YR;
 P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
 P1 Vlasuk GP;
 XX WPI: 1996-222997/22.
 DR
 XX Proteins with anticoagulant and/or serine protease inhibitory
 PT activity - isolated from nematodes and useful to inhibit blood
 PT coagulation
 XX
 PS Claim 26; Page 147; 243pp; English.
 XX
 CC Proteins with anticoagulant and/or serine protease inhibitory
 CC activity, isolated from nematodes, are useful to inhibit blood
 CC coagulation. The proteins can be added to blood collection tubes
 CC defining the collection of mammalian plasma. They are also useful
 CC to prevent or inhibit thrombosis, and may be given alone or in
 CC combination with other therapeutic or in vivo diagnostic agents.
 CC the proteins can serve as immunogens to raise antibodies for use in
 CC the diagnosis and identification of NAP concn. levels in biological
 CC fluids, e.g. to detect mammalian infection with a parasitic worm.
 CC They can also be used as immunogens in prophylactic and therapeutic
 CC vaccines against parasitic worm infection. The proteins may
 CC double the clotting time of human plasma in prothrombin time assays
 CC when present at 10-50 nMol, and double the clotting time of human
 CC plasma in activated partial thromboplastin time assays when present
 CC at 10-100 nMol
 CC The anticoagulant proteins are prot. derived from
 CC Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator
 CC americanus or Helicovermosiphid polygyrus.
 CC The proteins prot. have 2 NAP domains and specifically inhibit
 CC the catalytic activity of the factor VIIa/TF complex in the
 CC presence of factor Xa or a catalytically inactive factor Xa deriv.
 CC do not specifically inhibit the activation of factor VIIa in the
 CC absence of TF and do not specifically inhibit prothrombinase.
 CC Proteins given in AAF91729-E91732 are preferred subsequences
 CC of a genetic NAP sequence.

XX Sequence 7 AA:

Query Match 93.8%; Score 30; DB 17; Length 7;
 Best Local Similarity 100.0%; Prod. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFYRN 7
 DB 3 GFYRN 7

RESULT 5

AA140449
 ID AAY40449 standard; Peptide: 7 AA.

XX
 AC AAY40449;

XX
 DT 15-NOV 1999 (first entry)

DE Nematode extracted anticoagulant protein fragment.

XX Nematode extracted anticoagulant protein; NAP: anticoagulant;

KW serine protease inhibitor; NAP domain: factor VIIa/TF.

XX Unidentified.

OS US955294-A.

XX 21-SEP-1999.

PD 19-APR-1996; 96US-0644641.

XX 19 APR-1996; 96US-0644641.

PR 18-OCT-1994; 94OS-0326110.

PR 05-JUN-1995; 95OS-0461965.

PR 05-JUN-1995; 95OS-0455380.

PR 05-JUN-1995; 95OS-0486397.

PR 05-JUN-1995; 95OS-0486399.

PR 17-OCT-1995; 95WO-0513231.

XX (ORV-) CORVAS INT INC.

XX Bertram PM, Ganssmans YGJ, Jaspers LS, Laroché YR;

P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;

P1 Vlasuk GP;

XX WPI: 1999-539569/45.

DR Screening an isolated protein for Nematode extracted Anticoagulant

XX Protein domains

XX Disclosure: Volume 166; 167pp; English.

XX The present sequence represents a nematode extracted anticoagulant

CC protein (NAP) fragment. The protein has activity as an anticoagulant

CC and/or serine protease inhibitor. The protein contains at least one

CC NAP domain which has a factor VIIa/TF inhibitory activity. For factor VIIa/TF

CC The specification describes a method for screening an isolated protein

CC in at least one domain for factor VIIa/TF selective inhibitory activity.

CC The method comprises determining the time to clotting effected by a

CC concentration of the isolated protein, as *ex vivo* prothrombin time

CC (PT) assay and an *ex vivo* activated partial thromboplastin time (APTT)

CC assay; calculating prolongation of clotting effected by the isolated

CC protein in each of the PT and APTT assays, with respect to a baseline

CC clotting value for each assay, where prolongation of clotting is

CC calculated as fold elevation of clotting time relative to a baseline

CC clotting value, where a doubling of clotting time is deemed a two fold

CC elevation; and calculating a PT to APTT prolongation ratio, where a

CC ratio at least one is indicative of factor VIIa/TF inhibitory activity.

CC The method is useful for determining if a protein has factor VIIa/TF

CC inhibitory activity.

XX Sequence 7 AA:

Query Match 93.8%; Score 30; DB 20; Length 7;
 Best Local Similarity 100.0%; Prod. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 DB 3 GFYRN 7

RESULT 6

AA15334
 ID AAB15334 standard; Peptide: 7 AA.

XX
 AC AAB15334;

XX 19-DEC-2000 (first entry)

DE NAP domain fragment #11.

XX Nematode-extracted anticoagulant protein; NAP domain: blood clotting;

KW canine hookworm; thrombosis; vaccine.

OS Unidentified.

XX Key Location/Qualifiers

PH Misc-difference 1..2

FI /label= OTHER

FT /note= "one of these two residues must be either

FT Glu or Asp"

XX

XX

XX US6087487-A.

XX

XX 11-JUL-2000.

XX

XX 12-FEB-1999; 950S-0249451.

XX

XX 17-OCT-1995; 95WO-0513231.

XX

XX 17-APR-1997; 970S-0809455.

XX

XX 18-OCT-1994; 940S-026110.

XX

XX 05-JUN-1995; 950S-0461965.

XX

XX 05-JUN-1995; 950S-0465380.

XX

XX 05-JUN-1995; 950S-0486397.

XX

XX 05-JUN-1995; 950S-0486399.

XX

XX (CORV.) CORVAS INT INC.

XX

XX Lauwereys MJ, Stanssens PEH, Jaspers LS, Ganssema YCU, Moyle M.

XX Berquim PW, Messens JHL, Laboche YF, Vlaskuk GP;

XX WPI: 2000-531350/48

XX

XX New cDNA molecule encoding a protein having factor XI inhibitory

XX activity, for preventing and treating blood clotting disorders.

XX PT comprises nematode-extracted anticoagulant protein domains

XX

XX Claim 4: Column 286; 197pp; English.

XX

XX The present sequence is a fragment of the NAP domain (see AAB15347),

XX which is found in all nematode-extracted anticoagulant proteins (NAPs).

XX Proteins of this kind have been shown to be effective at preventing

XX blood clotting without causing excessive bleeding. They can be used in

XX blood collection tubes to aid the isolation of plasma from the blood, to

XX prevent thrombosis which may be linked to the rupture of an

XX atherosclerotic plaque, acute myocardial infarction, angina,

XX thrombolytic therapy, percutaneous transluminal coronary angioplasty,

XX disseminated intravascular coagulopathy, infection, cancer and septic

XX shock, and to produce antibodies. In the latter instance, the antibodies

XX can be raised in order to detect infection by nematodes (the coding

XX sequences can also be used for this) or as diagnostic tests. The proteins

XX can also be used as vaccines against nematode parasites.

XX

SQ Sequence 7 AA;

Query Match 93.8%; Score 30; PP 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 7; 80-06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

DB 3 GFYRN 7

RESULT 7

AAAY30420

LD AAY30420 standard; Protein: 78 AA.

XX

XX AAY30420;

XX

XX 15-NOV-1999 (first entry)

XX

XX Mature nematode extracted anticoagulant protein A-ANAP31.

XX

XX Nematode extracted anticoagulant protein, AANAP31; AANAP42; AANAP46;

XX serine protease inhibitor, NAP domain; Factor VIIa/TF.

XX

OS

OS Acyclostoma caninum.

XX

XX US5955294-A.

XX

XX 21-SEP-1999.

XX

XX 19-APR-1995; 960S-0634041

XX

XX 19-APR-1996; 960S-0634641.

XX

XX 18-OCT-1994; 940S-0426110.

XX

XX 05-JUN-1995; 950S-0461965.

XX

XX 05-JUN-1995; 950S-0465380.

XX

XX 05-JUN-1995; 950S-0486397.

XX

XX 05-JUN-1995; 950S-0486399.

XX

XX 17-OCT-1995; 95WO-0513231.

XX

XX (CORV.) CORVAS INT INC.

XX

XX Berquim PW, Ganssema YCU, Jaspers LS, Laboche YF,

XX Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;

XX Vlaskuk GP;

XX WPI: 1999-59556/45.

XX

XX Screening an isolated protein for Nematode extracted Anticoagulant

XX protein domains

XX

XX Disclosure: Columns 122-124; 197pp; English.

XX

XX The present sequence represents a nematode extracted anticoagulant

XX protein (NAP). The protein has activity as an anti-clotting and/or serine

XX protease inhibitor. The protein contains at least one NAP domain which

XX has selective inhibitory activity for factor VIIa/TF. The specification

XX describes a method for screening an isolated protein at least one domain

XX for factor VIIa/TF selective inhibitory activity. The method comprises

XX determining the time to clotting effected by a concentration of the

XX isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo

XX activated partial thromboplastin time (APTT) assay, calculating

XX a prolongation of clotting effected by the isolated protein in each of

XX the PT and APTT assay, with respect to a baseline clotting value for

XX each assay, where prolongation of clotting is calculated as fold

XX elevation of clotting time relative to a baseline clotting value, where

XX a doubling of clotting time is deemed a two fold elevation; and

XX calculating a PT to APTT prolongation ratio, where a ratio at least

XX one is indicative of factor VIIa/TF inhibitory activity. The method is

XX useful for determining if a protein has factor VIIa/TF inhibitory

XX activity.

XX

SQ Sequence 78 AA;

Query Match 93.8%; Score 30; PP 20; Length 78;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

DB 54 GFYRN 58

RESULT 8

AAB15305

LD AAB15305 standard; Protein: 78 AA.

XX

XX AAB15305;

XX

XX 19-DEC-2000 (first entry)

XX

XX A. caninum nematode-extracted anticoagulant protein A-ANAP31; A2.46.

XX

XX Nematode extracted anticoagulant protein, AcanAP31; AcanAP42; AcanAP46;

XX similar to factor blood clotting, the serine protease

XX Acyclostoma caninum.

XX

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XX  US6087487-A.
XX  11-JUL-2000.
XX  12-FEB-1999; 990S-0244451.
XX  17-OCT-1995; 95W0-0514241.
XX  17-APR-1997; 970S-0804455.
XX  18-OCT-1994; 940S-0326110.
XX  05-JUN-1995; 950S-0461965.
XX  05-JUN-1995; 950S-0465480.
XX  05-JUN-1995; 950S-0486497.
XX  05-JUN-1995; 950S-0486499.
XX  (CORV-) CORVAS INT INC.
XX  Lauwereys MJ, Staussens JHL, Laroché YP, Vlasuk GP;
XX  Borum PW, Messens JHL, Laroché YP, Vlasuk GP;
XX  WPI: 2000-541359/48.
XX  N-PSIB: AAY3378.
XX  New cDNA molecule encoding a protein having factor Xa inhibitory
XX  activity for preventing and treating blood clotting disorders.
XX  comprises nematode-extracted anticoagulant protein domains.
XX  Disclosure: Fig 16; 197pp; English.
XX  The present sequence comprises the Ancylostoma caninum
XX  nematode-extracted anticoagulant proteins AvenAP3, AvenAP4 and
XX  AvenAP4b. Proteins of this kind have been shown to be effective at
XX  preventing blood clotting without causing excessive bleeding. The
XX  proteins can be used in blood collection tubes to aid the isolation of
XX  plasma from the blood, to prevent thromboses which may be linked to the
XX  rupture of an atherosclerotic plaque, to prevent arterial infarction,
XX  angina, thrombolytic therapy, percutaneous transluminal coronary
XX  angioplasty, disseminated intravascular coagulopathy, infection, cancer
XX  and septic shock, and to produce antipeptides. In the latter instance, the
XX  antithrombotics can be raised in order to detect infection by nematodes (the
XX  coding sequence can also be used for this) or as diagnostic tests. The
XX  proteins can also be used as a vaccine against nematode parasites.
XX  Sequence 78 AA;
XX  Query Match 92.9%; Score 40; DB 21; Length 78;
XX  Best Local Similarity 100.0%; Pred. No. 44;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 3 GYRN 7
XX  DQ 54 GYRN 58
XX  RESULT 4
XX  AAY40499
XX  ID AAY40499 standard; Protein: 82 AA.
XX  AC AAY40499;
XX  DI 15-NOV-1999 (first entry)
XX  DE Nematode extracted anticoagulant protein AvenAP442.
XX  FW Nematode extracted anticoagulant protein AvenAP442;
XX  KW serine protease inhibitor; NAP domain; factor VIIa/TF.
XX  OS Ancylostoma ceylanicum.
XX  PN US5955294-A.
XX  PD 21-SEP-1999.
XX  PF 19-APR-1996; 960S-0644641.

XX  19-APR-1996; 960S-0644641.
XX  19-APR-1996; 960S-0644641.
XX  18-OCT-1994; 940S-0326110.
XX  05-JUN-1995; 950S-0461965.
XX  05-JUN-1995; 950S-0465480.
XX  05-JUN-1995; 950S-0486497.
XX  05-JUN-1995; 950S-0486499.
XX  17-OCT-1995; 95W0-0514241.
XX  (CORV-) CORVAS INT INC.
XX  Borum PW, Ganssens YJL, Jaspers JS, Laroché YP;
XX  Lauwereys MJ, Messens JHL, Moyle M, Staussens JHL;
XX  Vlasuk GP;
XX  WPI: 1999-539569/45.
XX  Screening an isolated protein for nematode extracted Anticoagulant
XX  Protein domains
XX  Disclosure: Column 111-112; 197pp; English.
XX  The present sequence represents a nematode extracted anticoagulant
XX  protein (NAP); the protein has activity as an anticoagulant and/or serine
XX  protease inhibitor. The protein contains at least one NAP domain which
XX  has selective inhibitory activity for factor VIIa/TF. The specification
XX  describes a method for screening an isolated protein at least one domain
XX  for factor VIIa/TF selective inhibitory activity. The method comprises:
XX  determining the time to clotting effected by a concentration of the
XX  isolated protein in an ex vivo prothrombin time (PT) assay; and
XX  activated partial thromboplastin time (APTT) assay; calculating
XX  prolongation of clotting effected by the isolated protein in each of
XX  the PT and APTT assay; with respect to a baseline clotting value for
XX  each assay, where prolongation of clotting is calculated as told
XX  clotting of clotting time relative to a baseline clotting value, where
XX  a doubling of clotting time is deemed a two-fold elevation; and
XX  calculating a PT to APTT prolongation ratio, where a ratio of at least
XX  one is indicative of factor VIIa/TF inhibitory activity. The method is
XX  useful for determining if a protein has factor VIIa/TF inhibitory
XX  activity.
XX  Sequence 82 AA;
XX  Query Match 93.8%; Score 40; DB 20; Length 82;
XX  Best Local Similarity 100.0%; Pred. No. 46;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 3 GYRN 7
XX  DQ 51 GYRN 55
XX  RESULT 10
XX  AAY30422
XX  ID AAY30422 standard; Protein: 82 AA.
XX  AC AAY30422;
XX  DI 15-NOV-1999 (first entry)
XX  DE Mature nematode extracted anticoagulant protein AvenAP442.
XX  FW Nematode extracted anticoagulant protein NAP; anticoagulant;
XX  KW serine protease inhibitor; NAP domain; factor VIIa/TF.
XX  OS Ancylostoma ceylanicum.
XX  PN US5955294-A.
XX  PD 21-SEP-1999.
XX  PF 19-APR-1996; 960S-0644641.

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XX 19-APR-1996; 9605-0634611.
XX 18-OCT-1994; 9405-0326110.
XX 05-JUN-1995; 9505-0461965.
XX 05-JUN-1995; 9505-0465380.
XX 05-JUN-1995; 9505-0486397.
XX 05-JUN-1995; 9505-0486399.
XX 17-OCT-1995; 9505-0513241.
XX (CORV-) CORVAS INT INC.
XX Berquim PW, Ganssens PH, Jespers LS, Ganssens YGL, Moyle M,
XX Lauwereys MJ, Messens JHL, Lafache YS, Vlaek GP;
XX Vlaek GP;
XX WPI: 1999-530560/45
XX Screening an isolated protein for Nematode-extracted Anticoagulant
XX Protein domains
XX Disclosure: Columns 135-136; 197pp; English.
XX
XX The present sequence represents a nematode extracted anticoagulant
XX protein (NAP). The protein has activity as an anticoagulant and/or serine
XX protease inhibitor. The protein contains at least one NAP domain which
XX has selective inhibitory activity for factor VIIa/TF. The specification
XX describes a method for screening an isolated protein at least one domain
XX for factor VIIa/TF selective inhibitory activity. The method comprises
XX determining the time to clotting effected by a concentration of the
XX isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX activated partial thromboplastin time (APTT) assay; calculating
XX prolongation of clotting effected by the isolated protein in each of
XX the PT and APTT assay, with respect to a baseline clotting value for
XX each assay, where prolongation of clotting is calculated as fold
XX elongation of clotting time relative to a baseline clotting value, where
XX a doubling of clotting time is deemed a two fold elevation; and
XX calculating a PT to APTT prolongation ratio, where a ratio at least
XX one is indicative of factor VIIa/TF inhibitory activity. The method is
XX useful for determining if a protein has factor VIIa/TF inhibitory
XX activity.
XX
XX Sequence 82 AA;
XX
XX Query Match 93.8%; Score 30; DB 20; Length 82;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 GFYRN 7
XX Db 51 GFYRN 55
XX
XX RESULT 11
XX AAB15293
XX ID AAB15293 standard; Protein: 82 AA
XX XX
XX AC AAB15293;
XX XX
XX DI 19-DEC-2000 (first entry)
XX XX
XX DE A. ceylanicum nematode-extracted anticoagulant protein AecNAP132 #1.
XX XX
XX FN US6087487-A.
XX XX
XX PD 11-JUL-2000.
XX XX
XX PF 12-FEB-1999; 9605-0249451.
XX XX

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PK 17-OCT-1995; 9505-0513241.
PK 17-APR-1997; 9705-0809455.
PK 18-OCT-1994; 9405-0326110.
PK 05-JUN-1995; 9505-0461965.
PK 05-JUN-1995; 9505-0465380.
PK 05-JUN-1995; 9505-0486397.
PK 05-JUN-1995; 9505-0486399.
XX (CORV-) CORVAS INT INC.
XX Lauwereys MJ, Stanssens PH, Jespers LS, Ganssens YGL, Moyle M,
XX Berquim PW, Messens JHL, Lafache YS, Vlaek GP;
XX WPI: 2000 531359/48.
XX
XX New DNA molecule encoding a protein having factor Xa inhibitory
XX activity for preventing and treating blood clotting disorders,
XX comprises nematode-extracted anticoagulant protein domains
XX
XX Disclosure: Fig 11; 197pp; English.
XX
XX The present sequence is the Ancylostoma ceylanicum nematode extracted
XX anticoagulant protein AecNAP132. Proteins of this kind have been shown to
XX be effective in preventing blood clotting without causing excessive
XX bleeding. The protein can be used in blood collection tubes to aid the
XX isolation of plasma from the blood, to prevent thrombosis which may be
XX linked to the capture of an atherosclerotic plaque, acute myocardial
XX infarction, angina, thrombolytic therapy, percutaneous transluminal
XX coronary angioplasty, disseminated intravascular coagulopathy, infection,
XX cancer and septic shock, and to produce antibodies. In the latter
XX instance, the antibodies can be raised in order to detect infection by
XX nematodes or as diagnostic tests. The protein can also be used as a
XX vaccine against nematode parasites.
XX
XX Sequence 82 AA;
XX
XX Query Match 93.8%; Score 30; DB 21; Length 82;
XX Best Local Similarity 100.0%; Pred. No. 46;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 GFYRN 7
XX Db 51 GFYRN 55
XX
XX RESULT 12
XX AAB15307
XX ID AAB15307 standard; Protein: 82 AA.
XX XX
XX AC AAB15307;
XX XX
XX DI 19-DEC-2000 (first entry)
XX XX
XX DE A. ceylanicum nematode-extracted anticoagulant protein AecNAP142 #2.
XX XX
XX FN US6087487-A.
XX XX
XX PD 11-JUL-2000.
XX XX
XX PF 12-FEB-1999; 9905-0249451.
XX XX
XX 17-OCT-1995; 9505-0513241.
XX 17-APR-1997; 9705-0809455.
XX 18-OCT-1994; 9405-0326110.
XX 05-JUN-1995; 9505-0461965.
XX 05-JUN-1995; 9505-0465380.
XX 05-JUN-1995; 9505-0486397.
XX 05-JUN-1995; 9505-0486399.

```

XX PA (CORV-) CORVAS INT INC.
 XX PT Lauwereys MJ, Stammsens PEB, Jaspers LS, Gansmans YGL, Moyle M;
 PT Berquin PW, Messens JHL, Labeche YG, Vlasuk GP;
 XX WP1: 2000-541459/48.
 XX PA New cDNA molecule encoding a protein having factor Xa inhibitory
 PT activity for preventing and treating blood clotting disorders,
 PT comprises nematode-extracted anticoagulant protein domains.
 XX PS Disclosure: Fig 16; 197pp; English.
 XX CC The present sequence is the Ancylostoma caninum nematode extracted
 CC anticoagulant protein AduNAP7d1. Proteins of this kind have been shown to
 CC be effective at preventing blood clotting without causing excessive
 CC bleeding. The protein can be used in blood collection tubes to aid the
 CC isolation of plasma from the blood, to prevent thrombosis which may be
 CC linked to the rupture of an atherosclerotic plaque, acute myocardial
 CC infarction, angina, thrombolytic therapy, percutaneous transluminal
 CC coronary angioplasty, disseminated intravascular coagulopathy, infection,
 CC cancer and septic shock, and to produce antibodies. In the latter
 CC instances, the antibodies can be raised in order to detect infection by
 CC nematodes or as diagnostic tests. The protein can also be used as a
 CC vaccine against nematode parasites.
 XX SQ Sequence 82 AA;
 Query Match 93.8%; Score 40; Db 21; Length 82;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 LB 51 GYRN 55
 RESULT 14
 AAY0425
 ID AAY0425 standard; Protein: R3 AA.
 XX AC AAY0425;
 XX 15-NOV-1999 (first entry)
 DT Mature nematode extracted anticoagulant protein AduNAP7d1.
 DE Nematode extracted anticoagulant protein, NAP, anticoagulant,
 KW serine protease inhibitor; NAP domain: factor VIIa/TF.
 XX OS Ancylostoma duodenale,
 XX US5955294 A.
 XX 21-SEP-1999.
 XX 19-APR-1996; 960S-0634641.
 XX 19-APR-1996; 960S-0634641.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465480.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 95WG-US14241.
 XX (CORV-) CORVAS INT INC.
 XX PT Berquin PW, Gansmans YGL, Jaspers LS, Labeche YG,
 PT Lauwereys MJ, Messens JHL, Moyle M, Stammsens PEB,
 PT Vlasuk GP;
 XX WP1: 2000-541459/48.

DR WP1: 1999-539569/45.
 XX Screening an isolated protein for Nematode extracted Anticoagulant
 PT Protein domains
 XX PS Disclosure: Columns 137-148; 197pp; English.
 XX CC The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein of at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an *ex vivo* prothrombin time (PT) assay and activating
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX SQ Sequence 83 AA;
 Query Match 93.8%; Score 40; 19-20; Length 83;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 LB 55 GYRN 59
 RESULT 14
 AAY0423
 ID AAY0423 standard; Protein: R4 AA.
 XX AC AAY0423;
 XX 15-NOV-1999 (first entry)
 DT Mature nematode extracted anticoagulant protein AduNAP45d1.
 DE Nematode extracted anticoagulant protein; NAP; anticoagulant;
 KW serine protease inhibitor; NAP domain: factor VIIa/TF.
 XX OS Ancylostoma caninum,
 XX US5955294 A.
 XX 21-SEP-1999.
 XX 19-APR-1996; 960S-0634641.
 XX 19-APR-1996; 960S-0634641.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465480.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 95WG-US14241.
 XX (CORV-) CORVAS INT INC.
 XX PT Berquin PW, Gansmans YGL, Jaspers LS, Labeche YG,
 PT Lauwereys MJ, Messens JHL, Moyle M, Stammsens PEB,
 PT Vlasuk GP;
 XX WP1: 1999-539569/45.

XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX
 PS Disclosure: Columns 135-136; 197pp; English.
 XX
 CC The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (aPTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and aPTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to aPTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 SQ Sequence 84 AA:
 Query Match 93.8%; Score 30; DP 20; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 Db 56 GYRN 60
 |||||
 RESULT 15
 ID AAY30424 standard; Protein; 84 AA.
 AC AAY30424;
 XX
 DT 15-NOV-1999 (first entry)
 DE Mature nematode extracted anticoagulant protein AcaNAP47d1.
 XX
 FW Nematode extracted anticoagulant protein. NAP, anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.
 XX
 OS Ancylostoma caninum.
 XX
 PN US5955294-A.
 XX
 PD 21-SEP-1999.
 XX
 PF 19-APR-1996; 960S-0634641.
 XX
 PR 19-APR-1996; 960S-0634641.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465380.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 95W0-US13231.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Berqum PW, Ganssems YGI, Jespers LS, Laroche YR;
 PI Lauwereys MJ, Meessens JHL, Moyle M, Staussens PEH;
 PI Vlasuk GP;
 XX
 DR WPI; 1999-549560/45.
 XX
 PT Screening an isolated protein for Nematode extracted Anticoagulant

PT Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX
 PS Disclosure: Columns 135-138; 197pp; English.
 XX
 CC The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (aPTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and aPTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to aPTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 SQ Sequence 84 AA:
 Query Match 93.8%; Score 30; DP 20; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 Db 56 GYRN 60
 |||||
 RESULT 16
 ID AAY30432 standard; Protein; 84 AA.
 AC AAY30432;
 XX
 DT 15-NOV-1999 (first entry)
 DE Mature nematode extracted anticoagulant protein AcaNAPe2.
 XX
 FW Nematode extracted anticoagulant protein. NAP, anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.
 XX
 OS Ancylostoma caninum.
 XX
 PN US5955294-A.
 XX
 PD 21-SEP-1999.
 XX
 PF 19-APR-1996; 960S-0634641.
 XX
 PR 19-APR-1996; 960S-0634641.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465380.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 95W0-US13231.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Berqum PW, Ganssems YGI, Jespers LS, Laroche YR;
 PI Lauwereys MJ, Meessens JHL, Moyle M, Staussens PEH;
 PI Vlasuk GP;
 XX
 DR WPI; 1999-549560/45.
 XX
 PT Screening an isolated protein for Nematode extracted Anticoagulant

PI Protein domains
 XX Discrepancy: Columns 142-144, 197pp; English.
 XX
 CC The present sequence represents a nematode extracted anticoagulant protein (RAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAB domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an *ex vivo* prothrombin time (PT) assay and an *ex vivo* activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.
 XX
 SQ Sequence 84 AA;
 Query Match 93.8%; Score 30; DB 20; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 II III
 Ib 55 GYRN 59
 RESULT 17
 AAR15417
 ID AAR15417 standard; Protein: 84 AA.
 AC AAR15417;
 XX
 XX 19 DEC-2000 (first entry)
 DT
 DE A. caninum nematode-extracted anticoagulant protein AcanAPE2(mature).
 XX
 XX Nematode-extracted anticoagulant protein: AcanAPE2; blood clotting;
 KW canine hookworm; thrombosis; vaccine.
 XX
 XX Ancylostoma caninum.
 OS
 XX D56047487-A
 PN
 XX 11-JUL-2000.
 XX
 XX 12-FEB-1999; 990S-0249451.
 PF
 PR 17-OCT-1995; 95W0-1S14241.
 PR 17-APR-1997; 970S-0809455.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465380.
 PR 05-JUN-1995; 950S-0486497.
 PR 05-JUN-1995; 950S-0486395.
 XX
 XX (CORV.) CORVAS INT INC.
 PA
 XX Lauwereys MJ, Staussens PER, Jespers LS, Gaussemans YGJ, Moyle M;
 P1 Borum PW, Messens JHL, Lapeere YK, Vlasak GP;
 XX WPL: 2000-531459/48
 XX N PSL0; AAR14475.
 XX
 XX New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders.

PI comprises nematode-extracted anticoagulant protein domains
 XX
 XX Example A: Fig 16; 197pp; English.
 XX
 CC The present sequence is the Ancylostoma caninum nematode-extracted anticoagulant protein AcanAPE2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an athero-sclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites.
 CC
 XX
 SQ Sequence 84 AA;
 Query Match 93.8%; Score 30; DB 21; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 II III
 Ib 55 GYRN 59
 RESULT 18
 AAM91998
 ID AAM91998 standard; Protein: 86 AA.
 XX
 XX AAM91998;
 XX
 XX 05-NOV-2001 (first entry)
 DT
 XX Human digestive system antigen SEQ ID NO: 1447.
 DE
 XX Human; digestive system antigen, gene therapy, cancer, appendicitis;
 KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
 XX digestive system disorder; Meckel's diverticulum.
 XX
 OS Homo sapiens.
 XX
 XX W0200155414-A2.
 PN
 XX 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001W-0501324.
 PF
 XX 31-JAN-2000; 2000US-0174065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0204467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215145.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220964.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225214.

RESULT 19

AA91701 ID AAY30421 standard: Protein: 89 AA.

XX AC AAY40421;
XX DT 15-NOV-1999 (first entry)
XX DE Mature nematode-extracted anticoagulant protein AcenAP4d1.
XX KW Nematode-extracted anticoagulant protein, NAP, anticoagulant,
KW serine protease inhibitor; NAP domain: factor VIIa/TF.
XX OS Ancylostoma ceylanicum.

XX PN US9595294 A.

XX PD 21-SEP-1999.

XX PF 19-APR-1996; 950S-06344641.

XX PR 19-APR-1996; 950S-06344641.

XX PR 18-OCT-1994; 940S-01261110.

XX PR 05-JUN-1995; 950S-0461965.

XX PR 05-JUN-1995; 950S-0465380.

XX PR 05-JUN-1995; 950S-0486397.

XX PR 05-JUN-1995; 950S-0486399.

XX PR 17-OCT-1995; 950S-0513231.

XX PA (CORV-) CORVAS INT INC.

XX PI Berquim PW, Gausemans YGJ, Jespers LS, Laroche YR,
PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH,
PI Vlasak GP;

XX WP1: 1999-539569/45.

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant
XX Protein domains

XX PS Disclosure: Columns 133-134; 197pp; English.

XX CC The present sequence represents a nematode-extracted anticoagulant
CC protein (NAP). The protein has activity as an anticoagulant and/or serine
CC protease inhibitor. The protein contains at least one NAP domain which
CC has selective inhibitory activity for factor VIIa/TF. The specification
CC describes a method for screening an isolated protein at least one domain
CC for factor VIIa/TF selective inhibitory activity. The method comprises
CC determining the time to clotting effected by a concentration of the
CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
CC activated partial thromboplastin time (APTT) assay; calculating
CC prolongation of clotting effected by the isolated protein in each of
CC the PT and APTT assay, with respect to a baseline clotting value for
CC each assay; where prolongation of clotting is calculated as fold
CC elevation of clotting time relative to a baseline clotting value, where
CC a doubling of clotting time is deemed a two-fold elevation; and
CC calculating a PT to APTT prolongation ratio, where a ratio at least
CC one is indicative of factor VIIa/TF inhibitory activity. The method is
CC useful for determining if a protein has factor VIIa/TF inhibitory
CC activity.

XX SQ Sequence 89 AA;

XX CC Query Match 93.8%; Score 30; DB 20; Length 89;

XX CC Best Local Similarity 100.0%; Prod. No. 50;

XX CC Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

07 4 GFEVN 7

10 61 GFEVN 65

RESULT 20

AA91701 ID AAR91701 standard: Protein: 91 AA.

XX AC AAR91701;

XX DT 17-NOV-1996 (first entry)

XX DE AcenAPe2.

XX KW AcenAP; HpcNAP; NamNAP; AcenAP; AcenAP; anticoagulant;
KW nematode-extracted anticoagulant protein; serine protease;
KW nematode; thrombosis; parasitic worm.
XX OS Ancylostoma caninum.

XX PN W09612021-A2.

XX PD 25-APR-1996.

XX PF 17-OCT-1995; 950S-0513231.

XX PR 05-JUN-1995; 950S-0486399.

XX PR 18-OCT-1994; 940S-01261110.

XX PR 05-JUN-1995; 950S-0461965.

XX PR 05-JUN-1995; 950S-0465380.

XX PR 05-JUN-1995; 950S-0486397.

XX PA (CORV-) CORVAS INT INC.

XX PI Berquim PW, Gausemans YGJ, Jespers LS, Laroche YR,
PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH,
PI Vlasak GP;

XX WP1: 1999-539569/45.

XX DR N-PSDB: AAT12947.

XX PT Proteins with anticoagulant and/or serine protease inhibitory
XX activity - isolated from nematodes and useful to inhibit blood
XX coagulation

XX PS Claim 89 - 96; Fig 9; 243pp; English.

XX CC Proteins with anticoagulant and/or serine protease inhibitory
CC activity, isolated from nematodes, are useful to inhibit blood
CC coagulation. The proteins can be added to blood collection tubes
CC defining the collection of mammalian plasma. They are also useful
CC to prevent or inhibit thrombosis, and may be given alone or in
CC combination with other therapeutic or in vivo diagnostic agents.
CC The proteins can serve as immunogens to raise antibodies for use in
CC the diagnosis and identification of NAP concn. levels in biological
CC fluids, e.g. to detect mammalian infection with a parasitic worm.
CC They can also be used as immunogens in prophylactic and therapeutic
CC vaccines against parasitic worm infection. The proteins may
CC double the clotting time of human plasma in prothrombin time assays
CC when present at 10-50 nMol, and double the clotting time of human
CC plasma in activated partial thrombin time assays when present
CC at 10-100 nMol.

XX CC The anticoagulant proteins are prot. derived from
XX Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator
XX americanus or Heligmosomoides polygyrus.

XX CC The proteins prot. have 2 NAP domains and specifically inhibit
XX the catalytic activity of the factor VIIa/TF complex in the
XX presence of factor Xa or a catalytically inactive factor Xa deriv.

XX CC do not specifically inhibit the activation of factor VIIIa in the
XX absence of TF and do not specifically inhibit prothrombinase.

XX SQ Sequence 91 AA;

XX CC Query Match 93.8%; Score 30; DB 17; Length 91;

XX CC Best Local Similarity 100.0%; Prod. No. 51;

XX CC Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
DB 62 GYRN 66

RESULT 21

AA30394
ID AAY30394 standard; Protein; 91 AA.

XX AC AAY30394;
XX DT 15-NOV-1999 (first entry)
XX DE Nematode extracted anticoagulant protein AcNAP2.

XX XX Nematode extracted anticoagulant protein AcNAP2.
XX FW Nematode extracted anticoagulant protein; MAP, anticoagulant;
XX KW serine protease inhibitor; NAP domain; factor VIIa/TF
XX XX
XX OS Ancylostoma caninum

XX PN US5955294-A.
XX XX 21-SEP-1999.
XX PF 19-APR-1996; 96US-0634641.

XX PR 19-APR-1996; 96US-0634641.
XX PR 18-OCT-1994; 94US-0326110.
XX PR 05-JUN-1995; 95US-0461965.
XX PR 05-JUN-1995; 95US-0465380.
XX PR 05-JUN-1995; 95US-0465380.
XX PR 05-JUN-1995; 95US-0465397.
XX PR 17-OCT-1995; 95WO-US13231.

XX PA (CORV-) CORVAS INT INC.

XX FI Belgium FW, Ganssens V&J, Jespers LS, Lathue Y&J
XX PI Lathue's MJ, Messens JHL, Moyle M, Stanssens PER,
XX PI Vlasuk GP;

XX DR WPI: 1996-529569/45
XX DR N-PSDB: AA299999

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant
XX PT Protein domains

XX PS Example 13; Fig 9; 197pp; English.

XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PT to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.

XX SQ Sequence 91 AA;

Query Match 91.8%; Score 30; DB 20; Length 91;
Best Local Similarity 100.0%; Prod No. 1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
DB 62 GYRN 66

RESULT 22

AA30454
ID AAY30454 standard; Protein; 91 AA.

XX AC AAY30454;
XX DT 15-NOV-1999 (first entry)
XX DE Nematode extracted anticoagulant protein AcNAP2.

XX XX Nematode extracted anticoagulant protein AcNAP2.
XX FW Nematode extracted anticoagulant protein; MAP, anticoagulant;
XX KW serine protease inhibitor; NAP domain; factor VIIa/TF.
XX XX
XX OS Ancylostoma caninum

XX PN US5955294-A.
XX XX 21-SEP-1999.
XX PF 19-APR-1996; 96US-0634641.

XX PR 19-APR-1996; 96US-0634641.
XX PR 18-OCT-1994; 94US-0326110.
XX PR 05-JUN-1995; 95US-0461965.
XX PR 05-JUN-1995; 95US-0465380.
XX PR 05-JUN-1995; 95US-0465397.
XX PR 17-OCT-1995; 95WO-US13231.

XX PA (CORV-) CORVAS INT INC.

XX FI Belgium FW, Ganssens V&J, Jespers LS, Lathue Y&J
XX PI Lathue's MJ, Messens JHL, Moyle M, Stanssens PER,
XX PI Vlasuk GP;

XX DR WPI: 1996-529569/45.

XX PT Screening an isolated protein for Nematode extracted Anticoagulant
XX PT Protein domains

XX PS Disclosure; Columns 175-176; 197pp; English.

XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PT to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.

XX SQ Sequence 91 AA;

Query Match 91.8%; Score 30; DB 20; Length 91;
Best Local Similarity 100.0%; Prod No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

Db 62 GYRN 66
|||||

RESULT 24

AA015346
ID AAB15346 standard; Protein: 91 AA.

XX AC AAB15346;

XX DT 19-DEC-2000 (first entry)

XX DE A. caninum nematode-extracted anticoagulant protein AcanAPc2.

XX KW Nematode-extracted anticoagulant protein: AcanAPc2; blood clotting
XX PW Cationic heparin; Thrombosis; parasitic worm.

XX OS Ancylostoma caninum.

XX PN US6087487-A.

XX PD 11 JUL-2000.

XX PF 12 FEB 1999; 950S-0249451.

XX PR 17 OCT 1995; 95WO-0814241.

XX PR 17 APR 1997; 97US-0809455.

XX PR 18 OCT 1994; 94US-0426110.

XX PR 05-JUN-1995; 95US-0461965.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 05-JUN-1995; 95US-0486397.

XX PR 05-JUN-1995; 95US-0486397.

XX PA (CORV-) CORVAS INT. INC.

XX PI Lauwereys MJ, Stanssens JGH, Jaspers LS, Gausemans YGJ, Moyle M;

XX PI Berdum PW, Messous JHL, Laroche YF, Vlasuk GP.

XX PR WP1: 2000-541459/48.

XX DR N PSD8; AA074474.

XX XX

XX PI New CLARA molecule encoding a protein having factor Xa inhibitory
XX PI activity for preventing and treating blood clotting disorders.
XX PI comprises nematode-extracted anticoagulant protein domains
XX PS Disclosure; Fig 11; 197pp; English.
XX CC The present sequence is the Ancylostoma caninum nematode-extracted
XX CC anticoagulant protein AcanAPc2. Proteins of this kind have been shown to
XX CC be effective at preventing blood clotting without causing excessive
XX CC bleeding. The protein can be used in blood collection tubes to aid the
XX CC isolation of plasma from the blood, to prevent thrombosis which may be
XX CC linked to the rupture of an atherosclerotic plaque, acute myocardial
XX CC infarction, angina, thrombolytic therapy, percutaneous transluminal
XX CC coronary angioplasty, disseminated intravascular coagulopathy, infection,
XX CC cancer and septic shock, and to produce antibodies. In the latter
XX CC instance, the antibodies can be raised in order to detect infection by
XX CC nematodes (the coding sequence can also be used for this) or as
XX CC diagnostic tests. The protein can also be used as a vaccine against
XX CC nematode parasites.

XX Sequence 91 AA;

Query Match

Best Local Similarity 92.8%; Score 40; DB 21; Length 91;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

Db 62 GYRN 66
|||||

RESULT 24

AA091709

ID AAR91709 standard; Protein: 97 AA.

XX AC AAR91709;

XX DT 17-NOV-1996 (first entry)

XX DE AcanAP31.

XX AC AcanAP; HpaNAP; NamNAP; AcanAP; AcanAP; anticoagulant;
XX KW nematode-extracted anticoagulant protein; serine protease;
XX KW nematode; thrombosis; parasitic worm.

XX OS Ancylostoma caninum.

XX PW W-9512021-A2.

XX PD 25-APR-1996.

XX PF 17-OCT-1995; 95WO-0814241.

XX PR 05-JUN-1995; 95US-0486397.

XX PR 18-OCT-1994; 94US-0426110.

XX PR 05-JUN-1995; 95US-0461965.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 05-JUN-1995; 95US-0486397.

XX PA (CORV-) CORVAS INT. INC.

XX PI Berdum PW, Gausemans YGJ, Jaspers LS, Laroche YF;

XX PI Lauwereys MJ, Messous JHL, Moyle M, Stanssens JGH;

XX PI Vlasuk GP;

XX PR WP1: 1996-222007/22.

XX DR N PSD8; AA112955.

XX PI Proteins with anticoagulant and/or serine protease inhibitory
XX PI activity - isolated from nematodes and useful to inhibit blood
XX PI coagulation

XX PS Claim 221; Fig 13D; 243pp; English.

XX CC Proteins with anticoagulant and/or serine protease inhibitory
XX CC activity, isolated from nematodes, are useful to inhibit blood
XX CC coagulation. The proteins can be added to blood collection tubes
XX CC defining the collection of mammalian plasma. They are also useful
XX CC to prevent or inhibit thrombosis, and may be given alone or in
XX CC combination with other therapeutic or in vivo diagnostic agents.
XX CC The proteins can serve as immunogens to raise antibodies for use in
XX CC the diagnosis and identification of NAP antigen. Levels in biological
XX CC fluids, e.g., to detect mammalian infection with a parasitic worm.
XX CC They can also be used as immunogens in prophylactic and therapeutic
XX CC vaccines against parasitic worm infection. The proteins may
XX CC double the clotting time of human plasma in prothrombin time assays
XX CC when present at 10-50 nMol, and double the clotting time of human
XX CC plasma in activated partial thromboplastin time assays when present
XX CC at 10-100 nMol.
XX CC The anticoagulant proteins are pref. derived from
XX CC Ancylostoma caninum, A. ceylanicum, A. de Bonte, Recator
XX CC Americanus or Helicoverma polydorus.
XX CC The proteins pref. have 2 NAP domains and specifically inhibit
XX CC the catalytic activity of the factor VIIa/TF complex in the
XX CC presence of factor Xa or a catalytically inactive factor Xa derivative.
XX CC do not specifically inhibit the activation of factor VIII in the
XX CC absence of TF and do not specifically inhibit prothrombinase.

XX Sequence 97 AA;

Query Match

Best Local Similarity 93.8%; Score 40; DB 17; Length 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 73 GFYEN 77

|||||

RESULT 25

AAV30407
ID AAV30407 standard; Protein; 97 AA.

XX AC AAV30407;

XX DT 15-NOV-1999 (first entry)

XX DE Nematode extracted anticoagulant protein AAVNAP1.
XX KW Nematode extracted anticoagulant protein; NAF, anticoagulant.
XX KW serine protease inhibitor; NAP domain; factor VIIa2/F.

OS Ancylostoma caninum.

XX FN US5955294-A.

XX PD 21-SEP-1999.

XX PF 16-APR-1996; 9608-0634641

XX PR 19-APR-1996; 9608-064641.

XX PR 18-OCT-1994; 9408-0326110.

XX PR 05-JUN-1995; 9508-0461565.

XX PR 05-JUN-1995; 9508-0465380.

XX PR 05-JUN-1995; 9508-0486397.

XX PR 05-JUN-1995; 9508-0486399.

XX PR 17-OCT-1995; 9508-0513231.

XX PA (CORV-) CORVAS INT INC.

XX PI Berquim PW, Gausemans YGI, Desroers LE, Laroche YR;

XX PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;

XX PI Vlasuk GP;

XX DR WPI: 1999-539569/45

XX DR N-PSDB; AA210455.

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant
XX PT Protein domains

XX PS Example 12, Fig 130; 197pp; English.

XX CC The present sequence represents a nematode-extracted anticoagulant
XX CC protein (NAF). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa. If the specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa2/F selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an assay with factor VIIa2/F, and an ex vivo
XX CC activated partial thromboplastin time (aPTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PI and aPTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PI to aPTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa2/F inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa2/F inhibitory
XX CC activity

XX SQ Sequence 97 AA;

Query Match 93.8%; Score 30; DB 20; length 97;
Best local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 9; Mismatches 0; Indels 3; Gaps 0.

QV 3 GFYEN 77

DB 73 GFYEN 77

|||||

RESULT 26

ABR14986
ID ABR14986 standard; Protein; 97 AA.

XX AC ABR14986;

XX DT 22-JAN-2002 (first entry)

XX DE Human nervous system related polypeptide SEQ ID NO 4643.
XX KW Human, neurologic, neurodegenerative, 57 status, demyelinated, zinc finger;
XX KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; zymogenic;
XX KW antiparkinsonian; antispasmodic; antitumor; antidiabetic; cancer;
XX KW antipneumatic; hepatotropic; neuroprotective; anti-inflammatory;
XX KW antiallergic; antidiabetic; antileukemic; antiparasitic; antitumor;
XX KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX FN W0200159063-A2.

XX PD 16-AUG-2001.

XX PF 17-JAN-2001; 2001W0-0801334.

XX PR 21-JAN-2000; 200008-0179065.

XX PR 04-FEB-2000; 200008-0180628.

XX PR 24-FEB-2000; 200008-0184664.

XX PR 02-MAR-2000; 200008-0186350.

XX PR 16-MAR-2000; 200008-0188874.

XX PR 17-MAR-2000; 200008-0190076.

XX PR 18-APR-2000; 200008-0198123.

XX PR 19-MAY-2000; 200008-0205515.

XX PR 07-JUN-2000; 200008-0209467.

XX PR 26-JUN-2000; 200008-0214986.

XX PR 30-JUN-2000; 200008-0215135.

XX PR 07-JUL-2000; 200008-0216647.

XX PR 07-JUL-2000; 200008-0216980.

XX PR 11-JUL-2000; 200008-0217487.

XX PR 13-JUL-2000; 200008-0217496.

XX PR 14-JUL-2000; 200008-0218290.

XX PR 26-JUL-2000; 200008-0220963.

XX PR 28-JUL-2000; 200008-0220964.

XX PR 14-AUG-2000; 200008-0221518.

XX PR 14-AUG-2000; 200008-0224519.

XX PR 14-AUG-2000; 200008-0224519.

XX PR 14-AUG-2000; 200008-0225214.

XX PR 14-AUG-2000; 200008-0225266.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX PR 14-AUG-2000; 200008-0225267.

XX Nematode extracted anticoagulant protein: NAP, anticoagulant;
 KW serine protease inhibitor; NAP domain, factor VIIa/TF.
 XX Ancylostoma duodenale.
 OS US5955294-A.
 PN 21-SEP-1999.
 XX 19-APR-1996; 96DS-0634541.
 XX 19-APR-1996; 96DS-0634541.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0461965.
 PR 05-JUN-1995; 95US-0463880.
 PR 05-JUN-1995; 95US-0486397.
 PR 05-JUN-1995; 95US-0486399.
 PR 17-OCT-1995; 95WO-0513231.
 XX (CORV-) CORVAS INT INC.
 XX Berquim PW, Gausemans YGJ, Jespers LS, Laroche YR;
 PI Lauwerrey MJ, Messens JHL, Moyle M, Stanssens PEH;
 PI Vlasuk GP;
 XX WPI: 1999-539569/45.
 DR Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX Disclosure: Column 111-112; 197pp; English.
 XX The present sequence represents a nematode-extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and a serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an assay platelet-rich plasma (PRP) assay and a factor
 CC activated partial thromboplastin time (APTT) assay, calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a twofold elevation, and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX Sequence 102 AA;
 SQ Query Match 93.8%; Score 30; DB 20; Length 102;
 Best local similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 Db 74 GYRN 78
 RESULT 28
 AAB15295
 ID AAB15295 standard; Protein: 102 AA.
 XX AAB15295.
 AC AAB15295.
 XX 19-DEC-2000 (first entry)
 DT 19-DEC-2000 (first entry)
 XX A. duodenale nematode-extracted anticoagulant protein: AduNAP7.
 DE Nematode extracted anticoagulant protein: AduNAP7.

KW Nematode extracted anticoagulant protein: AduNAP7. Blood clotting;
 KW serine protease inhibitor; NAP domain, factor VIIa/TF.
 XX Ancylostoma duodenale.
 OS US5955294-A.
 PN 21-SEP-1999.
 XX 19-APR-1996; 96DS-0634541.
 XX 19-APR-1996; 96DS-0634541.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0461965.
 PR 05-JUN-1995; 95US-0463880.
 PR 05-JUN-1995; 95US-0486397.
 PR 05-JUN-1995; 95US-0486399.
 PR 17-OCT-1995; 95WO-0513231.
 XX (CORV-) CORVAS INT INC.
 XX Berquim PW, Gausemans YGJ, Jespers LS, Laroche YR;
 PI Lauwerrey MJ, Messens JHL, Moyle M, Stanssens PEH;
 PI Vlasuk GP;
 XX WPI: 1999-539569/45.
 DR Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX Disclosure: Column 111-112; 197pp; English.
 XX The present sequence represents a nematode-extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and a serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an assay platelet-rich plasma (PRP) assay and a factor
 CC activated partial thromboplastin time (APTT) assay, calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a twofold elevation, and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX Sequence 102 AA;
 SQ Query Match 93.8%; Score 30; DB 20; Length 102;
 Best local similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 Db 74 GYRN 78
 RESULT 29
 AAY03098
 ID AAY03098 standard; Protein: 108 AA.
 XX AAY03098.
 AC AAY03098.
 XX 15-NOV-1999 (first entry)
 DT 15-NOV-1999 (first entry)
 XX Nematode extracted anticoagulant protein: AduNAP7.
 DE Nematode extracted anticoagulant protein: AduNAP7.

```

XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;
XX KW serine protease inhibitor; NAP domain; factor VIIa/TF.
XX CS Ancylostoma ceylanicum.
XX XX
XX PN US5955294-A.
XX PD 21-SEP-1999.
XX PF 19-APR-1996; 950S-0634641.
XX PR 19-APR-1996; 950S-0634641.
XX PR 18-OCT-1994; 940S-0326110.
XX PR 05-JUN-1995; 950S-0461965.
XX PR 05-JUN-1995; 950S-0465380.
XX PR 05-JUN-1995; 950S-0486397.
XX PR 17-OCT-1995; 950S-0486399.
XX PR 17-OCT-1995; 950S-0514241.
XX PA (CORV-) CORVAS INT INC.
XX PF Bertrum PW, Gansomans YGL, Jaspers LS, Laroché YR,
XX PF Lauwerijs MJ, Messens JHL, Moyle M, Stanssens PER,
XX PF Vlasak GP.
XX DR WPI: 1999-539569/45
XX XX
XX PS Screening an isolated protein for Nematode extracted Anticoagulant
XX PT Protein domains
XX XX
XX PS Disclosure; Column 109-110; 197pp; English.
XX XX
XX CC The present sequence represents a nematode-extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay.
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two fold elevation; and
XX CC calculating a PI to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.
XX XX
XX SQ Sequence 108 AA;
XX XX
XX Query Match 93.8%; Score 40; DB 20; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 61;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX XX
XX QY 3 GPNR 7
XX DB 80 GPNR 84
XX XX
XX RESULT 40
XX ID AAB15292
XX XX AAB15292 standard; protein; 108 AA.
XX AC AAB15292;
XX XX
XX DT 19-JUL-2000 (first entry)
XX XX
XX DE A. ceylanicum nematode extracted anticoagulant protein AncyNAP4.
XX XX

```

```

KW KW Nematode extracted anticoagulant protein; AncyNAP4; blood clotting;
KW vulture hawkmoth; thrombosis; vaccine.
XX XX
XX CS Ancylostoma ceylanicum.
XX XX
XX PF Key Location/Qualifiers
XX PF Peptide 1-19 "signal peptide"
XX PF Protein 20-108
XX PF /note "mature AncyNAP4"
XX XX
XX PN US6087487-A.
XX PD 11-JUL-2000.
XX PF 12 FEB 1999; 940S-0249451.
XX PR 17-OCT-1995; 950S-0514241.
XX PR 17-APR-1997; 970S-0809455.
XX PR 18-OCT-1994; 940S-0426110.
XX PR 05-JUN-1995; 950S-0461965.
XX PR 05-JUN-1995; 950S-0465380.
XX PR 05-JUN-1995; 950S-0486397.
XX PR 05-JUN-1995; 950S-0486399.
XX XX
XX PA (CORV-) CORVAS INT INC.
XX XX
XX PF Lauwerijs MJ, Stanssens PER, Jaspers LS, Gansomans YGL, Moyle M,
XX PF Bertrum PW, Messens JHL, Laroché YR, Vlasak GP.
XX DR WPI: 2000-531359/48.
XX DR N-PSDB: AAA73364.
XX XX
XX PT New cDNA molecule encoding a protein having factor Xa inhibitory
XX PT activity for preventing and treating blood clotting disorders,
XX PT comprises nematode-extracted anticoagulant protein domains.
XX PS Disclosure; Column 101-102; 197pp; English.
XX XX
XX CC The present sequence is the Ancylostoma ceylanicum nematode extracted
XX CC anticoagulant protein AncyNAP4. Proteins of this kind have been shown to
XX CC protect the plasma from the blood to prevent thrombosis which may be
XX CC isolated of plasma from the blood to prevent thrombosis which may be
XX CC linked to the rupture of an atherosclerotic plaque, acute myocardial
XX CC infarction, angina, thrombolytic therapy, percutaneous transluminal
XX CC coronary angioplasty, disseminated intravascular coagulation, infection,
XX CC cancer and septic shock, and to produce antibodies. In the latter
XX CC instance, the antibodies can be raised in order to detect infection by
XX CC nematodes (the coding sequence can also be used for this) or as
XX CC diagnostic tests. The protein can also be used as a vaccine against
XX CC nematode parasites.
XX XX
XX SQ Sequence 108 AA;
XX XX
XX Query Match 93.8%; Score 40; DB 21; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 61;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX XX
XX QY 3 GPNR 7
XX DB 80 GPNR 84
XX XX
XX RESULT 41
XX ID AAY70530
XX XX AAY70530 standard; peptide; 124 AA.
XX AC AAY70530;
XX XX
XX DT 04-JUL-2000 (first entry)
XX XX
XX DE Maize plastid targeting transit peptide (b).

```

XX Maize; plastid targeting sequence, transit peptide.
KW Plastid ribosomal protein C19; subcellular localisation.
XX Zea mays.
XX FvY Location/Qualifiers
FT Misc-difference 4
FT /label= Unknown
FT /note= "Encoded by CNG"
FT Misc-difference 51
FT /label= Unknown
FT /note= "Encoded by AAR"
FT Misc-difference 55
FT /label= Unknown
FT /note= "Encoded by CNG"
FT Misc-difference 109
FT /label= Unknown
FT /note= "Encoded by GAR"
FT Misc-difference 122
FT /label= Unknown
FT /note= "Encoded by TP"
XX W0200012732-A2.
FN 09-MAR-2000.
PD 25-AUG-1999; 95W0-US18455
XX 28-AUG-1998; 98US-0069225
XX (PION-) PIONEER HI-BRED INT INC.
XX Benson RJ;
XX WPT: 2000-256647/22
XX N-PSDB: AA251833.
XX New oranelle targeting ornelic acid and amino acid sequences are
XX useful in genetic engineering for modulating the subcellular
XX localization of heterologous proteins in plants
XX Claim 16; Page 44; 50pp; English.
XX The present sequence is a maize transit peptide which has homology to
XX the plastid ribosomal protein C19
XX this sequence can be used in genetic engineering for modulating
XX the subcellular localisation of heterologous proteins in plants. In
XX particular, the transit peptide finds use in the localisation of
XX proteins to plastids and compartments thereof.
SQ Sequence 124 AA;
Query Match 93.9%; Score 30; DE 21; Length 124;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 3 GFYRN 7
|||||
Db 76 GFYRN 80
RESULT 32
ABR03987
ID ABR03987 standard; Protein: 138 AA.
XX ABR03987;
XX
XX 08-JAN-2002 (first entry)
XX Human musculoskeletal system related polypeptide SEQ ID NO 1934.
XX
XX Cytostatin, immunosuppressive, non-lytic, non-antibiotic, antitumor.
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW adrenergic; androgenic; antitubercular; antitumoral; antiparasitic;
KW cardiotonic; chemotherapeutic; cytotoxic; immunosuppressive; antiparasitic;
KW neurological disorder; infection; human; secreted protein;
KW musculoskeletal system.
XX
XX Bone patients.
XX W020015367-A1.
XX 02-AUG-2001.
XX 17 JAN 2001. 2001W0-US01338.
XX 31-JAN-2000; 2000US-0179065.
XX 04 FEB 2000; 2000US-0186428.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16 MAR 2000; 2000US-0186874.
XX 17-MAR-2000; 2000US-0190076.
XX 19 APR 2000; 2000US-0198124.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28 JUN 2000; 2000US-0214886.
XX 30 JUN 2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216447.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26 JUL 2000; 2000US-0220963.
XX 24-JUL-2000; 2000US-0220964.
XX 14 AUG 2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14 AUG 2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225366.
XX 14-AUG-2000; 2000US-0225367.
XX 14-AUG-2000; 2000US-0225368.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 19 AUG 2000; 2000US-0226379.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226688.
XX 22 AUG 2000; 2000US-0227182.
XX 23 AUG 2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01 SEP 2000; 2000US-0229387.
XX 01 SEP 2000; 2000US-0229444.
XX 01-SEP-2000; 2000US-0229444.
XX 01-SEP-2000; 2000US-0229445.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230438.
XX 06-SEP-2000; 2000US-0230439.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08 SEP 2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14 SEP 2000; 2000US-0232398.
XX 14 SEP 2000; 2000US-0232399.
XX 14 SEP 2000; 2000US-0232400.
XX 14 SEP 2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0232403.
XX 14 SEP 2000; 2000US-0233064.
XX 14 SEP 2000; 2000US-0233064.

PR 05-JUN-1995; 96US-0461965.
 PR 05-JUN-1995; 96US-0465380.
 PR 05-JUN-1995; 96US-0486397.
 PR 05-JUN-1995; 96US-0486399.
 PR 17-OCT-1995; 96WO-US13231.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Berquim PW, Ganssema's YGL, Jespers LS, Laroche YR;
 PI Lauwerijs MJ, Messens JHL, Meyle M, Staessens PPH;
 PI Vlasuk GP;
 XX
 XX WPI: 1999-539569/45.
 XX
 XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PI Protein domains
 XX
 XX Disclosure: Fig 20: 197pp; English.
 XX
 XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 XX Sequence 161 AA:
 SQ
 Query Match 93.9%; Score 30; DP 20; Length 161.
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 Db 55 GYRN 59
 IIIII
 RESULT 34
 AAY30436
 ID AAY30436 standard; Protein: 162 AA.
 XX
 XX AAY30436;
 AC
 XX
 XX 15-NOV-1999 (first entry)
 DI
 XX
 XX Mature nematode extracted anticoagulant protein AcanAP45.
 DE
 XX Nematode extracted anticoagulant protein, NAP, anticoagulant,
 KW serine protease inhibitor; NAP domain; Factor VIIa/TF.
 KW
 XX Ancylostoma caninum.
 OS
 XX US5955294-A.
 PN
 XX 21-SEP-1999.
 PD
 XX
 XX 19-APR-1996; 96US-0634641.
 XX
 XX 19-APR-1996; 96US-0634641.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0461965.
 PR

PR 05-JUN-1995; 96US-0465380.
 PR 05-JUN-1995; 96US-0486397.
 PR 05-JUN-1995; 96US-0486399.
 PR 17-OCT-1995; 96WO-US13231.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Berquim PW, Ganssema's YGL, Jespers LS, Laroche YR;
 PI Lauwerijs MJ, Messens JHL, Meyle M, Staessens PPH;
 PI Vlasuk GP;
 XX
 XX WPI: 1999-539569/45.
 XX
 XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PI Protein domains
 XX
 XX Disclosure: Fig 18: 197pp; English.
 XX
 XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 XX Sequence 162 AA:
 SQ
 Query Match 93.8%; Score 40; DP 20; Length 162;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 Db 56 GYRN 60
 IIIII
 RESULT 35
 AAY30437
 ID AAY30437 standard; Protein: 162 AA.
 XX
 XX AAY30437;
 AC
 XX
 XX 15-NOV-1999 (first entry)
 DI
 XX
 XX Mature nematode extracted anticoagulant protein AcanAP47.
 DE
 XX Nematode extracted anticoagulant protein, NAP, anticoagulant,
 KW serine protease inhibitor; NAP domain; Factor VIIa/TF.
 KW
 XX Ancylostoma caninum.
 OS
 XX US5955294-A.
 PN
 XX 21-SEP-1999.
 PD
 XX
 XX 19-APR-1996; 96US-0634641.
 XX
 XX 19-APR-1996; 96US-0634641.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0461965.
 PR 05-JUN-1995; 95US-0465380.
 PR

PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 DR 17-OCT-1995; 950S-0813241.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Bertram PW, Ganssmans YSL, Jaspers LS, Laroché YF,
 PI Lauwereys MJ, Messens JHL, Moyle M, Stanstons PEH;
 PI Vlausk GP;
 XX
 DR WP1: 1999-531556/45.
 XX
 PI Screening an isolated protein for nematode extracted anticoagulant
 PI protein domains
 XX
 PS Disclosure: Fig 19; 197pp; English.
 XX
 CC The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or setting
 CC protease inhibitor, the protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and in ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 SQ Sequence 162 AA;

Query Match 93.8%; Score 30; BB 20; Length 162;
 Best Local Similarity 100.0%; Prod. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 DB 56 GFYRN 60
 |||||

RESULT 46
 AAB15321
 ID AAB15321 standard; Protein: 162 AA.
 XX
 AC AAB15321;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE A. caninum nematode-extracted anticoagulant protein AcanAP45.
 XX
 KW Nematode-extracted anticoagulant protein AcanAP45; blood clotting;
 KW canine hookworm; thrombosis; varicose
 XX
 OS Anacyclostoma caninum.
 XX
 PN US6087487-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 12-FEB-1999; 950S-0249451.
 XX
 PR 17-OCT-1995; 950S-0813241.
 PR 17-APR-1997; 950S-0809455.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465380.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 XX
 PA (CORV-) CORVAS INT INC.

PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Lauwereys MJ, Stanstons PEH, Jaspers LS, Ganssmans YSL, Moyle M,
 PI Bertram PW, Messens JHL, Laroché YF, Vlausk GP;
 XX
 DR WP1: 2000-531556/48.
 DR N-P5D8; AAA7380.
 XX
 PI New cDNA molecule encoding a protein having factor Xa inhibitory
 PI activity for preventing and treating blood clotting disorders,
 PI comprises nematode-extracted anticoagulant protein domains
 XX
 PS Disclosure: Fig 18; 197pp; English.

XX The present sequence is the Anacyclostoma caninum nematode extracted
 XX anticoagulant protein AcanAP45. Portions of this kind have been shown to
 XX be effective at preventing blood clotting without causing excessive
 XX blood loss. The protein can be used in blood substitution to all the
 XX isolation of plasma from the blood, to prevent thrombosis which may be
 XX linked to the therapy of an atherosclerotic plaque, acute myocardial
 XX infarction, anginal, thrombotic therapy, percutaneous transluminal
 XX coronary angioplasty, disseminated intravascular coagulopathy, infection,
 XX cancer and septic shock, and to produce antibodies. In the latter
 XX instance, the antibodies can be raised in order to detect infection by
 XX nematodes (the coding sequence can also be used for this) or as
 XX diagnostic tests. The protein can also be used as a vaccine against
 XX nematode parasites.
 XX
 SQ Sequence 162 AA;

Query Match 93.8%; Score 30; BB 21; Length 162;
 Best Local Similarity 100.0%; Prod. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 DB 56 GFYRN 60
 |||||

RESULT 47
 AAB15322
 ID AAB15322 standard; Protein: 162 AA.
 XX
 AC AAB15322;
 XX
 DT 19-DEC-2000 (first entry)
 XX
 DE A. caninum nematode-extracted anticoagulant protein AcanAP47.
 XX
 KW Nematode-extracted anticoagulant protein AcanAP47; blood clotting;
 KW canine hookworm; thrombosis; varicose.
 XX
 OS Anacyclostoma caninum.
 XX
 PN US6087487-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 12-FEB-1999; 950S-0249451.
 XX
 PR 17-OCT-1995; 950S-0813241.
 PR 17-APR-1997; 950S-0809455.
 PR 18-OCT-1994; 940S-0326110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465380.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 XX
 PA (CORV-) CORVAS INT INC.

Lauwereys MJ, Strausens PEH, Jaspers LS, Canssemaus YGJ, Moyle M;
 Bexum PW, Messens JHL, Laroche YE, Vlieghe GF.
 WPI: 2000-531359/48.
 N-PSDB: AAA7381.
 New cDNA molecule encoding a protein having factor Xa inhibitory
 activity for preventing and treating blood clotting disorders.
 comprises nematode-extracted anticoagulant protein domains -
 XX
 XX
 Disclosure, Fig 19, 197pp, English.
 The present sequence is the *Ancylostoma caninum* nematode-extracted
 anticoagulant protein AcanAP47. Proteins of this kind have been shown to
 be effective at preventing blood clotting without causing excessive
 bleeding. The protein can be used in blood collection tubes to aid the
 isolation of plasma from the blood, to prevent thrombosis which may be
 linked to the rupture of an atherosclerotic plaque, acute myocardial
 infarction, angina, thrombolytic therapy, intracerebral haematomas,
 coronary angioplasty, disseminated intravascular coagulopathy, infective,
 cancer and septic shock, and to produce antibodies. In the latter
 instance, the antibodies can be raised in order to detect infection by
 nematodes (the coding sequence can also be used for this) or as
 diagnostic tests. The protein can also be used as a vaccine against
 nematode parasites.
 CC
 CC
 Sequence 162 AA;
 SO

PR 05-JUN-1995; 95US-0486397.

XX (CORV-) CORVAS INT INC.

XX Berquim PW, Gansseman YGJ, Jespers LS, Laroché YP;

PI Lauwereys MJ, Messens JH, Moyle M, Stanssens PEH;

PI Vlasak GP;

XX WPI: 1996 222907/22.

DR N-PSDB: AAT12957.

XX Proteins with anticoagulant and/or serine protease inhibitory activity isolated from nematodes and useful to inhibit blood coagulation

ES Claim 221; Fig 13F; 243pp; English.

XX Proteins with anticoagulant and/or serine protease inhibitory activity, isolated from nematodes, are useful to inhibit blood coagulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis, and may be given alone or in combination with other therapeutic or *in vivo* diagnostic agents. CC The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP concn. levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm. CC They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may CC double the clotting time of human plasma in prothrombin time assays CC when present at 10-50 nmol, and double the clotting time of human CC plasma in activated partial thrombin time assays when present CC at 10-100 nmol

CC The anticoagulant proteins are pref. derived from: CC Ancylostoma caninum, A. ceylanicum, A. dendanale, Necator CC americanus or Heligmosomoides polygyrus.

CC The proteins pref. have 2 NAP domains and specifically inhibit CC the catalytic activity of the factor VIIa/TF complex in the CC presence of factor Xa or a catalytically inactive factor Xa deriv. CC do not specifically inhibit the activation of factor VIIa in the CC absence of TF and do not specifically inhibit prothrombinase.

XX Sequence 181 AA:

Query Match 93.8%; Score 30; DB 17; Length 181.

Best Local Similarity 100.0%; Pred. No. 10-22.

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

IIIII

Db 75 GFYRN 79

RESULT 42

AAR91712

Id AAR91712 standard; Protein: 181 AA.

XX AAR91712:

XX AAR91712:

DT 17-NOV-1996 (first entry)

XX AcanAP47.

XX AcanAP47.

XX AcanAP: IpoNAP, NamNAP, AcanNAP, AcanNAP; anticoagulant; CC nematode-extracted anticoagulant protein; serine protease; CC nematode; thrombosis; parasitic worm.

XX Ancylostoma caninum.

OS Ancylostoma caninum.

XX W09612021-A2.

XX W09612021-A2.

XX 25-APR-1996.

XX 17-OCT-1995; 95WO-US13231.

PN 17-OCT-1995; 95WO-US13231.

XX 05-JUN-1995; 95US-0486399.

PR 18-OCT-1994; 94US-0326110.

PR 05-JUN-1995; 95US-0461965.

PR 05-JUN-1995; 95US-0465380.

PR 05-JUN-1995; 95US-0486397.

XX (CORV-) CORVAS INT INC.

XX Berquim PW, Gansseman YGJ, Jespers LS, Laroché YP;

PI Lauwereys MJ, Messens JH, Moyle M, Stanssens PEH;

PI Vlasak GP;

XX WPI: 1996 222907/22.

DR N-PSDB: AAT12958.

XX Proteins with anticoagulant and/or serine protease inhibitory activity isolated from nematodes and useful to inhibit blood coagulation

ES Claim 221; Fig 13G; 244pp; English.

XX Proteins with anticoagulant and/or serine protease inhibitory activity, isolated from nematodes, are useful to inhibit blood coagulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis, and may be given alone or in combination with other therapeutic or *in vivo* diagnostic agents. CC The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP concn. levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm. CC They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may CC double the clotting time of human plasma in prothrombin time assays CC when present at 10-50 nmol, and double the clotting time of human CC plasma in activated partial thrombin time assays when present CC at 10-100 nmol. CC The anticoagulant proteins are pref. derived from: CC Ancylostoma caninum, A. ceylanicum, A. dendanale, Necator CC americanus or Heligmosomoides polygyrus. CC The proteins pref. have 2 NAP domains and specifically inhibit CC the catalytic activity of the factor VIIa/TF complex in the CC presence of factor Xa or a catalytically inactive factor Xa deriv. CC do not specifically inhibit the activation of factor VIIa in the CC absence of TF and do not specifically inhibit prothrombinase.

XX Sequence 181 AA:

Query Match 93.8%; Score 30; DB 17; Length 181;

Best Local Similarity 100.0%; Pred. No. 10-22;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

IIIII

Db 75 GFYRN 79

RESULT 43

AAV30409

Id AAV30409 standard; Protein: 181 AA.

XX AAV30409:

XX AAV30409:

DT 15-NOV-1999 (first entry)

XX AcanAP47.

XX AcanAP47.

XX AcanAP: IpoNAP, NamNAP, AcanNAP, AcanNAP; anticoagulant; CC nematode-extracted anticoagulant protein; serine protease; CC nematode; thrombosis; parasitic worm.

XX Ancylostoma caninum.

OS Ancylostoma caninum.

XX W09555294-A.

PN W09555294-A.

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XX PD 21-SEP-1999.
XX PF 19-APR-1996; 960S-0634641.
XX PR 19-APR-1996; 960S 0634641.
XX PR 18-OCT-1994; 940S-0326110.
XX PR 05-JUN-1995; 950S-0461965.
XX PR 05-JUN-1995; 950S-0465480.
XX PR 05-JUN-1995; 950S-0486397.
XX PR 05-JUN-1995; 950S-0486399.
XX PR 17-OCT-1995; 950S-0513241.
XX PA (CORV.) CORVAS INT. INC.
XX XX
XX PI Berquim PW, Ganssemaers YGL, Jaspers LS, Laroche YR;
XX PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PH;
XX PI Vlasuk GP;
XX DR WPI; 1999-539569/45.
XX DR N-PSDB; AAZ10457.
XX XX
XX PI Screening an isolated protein for Hematode extracted Anticoagulant
XX PI Protein domains
XX PS Example 12: Fig 13F; 157pp; English.
XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PI to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.
XX SQ Sequence 181 AA;
Query Match 93.8% Score 20; E0.20; Length 181;
Best Local Similarity 100.0%; Pred. No. 10402;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 GFEVN 7
DB 75 GFEVN 79
IIII
RESULT 44
AAY0410
ID AAY0410 standard; Protein; 181 AA.
XX AC AAY0410;
XX XX
XX DI 15-NOV-1999 (first entry)
XX XX
XX DE Nematode extracted anticoagulant protein AcanAP45.
XX XX
XX KW Nematode extracted anticoagulant protein AcanAP45.
XX XX
XX KW Serine protease inhibitor NAP domain; Factor VIIa/TF.
XX XX
XX OS Ancylostoma caninum.
XX XX
XX PN US9505294 A.

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XX PD 21-SEP-1999.
XX PF 19-APR-1996; 960S-0634641.
XX PR 19-APR-1996; 960S-0634641.
XX PR 18-OCT-1994; 940S-0326110.
XX PR 05-JUN-1995; 950S-0461965.
XX PR 05-JUN-1995; 950S-0465480.
XX PR 05-JUN-1995; 950S-0486397.
XX PR 05-JUN-1995; 950S-0486399.
XX PR 17-OCT-1995; 950S-0513241.
XX PA (CORV.) CORVAS INT. INC.
XX XX
XX PI Berquim PW, Ganssemaers YGL, Jaspers LS, Laroche YR;
XX PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PH;
XX PI Vlasuk GP;
XX DR WPI; 1999-539569/45.
XX DR N-PSDB; AAZ10458.
XX XX
XX PI Screening an isolated protein for Hematode extracted Anticoagulant
XX PI Protein domains
XX PS Example 12: Fig 13G; 197pp; English.
XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PI to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.
XX SQ Sequence 181 AA;
Query Match 93.8% Score 20; E0.20; Length 181;
Best Local Similarity 100.0%; Pred. No. 10402;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 GFEVN 7
DB 75 GFEVN 79
IIII
RESULT 45
ABH69726
ID ABH69726 standard; Protein; 184 AA.
XX AC ABH69726;
XX XX
XX DI 26-MAR-2002 (first entry)
XX XX
XX DE Drosophila melanogaster polypeptide SEQ ID No 45670.
XX XX
XX KW Drosophila developmental blood; cell signalling; insecticide;
XX XX
XX KW pharmaceutical.
XX XX
XX OS Drosophila melanogaster.
XX XX
XX PN W0200171042-A2.

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XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-050231.
XX
XX 23-MAR-2000; 2000US 15167P.
XX
XX 11-JUL-2000; 2000HS-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDH; ARL13829.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX PS Disclosure; SEQ ID NO 35970; 21pp - Sequence Listing; English.
XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ARL16176-ARL30511), expressed DNA
XX sequences (ABR01840-ABR16175) and the encoded proteins
XX (ABR7737-ABR72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences.
XX
XX SO Sequence 184 AA;
XX
XX Query Match 93.9%; Score 30; DB 22; Length 184;
XX Best local Similarity 100.0%; Pred. No. 1c+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 GFYRN 7
XX
XX Db 31 GFYRN 35
XX
XX Search completed: April 30, 2003, 14:34:08
XX Job time : 61.4545 secs

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GeoCore version 5.1.4_p5_4579
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OM protein - protein search, using sw model

Run on: April 30, 2003, 13:31:03; Search time 19.4545 Seconds
(without alignments)
36.466 Million cell updates/sec

Title: US-09-498-556C-79
Perfect score: 32
Sequence: 1 XXCFYRN 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

searched: 29,024 sets, 96124422 residues
Total number of hits satisfying the 500 kDa constraint: 28,997

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000

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Database :      PIR_73:★
1: pir1:
2: pir2:
3: pir3:
4: pir4:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		IP	Description
		Match	Length		
1	30	93.8	77	2	unknown protein
2	30	93.8	134	2	hypothetical protein
3	30	93.8	172	2	conserved hypothetical
4	30	93.8	175	2	hypothetical protein
5	29	93.8	175	2	hypothetical protein
6	30	93.8	223	2	adenosine triphosphatase III
7	30	93.8	226	2	probable endonuclease
8	30	93.8	227	2	hypothetical protein
9	30	93.8	361	2	hypothetical protein
10	30	93.8	362	2	phosphoserine aminotransferase
11	30	93.8	408	2	hypothetical protein
12	30	93.8	435	2	hypothetical protein
13	30	93.8	465	2	probable myosin
14	30	93.8	481	2	hypothetical protein
15	30	93.8	533	1	monophenol monooxygenase
16	30	93.8	747	2	hypothetical protein
17	30	93.8	824	2	hypothetical protein
18	30	93.8	900	2	hypothetical protein
19	30	93.8	940	2	hypothetical protein
20	30	93.8	1012	2	hypothetical protein
21	30	93.8	1564	2	probable transport
22	27	94.4	35	2	hypothetical protein
23	27	84.4	60	1	ribosomal protein
24	27	84.4	199	2	hypothetical protein
25	27	84.4	201	2	hypothetical protein
26	27	84.4	234	2	hypothetical protein
27	27	81.4	258	2	hypothetical protein
28	27	84.4	275	2	conserved hypothetical
29	27	84.4	279	2	hypothetical protein

103	24	81.2	10.4	2	A1673	H ₂ O ₂ exchanging A	176	25	78.1	229	2	A54274	sulfur, regulated
104	26	81.2	10.4	2	JN9094	H ₂ O ₂ exchanging A	177	25	78.1	342	2	B8976	hypothetical prote
105	26	81.2	10.4	2	A32992	H ₂ O ₂ exchanging A	178	25	78.1	345	2	C87228	hypothetical prote
106	26	81.2	10.4	2	S2406	H ₂ O ₂ exchanging A	179	25	78.1	348	2	C71174	hypothetical prote
107	26	81.2	10.4	2	F15621	hypothetical prote	180	25	78.1	352	2	C80924	bradykinin (B) rece
108	26	81.2	10.4	2	A56236	probable RNA helic	181	25	78.1	355	2	C81195	probably oxidoredu
109	26	81.2	10.4	2	A56158	eye developmental fr	182	25	78.1	356	2	T39408	hypothetical prote
110	26	78.1	7.0	2	B70790	hypothetical prote	183	25	78.1	357	2	S54603	hypothetical 39.8K
111	25	78.1	7.1	2	I51744	MHC class II alpha	184	25	78.1	357	2	G91295	hypothetical prote
112	25	78.1	7.1	2	I51750	MHC class II alpha	185	25	78.1	357	2	B86137	hypothetical prote
113	25	78.1	7.2	2	AH3473	lactoylglycathione	186	25	78.1	363	2	B81445	hypothetical prote
114	25	78.1	7.9	2	S51755	fibulin-10 - mouse	187	25	78.1	370	2	H74423	cytochrome-independent
115	26	78.1	9.0	2	S12849	maturation (pIva2)	188	25	78.1	381	2	AD1113	hypothetical prote
116	25	78.1	9.1	2	S72755	B1456_22_163 prote	189	25	78.1	381	2	AH1474	hypothetical prote
117	25	78.1	9.6	2	A25374	phospholipase	190	25	78.1	385	2	T23375	alk. MV2.3.3.3. open
118	25	78.1	10.0	2	B78202	ribosomal protein	191	25	78.1	397	1	K1B870	phosphorylase, kind
119	25	78.1	10.0	2	T23389	hypothetical prote	192	25	78.1	396	1	G71261	probable phenolase
120	25	78.1	12.3	2	E98040	conserved hypotet	193	25	78.1	398	2	C76680	hypothetical prote
121	26	78.1	12.4	2	A23279	hypothetical prote	194	25	78.1	400	2	T46383	hypothetical prote
122	25	78.1	12.7	2	T27227	hypothetical prote	195	25	78.1	401	2	T46661	probable RNA polym
123	25	78.1	13.8	2	P95060	acetyltransferase	196	25	78.1	405	2	T45117	probable secreted
124	25	78.1	13.9	2	E97901	conserved hypotet	197	25	78.1	409	2	T45118	probable secreted
125	25	78.1	14.3	2	C82467	conserved hypotet	198	25	78.1	414	1	HTK8AC	at red yin A (B) C
126	25	78.1	14.5	2	H85529	acetyltransferase	199	25	78.1	414	2	S41838	at red yin B (B) C
127	25	78.1	14.5	2	C64233	conserved hypotet	200	25	78.1	414	2	S41839	3-deoxy-D-ribose
128	25	78.1	16.4	2	C85238	peptidylprolyl iso	201	25	78.1	425	2	C39467	3-deoxy-D-ribose
129	25	78.1	16.4	2	C95702	peptidylprolyl iso	202	25	78.1	425	2	C39467	3-deoxy-D-ribose
130	25	78.1	16.4	2	P95552	peptidylprolyl ci	203	25	78.1	425	2	B86039	hypothetical prote
131	25	78.1	16.4	2	A96566	peptidylprolyl ci	204	25	78.1	427	2	B81978	probable glutamate
132	25	78.1	16.5	2	B86491	conserved hypotet	205	25	78.1	427	2	A91034	thiolamide 1, somal
133	25	78.1	16.8	2	H83643	peptide deform	206	25	78.1	427	2	A14341	phosphoribosylamin
134	25	78.1	16.9	2	S64047	peptidylprolyl iso	207	25	78.1	445	2	AH1598	hypothetical prote
135	25	78.1	19.0	1	C8587A	peptidylprolyl iso	208	25	78.1	445	2	AH1649	weakly methyltrans
136	25	78.1	19.0	1	C8587A	peptidylprolyl iso	209	25	78.1	452	2	T29116	hypothetical prote
137	25	78.1	19.6	2	C66001	peptidylprolyl iso	210	25	78.1	470	2	B64839	hypothetical prote
138	25	78.1	19.6	2	C66001	peptidylprolyl iso	211	25	78.1	477	2	C64833	4-phosphoribosyl a
139	25	78.1	19.6	2	C66001	peptidylprolyl iso	212	25	78.1	477	2	JL1880	4-phosphoribosyl a
140	25	78.1	20.0	1	H70409	conserved hypotet	213	25	78.1	491	1	TH2A2	alpha 2-antitrypsin
141	25	78.1	20.0	1	S15111	hemorrhagic factor	214	25	78.1	494	2	F84199	probable carboxydr
142	25	78.1	20.9	2	P83034	conserved hypotet	215	25	78.1	503	2	J35321	cytochrome P450 mo
143	25	78.1	20.9	2	P84482	hypothetical prote	216	25	78.1	505	2	E55246	4-alpha-albumin
144	25	78.1	21.0	2	A91438	hypothetical prote	217	25	78.1	505	2	B98111	4-alpha-albumin
145	25	78.1	21.4	2	B66630	acyl carrier prote	218	25	78.1	506	2	C39926	hypothetical prote
146	25	78.1	21.5	2	P84819	transcription regu	219	25	78.1	510	2	S64116	4-aminobutyrate tr
147	25	78.1	22.7	2	H65014	conserved hypotet	220	25	78.1	515	2	C84492	hypothetical prote
148	25	78.1	23.7	2	T12908	hypothetical prote	221	25	78.1	522	2	A45103	transmembrane glye
149	25	78.1	24.7	2	A97898	conserved hypotet	222	25	78.1	524	2	P96784	hypothetical prote
150	25	78.1	24.6	2	I51741	MHC class II alpha	223	25	78.1	526	2	T08541	hypothetical prote
151	25	78.1	24.9	2	A89967	serine proteinase	224	25	78.1	527	2	C95760	hypothetical prote
152	25	78.1	24.9	2	B89666	serine proteinase	225	25	78.1	527	2	H90858	hypothetical prote
153	25	78.1	24.4	2	A75118	phosphotransfer re	226	25	78.1	534	2	T19414	hypothetical prote
154	25	78.1	24.5	2	C72578	probable flagellin	227	25	78.1	538	2	H90329	p49.25 protein
155	25	78.1	24.5	2	C95798	hypothetical prote	228	25	78.1	540	2	T49874	hypothetical prote
156	25	78.1	24.5	2	C95667	hypothetical prote	229	25	78.1	547	2	A53833	glucan 1,4-alpha m
157	25	78.1	24.5	2	C95667	hypothetical prote	230	25	78.1	551	2	S05667	glucan 1,4-alpha m
158	25	78.1	24.6	2	C72352	probable endonuc	231	25	78.1	552	2	I54388	127R 1 human
159	25	78.1	24.7	2	A90273	probable AraC fami	232	25	78.1	553	2	C64149	adipocyte amino ac
160	25	78.1	24.8	2	P71936	probable transcrip	233	25	78.1	565	2	C70674	probable 2,3 dihyd
161	25	78.1	24.9	2	E64647	response regulator	234	25	78.1	573	2	T19523	azurin regulated pr
162	25	78.1	24.9	2	T19310	hypothetical prote	235	25	78.1	575	2	T19523	azurin regulated pr
163	25	78.1	24.9	2	P51717	caliculin protein	236	25	78.1	576	2	A81902	azurin-regulated pr
164	25	78.1	24.9	2	A54717	palmitoyl-protein	237	25	78.1	577	1	SYB001	arabinose TRNA lig
165	25	78.1	24.9	2	I58997	palmitoyl-protein	238	25	78.1	577	2	B99952	arabinose TRNA synt
166	25	78.1	24.9	2	T30061	hypothetical prote	239	25	78.1	577	2	P85900	arabinose TRNA synt
167	25	78.1	24.9	2	F64916	hypothetical prote	240	25	78.1	577	2	A12743	arabinose TRNA lig
168	25	78.1	24.9	2	E90917	hypothetical prote	241	25	78.1	591	2	B54665	metH, 2 precursor
169	25	78.1	24.9	2	C85766	hypothetical prote	242	25	78.1	585	2	B84941	Apo transporter (A
170	25	78.1	24.9	2	A20693	probable export	243	25	78.1	587	2	T48582	azurin regulated pr
171	25	78.1	24.9	2	T12729	structural protein	244	25	78.1	589	2	B66349	phosphotransfer, m
172	25	78.1	24.9	2	E90292	conserved hypotet	245	25	78.1	589	2	A22932	GRIFF family prote
173	25	78.1	24.9	2	T14451	hypothetical prote	246	25	78.1	594	2	T48583	azurin regulated pr
174	25	78.1	24.9	2	P97971	phosphoribosylamin	247	25	78.1	598	2	T48583	acid shock protein
175	25	78.1	24.9	2	B94660	probable peroxidase	248	25	78.1	599	2	C39712	heat shock protein

249	25	79.1	606	2	A51665	nitric oxide synthase
250	25	79.1	608	2	E90374	hypothetical protein
251	25	78.1	616	2	E84424	probable auxin transporter
252	25	78.1	625	2	G73429	oligonucleotide ABC transporter
253	25	79.1	621	2	G64874	probable membrane protein
254	25	78.1	633	2	G72284	oligonucleotide ABC transporter
255	25	79.1	638	2	G75739	hypothetical protein
256	25	79.1	645	2	G71261	probable membrane protein
257	25	78.1	670	2	E36790	hypothetical protein
258	25	78.1	679	2	E64192	DNA ligase (NAD ⁺)
259	25	78.1	682	2	G73612	hypothetical protein
260	25	78.1	686	2	A19047	amylase A (pH 5.2)
261	25	79.1	692	2	G70932	probable nucleic acid binding protein
262	25	79.1	710	2	G64979	hypothetical protein
263	25	78.1	733	2	G64058	outer membrane protein
264	25	78.1	725	2	A51149	outer membrane protein
265	25	79.1	729	2	G70539	hypothetical protein
266	25	78.1	735	2	A00711	probable membrane protein
267	25	78.1	736	2	H71006	ribosomal protein
268	25	78.1	737	2	G45040	hypothetical protein
269	25	78.1	737	2	A71094	ATP-dependent helix
270	25	78.1	802	2	A71094	outer membrane hem
271	25	78.1	803	2	A02088	hypothetical protein
272	25	78.1	905	2	E07094	membrane atrophy
273	25	78.1	917	2	E85649	probable transposase
274	25	78.1	960	2	G70623	probable sensor protein
275	25	78.1	973	2	T05199	glutathione S-transferase
276	25	78.1	982	2	G70789	aminopeptidase
277	25	78.1	984	2	T22677	hypothetical protein
278	25	78.1	984	2	E75189	conserved hypothetical protein
279	25	78.1	905	2	G73510	hypothetical protein
280	25	78.1	920	2	T12052	aminopeptidase
281	25	78.1	937	2	G70561	CS2 pilin synthase
282	25	78.1	955	2	A06990	alpha-amylase (EC 3.2.1.1)
283	25	78.1	962	2	A06990	membrane atrophy
284	25	78.1	965	2	A32852	membrane atrophy
285	25	78.1	967	2	A32852	membrane atrophy
286	25	78.1	995	2	V01390	carboxypeptidase
287	25	78.1	991	2	G71808	type I restriction enzyme
288	25	78.1	1000	2	G71808	DNA directed DNA polymerase
289	25	78.1	1009	2	T12925	DNA directed DNA polymerase
290	25	78.1	1055	2	T12925	DNA directed DNA polymerase
291	25	78.1	1074	2	G45534	probable histone H1
292	25	78.1	1083	2	A87647	DNA polymerase III
293	25	78.1	1121	2	E86495	hypothetical protein
294	25	78.1	1182	2	S14916	hypothetical protein
295	25	78.1	1195	2	A44018	lysine BCL chain
296	25	78.1	1233	2	T27045	nitrate reductase
297	25	78.1	1294	2	T18474	hypothetical protein
298	25	78.1	1309	2	S62457	hypothetical protein
299	25	78.1	1318	2	T28568	hypothetical protein
300	25	78.1	1335	2	T23210	hypothetical protein
301	24	75.0	26	2	STPPT4	stp protein - phage
302	24	75.0	26	2	S55799	stp protein - phage
303	24	75.0	26	2	S55799	stp protein - phage
304	24	75.0	26	2	S55799	stp protein - phage
305	24	75.0	26	2	S55799	stp protein - phage
306	24	75.0	26	2	S55799	stp protein - phage
307	24	75.0	26	2	S55799	stp protein - phage
308	24	75.0	26	2	S55799	stp protein - phage
309	24	75.0	51	1	INS2	insulin - casirau
310	24	75.0	51	1	INS2	insulin - casirau
311	24	75.0	52	2	H27804	hypothetical protein
312	24	75.0	55	2	A01194	50S ribosomal protein
313	24	75.0	60	2	E83273	50S ribosomal protein
314	24	75.0	62	2	E71277	probable ribosomal protein
315	24	75.0	62	2	E86516	hypothetical protein
316	24	75.0	62	2	G73105	hypothetical protein
317	24	75.0	62	2	S03103	hypothetical protein
318	24	75.0	62	2	A01194	hypothetical protein
319	24	75.0	62	2	A01194	hypothetical protein
320	24	75.0	72	2	T07369	ubiquinol-cytochrome c
321	24	75.0	73	2	G80665	cytochrome c oxidase
322	24	75.0	73	2	E90697	hypothetical protein
323	24	75.0	73	2	E90697	hypothetical protein
324	24	75.0	73	2	E90697	hypothetical protein
325	24	75.0	73	2	E90697	hypothetical protein
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429	24	75.0	73	2	E90697	hypothetical protein
430	24	75.0	73	2	E90697	hypothetical protein
431	24	75.0	73	2	E90697	hypothetical protein
432	24	75.0	73	2	E90697	hypothetical protein
433	24	75.0	73	2	E90697	hypothetical protein
434	24	75.0	73	2	E90697	hypothetical protein
435	24	75.0	73	2	E90697	hypothetical protein
436	24	75.0	73	2	E90697	hypothetical protein
437	24	75.0	73	2	E90697	hypothetical protein
438	24	75.0	73	2	E90697	hypothetical protein
439	24	75.0	73	2	E90697	hypothetical protein
440	24	75.0	73	2	E90697	hypothetical protein
441	24	75.0	73	2	E90697	hypothetical protein
442	24	75.0	73	2	E90697	hypothetical protein
443	24	75.0	73	2	E90697	hypothetical protein
444	24	75.0	73	2	E90697	hypothetical protein
445	24	75.0	73	2	E90697	hypothetical protein
446	24	75.0	73	2	E90697	hypothetical protein
447						

495	24	75.0	165	2	H90118	hypothetical prote	469	24	75.0	214	2	529794	hypothetical prote
496	24	75.0	165	2	H90469	3-isopropylmalate	469	24	75.0	215	2	529795	hypothetical prote
497	24	75.0	165	2	H97417	uncharacterized co	470	24	75.0	216	2	169400	conserved hypotet
498	24	75.0	165	2	H97546	probable ring-elec	471	24	75.0	216	2	115417	hypothetical prote
499	24	75.0	165	2	H97394	hypothetical prote	472	24	75.0	216	2	739520	hypothetical conse
400	24	75.0	167	2	H94904	atrial protein p	473	24	75.0	216	2	115174	hypothetical prote
401	24	75.0	167	2	S56544	fimbrial protein f	474	24	75.0	217	1	A65026	uracil phosphoribo
402	24	75.0	167	2	H00952	probable fimbrial	475	24	75.0	217	2	H01048	uracil phosphoribo
403	24	75.0	167	2	H91288	fimbrial morpholog	476	24	75.0	217	2	H85894	uracil phosphoribo
404	24	75.0	167	2	A86130	fimbrial morpholog	477	24	75.0	217	2	H86188	protein 125820.5 l
405	24	75.0	167	2	H87725	probable fimbrial	478	24	75.0	217	2	C70779	hypothetical prote
406	24	75.0	168	2	H94459	3-isopropylmalate	479	24	75.0	218	2	B94862	chitinase III (
407	24	75.0	170	2	E69210	3-isopropylmalate	480	24	75.0	218	2	T44287	translation initia
408	24	75.0	170	2	H64458	3-isopropylmalate	481	24	75.0	219	2	I40525	endonuclease III (
409	24	75.0	171	2	C96562	amino group acetyl	482	24	75.0	219	2	H99924	endonuclease-like
410	24	75.0	171	2	H72061	SSU ribosomal prot	483	24	75.0	219	2	AF1111	probable endonucle
411	24	75.0	172	2	H69545	hypothetical prote	484	24	75.0	219	2	AF1684	hypothetical endonuc
412	24	75.0	172	2	H95741	conserved hypotet	485	24	75.0	220	2	J05015	hypothetical 24.8K
413	24	75.0	172	2	H69646	transcription requ	486	24	75.0	220	2	D70114	chitinase III
414	24	75.0	173	2	C97430	cathapsin B-like p	487	24	75.0	220	2	D70659	probable lipoprote
415	24	75.0	174	2	H49454	N-methyltransferas	488	24	75.0	221	2	H94288	hypothetical prote
416	24	75.0	174	2	H94189	hypothetical prote	489	24	75.0	221	2	H72418	hypothetical prote
417	24	75.0	175	2	H24196	transcription requ	490	24	75.0	223	2	H59125	HWA 3-protein (HA
418	24	75.0	176	2	A86115	transcription requ	491	24	75.0	223	2	S16652	hypothetical prote
419	24	75.0	177	2	H75041	hypothetical prote	492	24	75.0	224	2	H95998	probable tail asso
420	24	75.0	178	2	H25570	hypothetical prote	493	24	75.0	224	2	A85742	probable tail comp
421	24	75.0	179	2	C96839	cat protein - vari	494	24	75.0	225	2	C95842	probable tail comp
422	24	75.0	179	2	A70154	B3c protein - vari	495	24	75.0	225	2	D81049	hypothetical prote
423	24	75.0	180	2	H36392	hypothetical prote	496	24	75.0	225	2	H51101	hypothetical prote
424	24	75.0	180	2	A99421	hypothetical 15.0K	497	24	75.0	225	2	A97271	probable tail-type
425	24	75.0	181	2	H88508	protein HMA12.1 l	498	24	75.0	226	2	D90464	insulin-like grow
426	24	75.0	181	2	H93442	N-methyl-D-asparta	499	24	75.0	226	2	T30199	carbohydrate (p-3
427	24	75.0	185	2	H49442	hypothetical prote	500	24	75.0	227	2	C25899	probable tail asso
428	24	75.0	185	2	A95086	transcription requ	501	24	75.0	227	2	G81118	hypothetical prote
429	24	75.0	186	2	A66984	transcription requ	502	24	75.0	229	2	A86944	conserved hypotet
430	24	75.0	185	2	H95988	transcription requ	503	24	75.0	231	2	AF0336	aspartate tase
431	24	75.0	185	2	H95952	conserved hypotet	504	24	75.0	231	2	A10722	hypothetical prote
432	24	75.0	185	2	H97690	hypothetical prote	505	24	75.0	233	2	AB2073	hypothetical prote
433	24	75.0	186	2	AF0348	conserved hypotet	506	24	75.0	234	2	G46098	phosphatase, Pup
434	24	75.0	187	2	H74872	basalB protein hem	507	24	75.0	236	1	D941	lectin - common sa
435	24	75.0	188	2	C31952	penicillin binding	508	24	75.0	236	2	AF4104	endonuclease III l
436	24	75.0	189	2	H95966	probable tail asso	509	24	75.0	236	2	A84319	RNA repair protein
437	24	75.0	189	2	AF0197	hypothetical prote	510	24	75.0	236	2	E73453	hypothetical prote
438	24	75.0	192	2	H84601	hypothetical prote	511	24	75.0	236	2	H95745	hypothetical prote
439	24	75.0	195	2	H95297	probable allantoic	512	24	75.0	237	2	C82002	probable cell divi
440	24	75.0	196	2	H64968	acetyl CoA acetyl	513	24	75.0	237	2	H81240	septum site determ
441	24	75.0	197	2	H94489	unknown protein f	514	24	75.0	237	2	114770	hypothetical prote
442	24	75.0	200	2	H90522	hypothetical prote	515	24	75.0	237	2	D89990	hypothetical prote
443	24	75.0	200	2	H74059	hypothetical prote	516	24	75.0	238	2	I48605	insulin-like grow
444	24	75.0	201	2	A34710	beta-lactamase int	517	24	75.0	238	2	S62809	type I restriction
445	24	75.0	202	2	A71995	tumor-specific tra	518	24	75.0	239	2	H71543	probable lipoprote
446	24	75.0	202	2	A44357	hypothetical prote	519	24	75.0	240	2	A39242	insulin-like grow
447	24	75.0	202	2	H95929	ribosomal protein	520	24	75.0	242	2	H75143	hypothetical prote
448	24	75.0	204	1	A54204	ribosomal protein	521	24	75.0	243	2	T09646	translation initia
449	24	75.0	204	2	S20529	ribosomal protein	522	24	75.0	243	2	C54120	kinA protein Bar
450	24	75.0	207	2	H70149	transplantation an	523	24	75.0	245	2	F00823	probable tail asso
451	24	75.0	205	2	A92024	conserved hypotet	524	24	75.0	245	2	C95692	probable tail asso
452	24	75.0	205	2	H44646	hypothetical prote	525	24	75.0	245	2	S48395	PEW7 protein, yes
453	24	75.0	207	2	C82941	uracil phosphoribo	526	24	75.0	246	1	P58994	polyhedrin - Arct
454	24	75.0	207	2	H84110	hypothetical prote	527	24	75.0	246	1	C54705	acetylase (p-3.2)
455	24	75.0	207	2	S25990	hypothetical prote	528	24	75.0	246	2	S27441	chitinase (p-3.2)
456	24	75.0	207	2	H36086	hypothetical prote	529	24	75.0	246	2	C71917	chitinase (p-3.2)
457	24	75.0	207	2	AF17925	multibacterial gran	530	24	75.0	246	2	A80793	probably exported
458	24	75.0	208	1	H41111	uracil phosphoribo	531	24	75.0	247	2	S37412	chitinase (p-3.2)
459	24	75.0	208	2	A00918	uracil phosphoribo	532	24	75.0	247	2	H95977	probable tail asso
460	24	75.0	209	2	H94961	endonuclease III (533	24	75.0	247	2	B00997	probable tail asso
461	24	75.0	209	2	H55148	endonuclease III (534	24	75.0	247	2	A11754	hypothetical prote
462	24	75.0	209	2	H39016	DNA (apurinic or a	535	24	75.0	248	2	AL2175	hypothetical prote
463	24	75.0	209	2	S25980	hypothetical prote	536	24	75.0	249	2	S32609	phycocyanin asso
464	24	75.0	209	2	H90209	conserved hypotet	537	24	75.0	249	2	S73553	translation initia
465	24	75.0	211	2	H95768	probable tail asso	538	24	75.0	249	2	H71442	probable tail asso
466	24	75.0	211	2	H94723	hypothetical prote	539	24	75.0	250	2	S51588	chitinase (p-3.2)
467	24	75.0	214	2	H70425	endonuclease III -	540	24	75.0	251	2	A64395	hypothetical prote

541	24	75.0	351	0	859312	hypothetical prote	611	75.0	351	0	859312	hypothetical prote
542	24	75.0	352	0	859364	ribosomal protein	615	75.0	352	0	859364	transcription requ
543	24	75.0	353	0	859389	chitinase (EC 3.2.	616	75.0	353	0	859389	probable retrocon
544	24	75.0	354	0	859393	chitinase (EC 3.2.	617	75.0	354	0	859393	chitinase (EC 3.2.
545	24	75.0	355	0	859384	ribosomal protein	618	75.0	355	0	859384	probable trans
546	24	75.0	356	0	859399	endonuclease III 1	619	75.0	356	0	859399	probable mitochond
547	24	75.0	357	0	859380	conserved hypotet	620	75.0	357	0	859380	ADP-ribosyl cyclas
548	24	75.0	358	0	859463	high affinity brom	621	75.0	358	0	859463	lactacin transpo
549	24	75.0	359	0	859499	adenylyl kinase	622	75.0	359	0	859499	beta protein - bar
550	24	75.0	360	0	859519	proteoglycanase 3,	623	75.0	360	0	859519	protein p118 hem
551	24	75.0	361	0	859481	conserved hypotet	624	75.0	361	0	859481	hypothetical prote
552	24	75.0	362	0	859599	chemotactic methyl	625	75.0	362	0	859599	chitinase (EC 3.2.
553	24	75.0	363	0	859567	hypothetical prote	626	75.0	363	0	859567	hypothetical prote
554	24	75.0	364	0	859536	RNA-directed RNA p	627	75.0	364	0	859536	conserved hypotet
555	24	75.0	365	0	859618	endonuclease III 1	628	75.0	365	0	859618	conserved hypotet
556	24	75.0	366	0	859420	hypothetical prote	629	75.0	366	0	859420	thioredoxin reduct
557	24	75.0	367	0	859406	protein p108B.7 (1	630	75.0	367	0	859406	thioredoxin reduct
558	24	75.0	368	0	859484	hypothetical prote	631	75.0	368	0	859484	thioredoxin reduct
559	24	75.0	369	0	859484	chitinase (EC 3.2.	632	75.0	369	0	859484	chitinase (EC 3.2.
560	24	75.0	370	0	859625	chitinase (EC 3.2.	633	75.0	370	0	859625	probable dihydrol
561	24	75.0	371	0	859507	hypothetical prote	634	75.0	371	0	859507	hypothetical prote
562	24	75.0	372	0	859402	hypothetical prote	635	75.0	372	0	859402	hypothetical prote
563	24	75.0	373	0	859402	hypothetical prote	636	75.0	373	0	859402	conserved hypotet
564	24	75.0	374	0	859402	hypothetical prote	637	75.0	374	0	859402	thioredoxin disulf
565	24	75.0	375	0	859402	hypothetical prote	638	75.0	375	0	859402	thioredoxin reduct
566	24	75.0	376	0	859402	hypothetical prote	639	75.0	376	0	859402	chitinase (EC 3.2.
567	24	75.0	377	0	859402	hypothetical prote	640	75.0	377	0	859402	chitinase (EC 3.2.
568	24	75.0	378	0	859402	hypothetical prote	641	75.0	378	0	859402	chitinase (EC 3.2.
569	24	75.0	379	0	859402	hypothetical prote	642	75.0	379	0	859402	chitinase (EC 3.2.
570	24	75.0	380	0	859402	hypothetical prote	643	75.0	380	0	859402	chitinase (EC 3.2.
571	24	75.0	381	0	859402	hypothetical prote	644	75.0	381	0	859402	chitinase (EC 3.2.
572	24	75.0	382	0	859402	hypothetical prote	645	75.0	382	0	859402	chitinase (EC 3.2.
573	24	75.0	383	0	859402	hypothetical prote	646	75.0	383	0	859402	chitinase (EC 3.2.
574	24	75.0	384	0	859402	hypothetical prote	647	75.0	384	0	859402	chitinase (EC 3.2.
575	24	75.0	385	0	859402	hypothetical prote	648	75.0	385	0	859402	chitinase (EC 3.2.
576	24	75.0	386	0	859402	hypothetical prote	649	75.0	386	0	859402	chitinase (EC 3.2.
577	24	75.0	387	0	859402	hypothetical prote	650	75.0	387	0	859402	chitinase (EC 3.2.
578	24	75.0	388	0	859402	hypothetical prote	651	75.0	388	0	859402	chitinase (EC 3.2.
579	24	75.0	389	0	859402	hypothetical prote	652	75.0	389	0	859402	chitinase (EC 3.2.
580	24	75.0	390	0	859402	hypothetical prote	653	75.0	390	0	859402	chitinase (EC 3.2.
581	24	75.0	391	0	859402	hypothetical prote	654	75.0	391	0	859402	chitinase (EC 3.2.
582	24	75.0	392	0	859402	hypothetical prote	655	75.0	392	0	859402	chitinase (EC 3.2.
583	24	75.0	393	0	859402	hypothetical prote	656	75.0	393	0	859402	chitinase (EC 3.2.
584	24	75.0	394	0	859402	hypothetical prote	657	75.0	394	0	859402	chitinase (EC 3.2.
585	24	75.0	395	0	859402	hypothetical prote	658	75.0	395	0	859402	chitinase (EC 3.2.
586	24	75.0	396	0	859402	hypothetical prote	659	75.0	396	0	859402	chitinase (EC 3.2.
587	24	75.0	397	0	859402	hypothetical prote	660	75.0	397	0	859402	chitinase (EC 3.2.
588	24	75.0	398	0	859402	hypothetical prote	661	75.0	398	0	859402	chitinase (EC 3.2.
589	24	75.0	399	0	859402	hypothetical prote	662	75.0	399	0	859402	chitinase (EC 3.2.
590	24	75.0	400	0	859402	hypothetical prote	663	75.0	400	0	859402	chitinase (EC 3.2.
591	24	75.0	401	0	859402	hypothetical prote	664	75.0	401	0	859402	chitinase (EC 3.2.
592	24	75.0	402	0	859402	hypothetical prote	665	75.0	402	0	859402	chitinase (EC 3.2.
593	24	75.0	403	0	859402	hypothetical prote	666	75.0	403	0	859402	chitinase (EC 3.2.
594	24	75.0	404	0	859402	hypothetical prote	667	75.0	404	0	859402	chitinase (EC 3.2.
595	24	75.0	405	0	859402	hypothetical prote	668	75.0	405	0	859402	chitinase (EC 3.2.
596	24	75.0	406	0	859402	hypothetical prote	669	75.0	406	0	859402	chitinase (EC 3.2.
597	24	75.0	407	0	859402	hypothetical prote	670	75.0	407	0	859402	chitinase (EC 3.2.
598	24	75.0	408	0	859402	hypothetical prote	671	75.0	408	0	859402	chitinase (EC 3.2.
599	24	75.0	409	0	859402	hypothetical prote	672	75.0	409	0	859402	chitinase (EC 3.2.
600	24	75.0	410	0	859402	hypothetical prote	673	75.0	410	0	859402	chitinase (EC 3.2.
601	24	75.0	411	0	859402	hypothetical prote	674	75.0	411	0	859402	chitinase (EC 3.2.
602	24	75.0	412	0	859402	hypothetical prote	675	75.0	412	0	859402	chitinase (EC 3.2.
603	24	75.0	413	0	859402	hypothetical prote	676	75.0	413	0	859402	chitinase (EC 3.2.
604	24	75.0	414	0	859402	hypothetical prote	677	75.0	414	0	859402	chitinase (EC 3.2.
605	24	75.0	415	0	859402	hypothetical prote	678	75.0	415	0	859402	chitinase (EC 3.2.
606	24	75.0	416	0	859402	hypothetical prote	679	75.0	416	0	859402	chitinase (EC 3.2.
607	24	75.0	417	0	859402	hypothetical prote	680	75.0	417	0	859402	chitinase (EC 3.2.
608	24	75.0	418	0	859402	hypothetical prote	681	75.0	418	0	859402	chitinase (EC 3.2.
609	24	75.0	419	0	859402	hypothetical prote	682	75.0	419	0	859402	chitinase (EC 3.2.
610	24	75.0	420	0	859402	hypothetical prote	683	75.0	420	0	859402	chitinase (EC 3.2.
611	24	75.0	421	0	859402	hypothetical prote	684	75.0	421	0	859402	chitinase (EC 3.2.
612	24	75.0	422	0	859402	hypothetical prote	685	75.0	422	0	859402	chitinase (EC 3.2.
613	24	75.0	423	0	859402	hypothetical prote	686	75.0	423	0	859402	chitinase (EC 3.2.

687	34	75.0	641	2	AP2797	conserved hypothetical	760	24	75.0	662	2	146079	hypothetical prote
688	24	75.0	631	2	S76480	hypothetical prote	761	24	75.0	363	2	S72661	hypothetical prote
689	24	75.0	342	2	T15561	G protein-coupled	762	24	75.0	363	2	E4616	hypothetical prote
690	24	75.0	343	2	D21748	glutaryl tRNA red	763	24	75.0	363	2	A21696	hypothetical prote
691	24	75.0	344	2	G95211	anthranilate phosph	764	24	75.0	363	2	T42240	amino acid transpo
692	24	75.0	344	2	A08076	hypothetical prote	765	24	75.0	364	2	H69831	acetyl CoA transac
693	24	75.0	344	2	I25427	hypothetical prote	766	24	75.0	364	2	355529	p46 bet a2 mitoch
694	24	75.0	344	2	S20962	chitinase (EC 3.2.	767	24	75.0	364	2	G84367	hypothetical prote
695	24	75.0	344	2	G54961	hypothetical prote	768	24	75.0	365	2	D89980	conserved hypotet
696	24	75.0	344	2	E90967	probable reductase	769	24	75.0	366	1	T25259	phosphoprotein pho
697	24	75.0	344	2	D85816	probable reductase	770	24	75.0	366	2	AH0445	conserved hypotet
698	24	75.0	344	2	AF0912	conserved hypotet	771	24	75.0	366	2	JH0368	double-strand break
699	24	75.0	345	1	S35194	anthranilate phosph	772	24	75.0	367	2	J56129	ester and beta-alm
700	24	75.0	346	2	I48171	PC gamma (14C) ox	773	24	75.0	367	2	S68683	stress activated p
701	24	75.0	346	2	T23849	hypothetical prote	774	24	75.0	367	2	J57292	adhesin, activated
702	24	75.0	346	2	S52591	probable membrane	775	24	75.0	367	2	S66592	fast asium channel
703	24	75.0	347	1	W08922	ribonucleoside dip	776	24	75.0	367	2	A51131	beta-142 protein
704	24	75.0	347	1	W08922	ribonucleoside dip	777	24	75.0	367	2	S45312	hypothetical prote
705	24	75.0	347	2	F69890	dolichol phosphate	778	24	75.0	367	2	G96776	hypothetical prote
706	24	75.0	347	2	C84059	conserved hypotet	779	24	75.0	370	1	G64650	probable membrane
707	24	75.0	349	2	T34423	hypothetical prote	780	24	75.0	370	1	H71937	probable membrane
708	24	75.0	342	2	D85898	hypothetical prote	781	24	75.0	370	2	A72403	stomach 1 phosphat
709	24	75.0	342	2	D21558	protein tp33 prote	782	24	75.0	371	2	T34253	phosphatase homol
710	24	75.0	342	2	A70162	hypothetical prote	783	24	75.0	372	2	S32524	MAP kinase (p32.7
711	24	75.0	343	1	H01V1A	hemagglutinin HA1	784	24	75.0	372	2	A85249	hypothetical prote
712	24	75.0	343	2	J62470	hemagglutinin in	785	24	75.0	372	2	I48416	probable mitochond
713	24	75.0	343	2	T23271	hemagglutinin in	786	24	75.0	373	2	I27463	acetylserine amin
714	24	75.0	343	2	J62372	hemagglutinin in	787	24	75.0	373	2	T05462	hypothetical prote
715	24	75.0	343	2	G96533	hypothetical prote	788	24	75.0	375	1	I27314	phosphoprotein pho
716	24	75.0	343	2	AH1419	weakly ATP synthas	789	24	75.0	377	2	A43234	pyruvate kinase q
717	24	75.0	344	2	J61543	hemagglutinin - in	790	24	75.0	377	2	T59643	zinc metalloprotei
718	24	75.0	344	2	P90319	hemagglutinin - in	791	24	75.0	378	2	T11713	probable alpha 1-2
719	24	75.0	344	2	P06321	hemagglutinin - in	792	24	75.0	378	2	G71244	hypothetical prote
720	24	75.0	344	2	E84377	protein export (im	793	24	75.0	379	1	G9624W	citrate utilization
721	24	75.0	344	2	T16630	hypothetical prote	794	24	75.0	379	2	G82233	phosphoserine amin
722	24	75.0	345	2	C86195	hypothetical prote	795	24	75.0	380	2	T29181	hypothetical prote
723	24	75.0	345	2	A91204	hypothetical prote	796	24	75.0	380	2	S23157	light protein, Kle
724	24	75.0	346	2	S21255	acetylserine amin	797	24	75.0	381	2	D23397	hypothetical prote
725	24	75.0	346	2	P06660	probable reductase	798	24	75.0	382	2	T73345	hypothetical prote
726	24	75.0	346	2	P06660	probable reductase	799	24	75.0	382	2	P95904	probable alpha-act
727	24	75.0	346	2	H22437	gamma protein prec	800	24	75.0	384	2	G96689	probable fructokin
728	24	75.0	346	2	I31179	hypothetical prote	801	24	75.0	384	2	T25587	probable histidin
729	24	75.0	348	2	C37693	thioredoxin reduct	802	24	75.0	384	2	I27312	conserved beta-oxyl
730	24	75.0	348	2	H71487	probable glutamyl	803	24	75.0	384	2	I32312	aqueous 111 protein
731	24	75.0	349	2	A40141	mitochondrial solu	804	24	75.0	384	2	T95201	hypothetical prote
732	24	75.0	349	2	S38321	recombination prot	805	24	75.0	385	2	S05113	calreticulin (M60F)
733	24	75.0	351	2	D87991	hypothetical prote	806	24	75.0	387	2	T40339	cytochrome c oxid
734	24	75.0	352	2	A82249	N-acetyl glutamate	807	24	75.0	389	2	T27240	hypothetical prote
735	24	75.0	353	2	S16785	hemagglutinin in	808	24	75.0	389	2	G82140	conserved hypotet
736	24	75.0	353	2	S16785	hemagglutinin in	809	24	75.0	389	2	T25271	conserved hypotet
737	24	75.0	354	2	C91674	probable mitochond	810	24	75.0	391	2	T25263	hypothetical prote
738	24	75.0	354	2	A95788	sorbitol dehydrog	811	24	75.0	391	2	S22663	S-sadenosylmet hion
739	24	75.0	355	2	S24785	hemagglutinin - in	812	24	75.0	394	2	A52211	14S ribonucleosid
740	24	75.0	355	2	T21129	peroxidase (EC 1.1	813	24	75.0	395	2	H65147	glutamate transpo
741	24	75.0	355	2	T21129	hypothetical prote	814	24	75.0	395	2	I11248	glutamate transpo
742	24	75.0	355	2	T10482	hypothetical prote	815	24	75.0	396	2	A92107	phosphatase synth
743	24	75.0	356	2	S61765	protein kinase AIN	816	24	75.0	397	2	A95681	putative nucleolar
744	24	75.0	356	2	A51230	class I histocompa	817	24	75.0	400	2	A52280	hypothetical prote
745	24	75.0	356	2	C95134	interase/recombin	818	24	75.0	401	1	V33780	sodium glutamate S
746	24	75.0	356	2	H96779	interase/recombin	819	24	75.0	401	2	A98195	glutamate transpo
747	24	75.0	356	2	E84192	hypothetical prote	820	24	75.0	401	2	B86042	glutamate transpo
748	24	75.0	356	2	F08002	interase/recombin	821	24	75.0	401	2	A00969	glutamate transpo
749	24	75.0	357	2	A21972	conserved hypotet	822	24	75.0	402	2	T23701	hypothetical prote
750	24	75.0	358	2	S69886	hypothetical prote	823	24	75.0	402	2	T34541	probable membrane
751	24	75.0	361	1	XN8974	hemagglutinin prec	824	24	75.0	403	2	R52778	probable proteasin
752	24	75.0	361	2	H95260	phosphoserine tran	825	24	75.0	403	2	H83783	hypothetical prote
753	24	75.0	361	2	G82540	conserved hypotet	826	24	75.0	404	2	A46480	PC gamma (14C) rec
754	24	75.0	362	1	S30512	hypothetical prote	827	24	75.0	404	2	A60395	sodium glutamate S
755	24	75.0	362	1	B64838	phosphoserine tran	828	24	75.0	404	2	B84593	hypothetical prote
756	24	75.0	362	2	S21149	phosphoserine tran	829	24	75.0	407	2	T12386	conserved hypotet
757	24	75.0	362	2	F92752	3-phosphoserine am	830	24	75.0	407	2	A46072	reverse transcripta
758	24	75.0	362	2	S32636	3-phosphoserine am	831	24	75.0	407	2	A00706	alpha and beta poly
759	24	75.0	362	2	AQ0613	phosphoserine amin	832	24	75.0	408	2	T19463	hypothetical prote

979 24 75.0 505 2 089 391
 980 24 75.0 506 2 069963
 981 24 75.0 506 2 F88954
 982 24 75.0 508 2 D81225
 983 24 75.0 509 2 S45413
 984 24 75.0 509 2 G83442
 985 24 75.0 510 2 H82197
 986 24 75.0 511 1 S54720
 987 24 75.0 512 2 T41982
 988 24 75.0 512 2 G24505
 989 24 75.0 513 2 E72495
 990 24 75.0 514 2 B86355
 991 24 75.0 516 2 A69527
 992 24 75.0 516 2 F84019
 993 24 75.0 516 2 T40181
 994 24 75.0 520 2 H75419
 995 24 75.0 520 2 P90494
 996 24 75.0 521 2 T27192
 997 24 75.0 525 2 T30445
 998 24 75.0 525 2 T17443
 999 24 75.0 525 2 A62342
 1000 24 75.0 525 2 P46639

ALIGNMENTS

RESULT 1
 B85684
 unknown protein encoded by prophage CP-933C [imported] - Escherichia coli (strain O157:H7)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 15 Feb-2001 #text_change 14 Sep-2001
 C:Accession: B85684
 P:Porra, N.T.; Plunkett, III, G.; Borland, V.; Mau, R.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.J.; Grobeck, P.; Davis, N.W.; Im, A.; Pimulunta, E.; Potamousis, K.; Apedaca,
 Nature 409, 529-533, 2001
 A:Title: Genomic sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MIMD:21074935; PMID:11206551
 A:Accession: B85684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 -STO-
 A:Cross-references: GB:AE025374; EMBL:AF2514756; FIDB:AA055934.1; GSPDB:GM03145; UMRP:218
 A:Description: 41 sequence entries for enterohemorrhagic Escherichia coli O157:H7.
 C:Genetics:
 A:Gene: Z1846

Query Match 93.8% Score 40; Db 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 9; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GYRN 7
 DB 15 GYRN 19

RESULT 2
 S76180
 hypothetical protein - Synecochystis sp. (strain pcc 6803)
 C:Species: Synecochystis sp.
 A:Variety: pcc 6803
 C:Date: 25-Apr-1997 #sequence_revision 25 Apr 1997 #text_change 08 Oct 1999
 C:Accession: S76180
 E:Kaneko, T.; Sato, S.; Katami, H.; Tanaka, A.; Asanuma, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 4, 109-146, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecochystis
 sp.
 A:Reference number: S74322; MIMD:97061291; PMID:8905241
 A:Accession: S76180
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-144 -KAN-

A:Cross-references: EMBL:AF59314; GB:AA061339; K004165477; FIDB:AA18459.1; PDB:1J0
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 93.8% Score 40; Db 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GYRN 7
 DB 27 GYRN 41

RESULT 3
 B87703
 conserved hypothetical protein Y5660 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20 Apr 2001 #sequence_revision 23 Apr 2001 #text_change 20 Apr 2001
 C:Accession: B87703
 R:Norman, W.C.; Goldblum, T.V.; Paulson, L.L.; Nelson, K.E.; Elson, J.; Beidell, R.;
 B. Ladd, H.C.; Brey, R.L.; Kadosh, R.J.; Linking, A.S.; Glick, M.H.; Hall, D.H.; Ko
 n. S.; Emolteva, M.; White, G.; Sakhara, S.; Shapira, E.; Venter, J.C.; Fraser, R.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4197-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MIMD:2117698; PMID:11259647
 A:Accession: B87703
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 -STO-
 A:Cross-references: GB:AE005673; NID:q13425419; FIDB:AA025622.1; GSPDB:GM00148
 C:Genetics:
 A:Gene: CC3660

Query Match 93.8% Score 40; Db 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GYRN 7
 DB 73 GYRN 77

RESULT 4
 S74396
 hypothetical protein p03613, phage phi-22, tail fiberase 145 - Mycoplasma pneumoniae (strain AT
 N:Alternate names: hypothetical protein K05_01175
 C:Species: Mycoplasma pneumoniae
 A:Variety: ATCC 29442
 C:Date: 27-Feb-1997 #sequence_revision 25 Apr 1997 #text_change 07 Jan 1999
 C:Accession: S74396
 E:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pohl, E.; Li, R.; Hermann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumo
 A:Reference number: S74327; MIMD:97105985; PMID:8948634
 A:Accession: S74396
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-175 -HIM-
 A:Cross-references: EMBL:AF000018; GB:000089; NID:q1674827; FIDB:AA069818.1; PDB:1J2
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Gene: hpt
 A:Gene code: 3383
 C:Superfamily: hypoxanthine phosphoribosyl transferase

Query Match 93.8% Score 40; Db 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GYRN 7
 DB 159 GYRN 164

C:Keywords: aminotransferase

Query Match 94.8%; Score 30; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
|||||
DB 284 GFYRN 287

RESULT 10

CP82572
phosphoserine aminotransferase XP2426 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa
C:Date: 18 Aug 2000 #sequence_revision 29 Aug 2000 #text_change 02-Sep-2000

C:Accession: CP82572

C:Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB2515; MIMB:20045717; PMID:10910347

A:Note: for a complete list of authors see reference number AF9328 below

A:Accession: CP82572

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-362 <SIM>

A:Cross-references: GB:AE004043; GB:AE003849; NID:q107486; PIDN:AAF85125.1; GSPDR:GN001

R:Simpton, A.J.G.; Reinauch, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Brites, M.R.S.; Bueno, M.R.F.; Camargo, A.A.; Camargo, E.E.A.; Carraro, D.M.; Carrer, H

de Nêto, E.; Dorena, P.; El-Berry, H.; Faciniani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froim

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramao, E.E.; Lajolo

Chado, M.A.; Madeira, A.M.B.N.; Madeira, R.M.P.; Marico, C.L.; Marques, M.V.; Martins, F

A:Authors: Martins, F.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.;

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jrs, V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.P.; da Silva, P.P.; da Silva, A.M.; Silva Jrs, W.A.; da Silveir

M.; Tsubota, M.H.; Vilella, H.; Van Elteren, M.A.; Vojtowski, Almeida, S.; Vettore, A.;

A:Reference number: AF9328

A:Contents: annotation

C:Genetics:

A:Gene: XP2426

C:Superfamily: phosphoserine aminotransferase

Query Match 94.8%; Score 30; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

|||||

DB 284 GFYRN 298

RESULT 11

CP82572

hypothetical protein CP06A5.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15 Oct 1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: CP82572

R:Davidson, S.; Wohldmann, P.

submitted to The EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid CP06A5.

A:Reference number: Z25044

A:Accession: Z25044

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-408 <DAY>

A:Cross-references: EMBL:097193; PIDN:AAF52442.1; GSPDR:GN00019; GSP:CP06A5.9

A:Experimental source: strain Bristol N2; clone CP06A5

C:Genetics:

A:Gene: GSP-CP06A5.9

A:Map position: 1
A:Features: 3; 273; 283; 293; 303; 313; 323; 333; 343; 353; 363; 373; 383; 393; 403

Query Match 94.8%; Score 30; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
|||||
DB 229 GFYRN 233

RESULT 12

T46716

hypothetical protein L4326.05 [imported] - Leishmania major

C:Species: Leishmania major

C:Date: 28 Feb 2000 #sequence_revision 19-Feb-2000 #text_change 19-Feb-2000

C:Accession: T46716

R:Volckaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G

submitted to the EMBL Data Library, December 1999

A:Reference number: Z31137

A:Accession: T46716

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-415 <VOL>

A:Cross-references: EMBL:AL121861; PIDN:CAR58481.1

A:Experimental source: strain Friedlin

C:Genetics:

A:Note: L4326.05

Query Match 93.8%; Score 30; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

|||||

DB 225 GFYRN 229

RESULT 13

AF9553

probable myrosinase precursor 5432c-50499 [imported] Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Mar-2001

C:Accession: AF9553

R:Theologis, A.; Ecker, J.R.; Palm, C.L.; Federspiel, N.A.; Kaul, S.; White, O.; Aki

Chin, C.W.; Chum, M.K.; Comai, L.; Conway, A.R.; Conway, A.R.; Cressy, L.H.; Dewar,

anson, N.P.; Hughes, R.; Huizar, L.

Nature 409, 916-920, 2000

A:Authors: Butler, J.L.; Jenkins, J.; Johnson-Hopson, C.; Flinn, S.; Kunkin, J.; Kim,

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Martin, R.; Marzita

Rizzo, M.; Rooney, J.; Rowley, D.; Sakano, H.

A:Authors: Salter, S.L.; Schwartz, J.R.; Shino, P.; Southwick, A.M.; Song, H.; Tallo

ver, M.; Wu, D.; Yu, C.; Fraser, C.M.; Venter, C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AF9553

A:Accession: AF9553

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-465 <SPO>

A:Cross-references: GB:AF9553.1; NID:q10042498; PIDN:AA12763.1; GSPDR:CP06A5.9

C:Genetics:

A:Gene: F5D21.17

A:Map position: 1

C:Superfamily: Agrobacterium beta-glucosidase

Query Match 92.8%; Score 30; DB 2; Length 465;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

|||||

DB 331 GFYRN 335

RESULT 14

S50053

tryptophan-tRNA ligase (EC 6.1.1.2) alpha 2 chain mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-May-1996 #sequence revision: 10-Nov-1995 #prev_change 02-Jan-2002

C:Accession: S50053; S50053; 149301; S31461; S31462

R:Palot, B.; Sargor, G.; Bonnot, J.; Garrel, M.

J. Mol. Biol. 242, 509-503, 1994

A:Title: An alternative splicing modifies the regulatory role of tryptophan-tRNA synthetase

A:Reference number: S50052; MIM:95018226; PMID:2932716

A:Accession: S50053

A:Molecule type: mRNA

A:Residues: 1-481 <RAW>

A:Cross-references: EMBL:X66677; MIM:955477; FIDR:CAA49312.1; FID:q55438

A:Genetics: LSP

A:Note: Intron position was determined by sequencing of genomic DNA

A:Accession: S50052

A:Molecule type: mRNA

A:Residues: 1-475 <RAW>

A:Cross-references: EMBL:X66676; MIM:955435; FIDR:CAA49447.1; FID:q55436

A:Genetics: SSP

R:Kisselev, L.L.

Biochimie 75, 1027-1039, 1993

A:Title: Mammalian tryptophan-tRNA synthetase

A:Reference number: 149391; MIM:9457799; PMID:9515982

A:Accession: 149391

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-481 <RRS>

A:Cross-references: EMBL:X55657; MIM:955437; FIDR:CAA49348.1; FID:q55438

C:Genetics: <LSP>

A:Gene: WRS

A:Introns: 475/2

A:Note: the list of introns may be incomplete; clone W13

C:Genetics: <SSP>

A:Gene: WRS

A:Note: clone S5

C:Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat family

C:Keywords: alternative splicing; aminoacyl-tRNA synthetase; ligase; protein kinases

F1:481-trp-trp-trp-tRNA ligase alpha-2; trp-1-13 splice form #status: full

F12:475-trp-trp-trp-tRNA ligase alpha-2 chain; short splice form #status: predicted

F123:58-trp-trp-trp-tRNA ligase repeat family <RAW>

Query Match 93.8% Score 30; DB 2; Length 481;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

|||||

DB 250 GFYRN 254

RESULT 15

YHMS2S

monophenol monooxygenase (EC 1.14.18.1) precursor [uncloned] mouse

N:Alternate names: cresolase; monophenol oxidase; phenolase; tyrosinase

C:Species: Mus musculus (house mouse)

C:Date: 31 Mar 1989 #sequence revision: 31 Mar 1995 #prev_change 29 Apr 2000

C:Accession: A27111; A60778; A32429; S01170; S02278; S15757; 149391

R:Kahn, B.S.; Wajsbich, M.; Haq, A.K.; Kestler, D.; Barton, D.F.

Biochem. Biophys. Res. Commun. 157, 1301-1309, 1989

A:Title: Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its

A:Reference number: A27111; MIM:89268910; PMID:8124290

A:Accession: A27111

A:Molecule type: mRNA

A:Residues: 1-533 <RAW>

A:Cross-references: GR:X29244; MIM:89268910; FIDR:AAA45517.1; FID:q50248

A:Experimental sources: Goodman, S-91 melanoma cells

R:Kahn, B.S.; Haq, A.K.; Wajsbich, M.; Kestler, D.; Barton, D.F.; Francke, U.; Hametov

J. Invest. Dermatol. 93, 589-594, 1989

A:Title: Isolation, chromosomal mapping, and expression of the mouse tyrosinase gene.

A:Reference number: A60778; MIM:90018220; PMID:2507645

A:Accession: A60778

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-273 <RW>

A:Experimental source: K1487C

R:Taib, M.; Takai, E.; Cortali, E.; Studer, M.; Mintz, B.

Biochem. Biophys. Res. Commun. 159, 949-957, 1989

A:Title: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.

A:Reference number: A32429; MIM:99199579; PMID:2494997

A:Accession: A32429

A:Molecule type: mRNA

A:Residues: 1-102, 104, 105, 107, 347-533 <RRS>

A:Cross-references: GR:M24560; MIM:902249; FIDR:AAA45517.1; FID:q502250

A:Accession: B32429

A:Molecule type: mRNA

A:Residues: 1-77, 155-245, 347-533 <RRS>

A:Cross-references: GR:M24560

A:Experimental source: B16 melanoma cells

R:Mueller, G.; Ruppert, S.; Schmid, R.; Schuetz, G.

EMBO J. 7, 2723-2730, 1988

A:Title: Functional analysis of alternatively spliced tyrosinase gene transcripts.

A:Reference number: S01170; MIM:89040636; PMID:3141148

A:Accession: S01170

A:Molecule type: mRNA

A:Residues: 1-102, 105, 114, 253, 347-533 <RRS>

A:Cross-references: GR:X12792; MIM:955941; FIDR:AAA41274.1; FID:q55942

R:Yamamoto, H.; Takeuchi, S.; Kato, T.; Miyano, K.; Nakai, A.; Shiohara, T.; Takeuchi

Jpn. J. Genet. 62, 271-274, 1987

A:Title: Cloning and sequencing of mouse tyrosinase cDNA.

A:Reference number: S02278

A:Accession: S02278

A:Molecule type: mRNA

A:Residues: 1-182, 194, 253, 347-533 <RRS>

A:Cross-references: EMBL:X12782

A:Note: part of this sequence was confirmed by protein sequencing

R:Shiohara, S.; Okamoto, S.; Tamita, Y.; Takada, A.; Yamamoto, H.; Sato, M.; Takeuchi

Eur. J. Biochem. 189, 455-461, 1990

A:Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the c

A:Reference number: S15753

A:Accession: S15753

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-13 <RRS>

A:Cross-references: EMBL:X51741; MIM:955057; FIDR:CAA36043.1; FID:q55058

A:Experimental source: strain K1487C

R:Kahn, B.S.; Halaiban, R.; Chintamaneni, C.

Biochem. Biophys. Res. Commun. 141, 252-260, 1989

A:Title: Molecular basis of mouse Himalayan mutation.

A:Reference number: 149746; MIM:9927444; PMID:2567165

A:Accession: 149746

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-39, 1741-1024, 104-196, 107, 198-345, 347-419, 421-533 <RRS>

A:Cross-references: GR:M26729; MIM:949495; FIDR:AAA47806.1; FID:q309296

C:Comment: This cell-specific oxidase is a glycoprotein containing two 60 per centyme-

reactions in the formation of pigments such as melanin and other polypheolic compo-

nogenetics.

A:Gene: Tyr1

A:Map position: 7

C:Superfamily: monophenol monooxygenase

C:Keywords: alternative splicing; tyrosinase; tyrosinase; tyrosinase; tyrosinase

F1:1270-melanin; signal sequence; status: predicted; size

F12:532-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

F123:147-trp-trp-trp-tRNA monooxygenase related protein M21

Db 458 GYRN 462

RESULT 16

116274

hypothetical protein F45D2.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20 Sep 1999 #sequence_revision 20 Sep 1999 #text_change 24 Nov 1999

C:Accession: 116274

C:Gene: C01A1.6

submitted to the EMBL data library, June 1995

A:Description: the sequence of C. elegans cosmid F35D2.

A:Reference number: Z18488

A:Accession: 116274

A>Status: preliminary; translated from ORF4MP5/D0R3

A:Molecule type: DNA

A:Residues: 1747 <UN>

A:Cross-references: EMBL:Z18488; R15:961200; F15:961204; P15:961204

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: C01A1.6

A:Introns: 1747, 581, 1757, 1763, 241, 3, 372, 471, 541, 5, 595, 6, 672,

C:Superfamily: Caenorhabditis elegans hypothetical protein F45D2.4

Query Match:

Best Local Similarity 94.8%; Score 40; DB 2; Length 747;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7

|||||

Db 106 GYRN 110

RESULT 17

S40937

hypothetical protein Z642.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 06 Jan 1995 #sequence_revision 06 Jan 1995 #text_change 24 Nov 1999

C:Accession: S40937

C:Gene: C01A1.6

submitted to the EMBL data library, February 1994

A:Reference number: S40934

A:Accession: S40937

A:Molecule type: DNA

A:Residues: 1824 <HER>

A:Cross-references: EMBL:Z642.6; R15:929790; F15:929790

C:Genetics:

A:Introns: 1824, 241, 3, 372, 471, 541, 5, 595, 6, 672,

C:Superfamily: Caenorhabditis elegans hypothetical protein Z642.6

Query Match:

Best Local Similarity 94.8%; Score 40; DB 2; Length 824;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7

|||||

Db 206 GYRN 210

RESULT 18

S70630

Xeroderma pigmentosum group C - mouse

C:Species: Mus musculus (house mouse)

C>Date: 14 Feb 1997 #sequence_revision 14 Mar 1997 #text_change 05 Nov 1999

C:Accession: S70630

C:Gene: C01A1.6

Submitted to the EMBL data library, February 1996

A:Reference number: S70630

A:Accession: S70630

A:Molecule type: mRNA

A:Description: Sequence of the mouse XPC cDNA and genomic structure of human XPC gene.

A:Reference number: S70630; M111:9618489; PMID:860433

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-900 <LIL>

A:Cross-references: EMBL:U27498; N111:127472; F111:AA76250; L111:127474

A:Note: the nucleotide sequence was submitted to the EMBL data library, May 1995.

C:Genetics:

A:Gene: mXPC

Query Match:

Best Local Similarity 94.8%; Score 40; DB 2; Length 900;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

|||||

Db 182 GYRN 186

RESULT 19

S44345

Xeroderma pigmentosum group C repair complementing protein 125 - human

N:Alternate names: DNA repair protein

C:Species: Homo sapiens (man)

C>Date: 25 Dec 1994 #sequence_revision 28 Jul 1995 #text_change 08 Oct 1999

C:Accession: S44345; S28906

Kikuchi, C.; Saito, K.; Yanagisawa, J.; Saito, M.; Kikuchi, T.; Takai

EMBO J. 13, 1831-1843, 1994

A:Title: Purification and cloning of a nucleotide excision repair complex involving a

A:Reference number: S44345; M111:9422030; PMID:816482

A:Accession: S44345

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-940 <MAS>

A:Cross-references: GR:D21089; N111:47319; F111:BA04043; L111:PID:1005180; PMID:1519

Kikuchi, K.; Peterson, C.

Nature 359, 70-73, 1992

A:Title: Expression cloning of a human DNA repair gene involved in xeroderma pigmento

A:Reference number: S28357; M111:9246248; PMID:1522891

A:Accession: S28357

A:Molecule type: mRNA

A:Residues: 119, 259, 371, 262-498, 7A, 500-940 <LEZ>

A:Cross-references: EMBL:X65024

A:Note: this sequence has been revised in reference S28906

Kikuchi, K.; Peterson, C.

Nature 360, 610, 1992

A:Reference number: S28906; M111:9409605; PMID:1461286

A:Contents: erratum: correction to residues 260 and 261

A:Accession: S28906

A:Molecule type: mRNA

A:Residues: 259, 262 <LEZ>

Query Match:

Best Local Similarity 94.8%; Score 40; DB 2; Length 940;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

|||||

Db 217 GYRN 221

RESULT 20

C87645

Xeroderma pigmentosum group C - mouse

C:Species: Caenorhabditis elegans

C>Date: 20 Apr 2001 #sequence_revision 20 Apr 2001 #text_change 20 Apr 2001

C:Accession: C87645

Kikuchi, K.; Saito, K.; Yanagisawa, J.; Saito, M.; Kikuchi, T.; Takai

EMBO J. 13, 1831-1843, 1994

A:Title: Purification and cloning of a nucleotide excision repair complex involving a

A:Reference number: S44345; M111:9422030; PMID:816482

A:Accession: S44345

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1041 <STO>

ACross-references: GB:AF006674; NID:q13424873; PDB:AAV5150 1; GSTP:GM20148
 C:Genetics:
 A:Gene: GC3157

Query Match 93.8%, Score 38, PB 2; Length 1041,
 Best Local Similarity 100.0%, Pdb. No. 1-46-22,
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GYRN 7
 DB 516 GYRN 520

RESULT 21

S55517

probable transport protein PDR10 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: probable ABC transporter PDR10; Protein YOR328W
 C:Species: Saccharomyces cerevisiae
 C>Date: 01-Aug-1995 sequence_s61957; s67245; s71958
 C:Accession: s55517; s62060; s61957; s67245; s71958
 R:Parle, A.G., Rand, N.J., Goulding, S.E., Wolfe, K.H.
 submitted to the EMBL Data Library, June 1995
 A:Description: PDR10, a candidate pleiotropic drug resistance locus encoding a new ABC B
 A:Reference number: s55517
 A:Accession: S55517
 A:Molecule type: DNA
 A:Residues: 1-1564 <PAF>
 A:Cross references: EMBL:Z49821; NID:q13424873; PDB:AAV5150 1; PIR:J42571
 R:Parle, A.G.; Hand, N.J.; Goulding, S.G.; Wolfe, K.H.
 submitted to the EMBL Data Library, June 1995
 A:Description: Sequence of 29 kilobases around the PDR10 locus on the right arm of Sacch
 A:Reference number: s62058
 A:Accession: s62058
 A:Molecule type: DNA
 A:Residues: 1-1564 <PAW>
 A:Cross-references: EMBL:Z49821; NID:q13424873; PDB:AAV5150 1; PIR:J42571
 R:Song, J.M.; Cheung, E.; Rabinowitz, J.C.
 submitted to the EMBL Data Library, December 1995
 A:Description: Cloning and characterization of the Saccharomyces cerevisiae FBR1 gene.
 A:Reference number: s61955
 A:Accession: s61955

A:Accession: s61957

A:Molecule type: DNA

A:Residues: 1992-1427, 1426-1564 <SN>

A:Cross-references: EMBL:Z4222; NID:q1147766; PDB:AAV5144 1; PIR:J42571

R:Goulding, S.E.; Hand, N.J.; Parle-McDermott, A.G.; Wolfe, K.H.

submitted to the Protein Sequence Database, July 1996

A:Reference number: s67233

A:Accession: s67235

A:Molecule type: DNA

A:Residues: 1-1564 <GOU>

A:Cross-references: EMBL:Z4222; NID:q1420710; PDB:AAV5144 1; PIR:J42571

R:Parle-McDermott, A.G.; Hand, N.J.; Goulding, S.E.; Wolfe, K.H.

Yeast 12, 994-1004, 1996

A:Title: Sequence of 29 kb around the PDR10 locus on the right arm of Saccharomyces cere

A:Reference number: s71966; MIM:47061586; PMID:8496243

A:Accession: s71968

A:Molecule type: DNA

A:Residues: 1-1564 <PAF>

A:Cross-references: EMBL:Z49821; NID:q1163052; PDB:AAV5150 1; PIR:J42571

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

C:Genetics:

A:Gene: SGP:PDR10

A:Cross references: SGP:S0000956; MIM:340328W

A:Map position: 15p

C:Keywords: ATP-binding cassette, first two, ABC, transmembrane protein

P:196-406/Domain: ATP-binding cassette homology (ABC)

P:544-560/Domain: transmembrane #status predicted (TM)

P:580-600/Domain: transmembrane #status predicted (TM)

P:653-669/Domain: transmembrane #status predicted (TM)

P:689-705/Domain: transmembrane #status predicted (TM)

P:797-812/Domain: transmembrane #status predicted (TM)
 P:942-1141/Domain: ATP binding cassette homology (ABC)
 P:959-966/Region: nucleotide-binding motif A (P-loop)
 P:1340-1350/Domain: transmembrane #status predicted (TM)
 P:1394-1400/Domain: transmembrane #status predicted (TM)
 P:1422-1428/Domain: transmembrane #status predicted (TM)
 P:1447-1450/Domain: transmembrane #status predicted (TM)
 P:1533-1549/Domain: transmembrane #status predicted (TM)

Query Match 93.8%, Score 40; PB 2; Length 1564;
 Best Local Similarity 100.0%, Pdb. No. 20-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7

DB 163 GYRN 1467

P:1001

P:1001

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Query Match 84.4% Score 27; DB 1; Length 60;
 Best local Similarity 80.0%; Pred. No. 35;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 |||||
 DB 48 GYKRN 52

RESULT 24

139498
 hypothetical protein ynfH41_16; taxon: ynfH41_16; Schizosaccharomyces pombe
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39498
 E:Beck, A.; Reinhardt, F.; Lyne, M.; Rajandream, M.A.; Barrett, B.G.
 submitted to the EMBL Data Library, December 1998

A:Reference number: 221859

A:Accession: T39498

A:Status: preliminary; translated from GB/EMBL/GenBank

A:Molecule type: DNA

A:Residues: 1-199 <DEC>

A:Cross-references: EMBL:AL034413; FIDN:AA223471.1; SFE8:AB30066; SFE8:SF01564.16c

A:Experimental source: strain 972b; csmid:cl604

C:Genetics:

A:Gene: SPOB:SP0B1604.16c

A:Map position: 1

Query Match 84.4% Score 27; DB 2; Length 199;
 Best local Similarity 80.0%; Pred. No. 1,200-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 |||||
 DB 14 GYKRN 18

RESULT 25

AB6636
 hypothetical protein ynfH (imported) - Lactococcus lactis subsp. lactis (strain 111493)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 20-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Apr-2001
 C:Accession: AB6636
 E:Bohlin, A.; Wincor, P.; Mauger, S.; Wallen, O.; Malarre, F.; Weissbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A:Reference number: AB6625; M010:21345186; PMID:11337471

A:Accession: AB6636

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-201 <STO>

A:Cross-references: GB:AF005176; PID:q12722933; FIDN:AAK04187.1; GSPB:GN0511c

A:Experimental source: strain 111404

C:Genetics:

A:Gene: ynfH

Query Match 84.4% Score 27; DB 2; Length 201;
 Best local Similarity 80.0%; Pred. No. 1,200-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 |||||
 DB 67 GYKRN 71

RESULT 26

AB4994
 putative-nucleoside phosphorylase (EC 2.4.2.1) [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: AB4994

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakurai, Y.; Ishikawa, H.

Nature 407, 81-86, 2000
 A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
 A:Reference number: AB4994; M010:23445173; PMID:10974077

A:Accession: AB4994

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <STO>

A:Cross-references: GB:AP000498; GSPB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: doob; H0541

A:Superfamily: putative-nucleoside phosphorylase pap

C:Keywords: 117307;translocase, peptidyl transferase

Query Match 84.4% Score 27; DB 2; Length 243;
 Best local Similarity 80.0%; Pred. No. 1,200-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 |||||
 DB 51 GYKRN 55

RESULT 27

122092
 hypothetical protein F42E11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22092

R:Donnard, N.

submitted to the EMBL Data Library, November 1995

A:Reference number: Z19512

A:Accession: T22092

A:Status: preliminary; translated from gb/EMBL/GenBank

A:Molecule type: DNA

A:Residues: 1-258 <WIL>

A:Cross-references: EMBL:Z66562; FIDN:AAV1455.1; GSPB:GN00028; CESP:F42E11.4

A:Experimental source: clone F42E11

C:Genetics:

A:Gene: CESP:F42E11.3

A:Map position: X:1,763,157-1,773,233

A:Accession: 941,763,157-1,773,233

Query Match 84.4% Score 27; DB 2; Length 278;
 Best local Similarity 80.0%; Pred. No. 1,200-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 |||||
 DB 242 GYKRN 246

RESULT 28

A69413
 conserved hypothetical protein APL06 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Feb-1997 #sequence_revision 05-Feb-1997 #text_change 22-Jul-1999

C:Accession: A69413

E:Kleck, H.F.; Clayton, S.A.; Tully, J.F.; White, C.; Nelson, K.E.; Kachala, K.A.; Ped

Archaeoglobus fulgidus genome project, J. Biol. Chem. 272, 11111-11115, 1997

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; M010:98049445; PMID:9386475

A:Accession: A69413

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-275 <KLE>

A:Cross-references: GB:AF001014; GB:AF000762; FIDN:AAV04552.1; GB:AA00904.1; FIDN:AA

Query Match 94.1% Score 27; DB 2; Length 278;

Query Match 84.4%; Score 27; LH 2; Length 340;
 Best Local Similarity 80.0%; Pred. No. 2.5e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 11111
 DB 254 GYKRN 258

RESULT 34
 E64376
 endonuclease III - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 14-Sep-1996 #sequence_revision 14-Sep-1996 #text_change 10-Oct-1997
 C:Accession: E64376
 R:Belk, C.J.; White, G.J.; Zhou, L.; Fleischmann, P.B.; Satchell, G.O.; Blake,
 rson, J.D.; Sakaguchi, F.W.; Hama, M.C.; Gotten, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 274, 1058-1073, 1996
 A:Authors: Kaine, R.P.; Porceddu, M.; Plunkett, H.P.; Fraser, C.M.; Smith, H.C.; Woese,
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MIMD:9637044; PMID:8686087
 A:Accession: E64376
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-453-801
 A:Cross-references: GR:067599; GH:177117; NID:41591415; PID:41591323; TIGR:MJ0614; PID:4
 A:Map position: REV54497-54498
 A:Start codon: 165

Query Match 84.4%; Score 27; LH 2; Length 353;
 Best Local Similarity 80.0%; Pred. No. 2.1e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 11111
 DB 96 GYKRN 90

RESULT 35
 E69193
 acetyl-CoA synthetase related protein - Methanobacterium thermoautotrophicum (strain Del
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Oct-1999
 C:Accession: E69193
 R:Smith, D.K.; Leontovich-Stamm, L.A.; Delongchery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Gu, D.; Scudatore, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, K.; Jiwani, N
 k, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. bacteriol. 179, 7136-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
 A:Reference number: A69000; MIMD:98037514; PMID:9371463
 A:Accession: E69193
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-425-2111
 A:Cross-references: GR:AE000949; GR:AE000946; NID:42521789; PID:AA85205.1; PID:4252178
 A:Experimental source: strain Delta H
 C:Genetics: MIM701
 C:Superfamily: human SA protein; acetate-CoA ligase homology
 F:84-47%2; human SA protein; acetate-CoA ligase homology #status: typical <AC>

Query Match 84.4%; Score 27; LH 2; Length 425;
 Best Local Similarity 80.0%; Pred. No. 2.5e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 11111
 DB 411 GYKRN 415

RESULT 36
 F96994
 uncharacterized conserved protein (FA0769 [imported]) - Clostridium acetabutylicum
 C:Species: Clostridium acetabutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: F96994
 R:Noelling, J.; Brelvi, G.; Melchenko, M.V.; Markovica, K.S.; Zeng, Q.; Gibson, K.; L
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4824-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MIMD:21459425; PMID:21459425
 A:Accession: F96994
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-426-200
 A:Cross-references: GR:AE001437; PIR:AAK78745.1; PID:15024654; GSRI:G000168
 A:Experimental source: Clostridium acetabutylicum A95924
 C:Genetics: CA0769
 A:Gene: CA0769

Query Match 94.4%; Score 27; LH 2; Length 426;
 Best Local Similarity 80.0%; Pred. No. 2.5e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 11111
 DB 329 GYKRN 333

RESULT 37
 E95152
 v-type sodium ATP synthase, chain B [imported] - Streptococcus pneumoniae (strain TIC
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
 C:Accession: E95152
 R:Reitelin, B.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Kadane, D.; Holtzappel
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, R.J.; Yang, F.; Smith, H.C.; Venter, J.C.; Donnelly, K.A.; Morris
 A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae
 A:Reference number: A95000; MIMD:21457209; PMID:11460916
 A:Accession: E95152
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-441-200
 A:Cross-references: GR:AE096472; PIR:AAK76414.1; PID:1472747; GSRI:G000164; TIGR
 C:Genetics: strain TIC84
 A:Gene: SPI316
 C:Superfamily: B-transported ATP synthase alpha chain; B-transported ATP synthase

Query Match 84.4%; Score 27; LH 2; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.7e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKRN 7
 11111
 DB 418 GYKRN 422

RESULT 38
 H85745
 unknown protein encoded within prophage CP-948k [imported] - Escherichia coli (strain
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: H85745
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, R.; Glasner, J.B.; Rose, J.; May
 ilier, L.; Grothbeck, C.J.; Davis, N.W.; Lim, A.; Binstadt, E.; Beckmann, K.; Arpa
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MIMD:21074966; PMID:11266561
 A:Accession: H85745

A:Authors: Parry, C.; Small, M.; Pothoford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A:Reference number: AR0502; PMID:11677638
 A:Accession: A20659
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-467-146
 A:Cross-references: GB:AL513382; FIDN:CAU01644.1; FID:g16562466; GSPDR:GN00176
 C:Genetics: STY1476
 A:Gene: STY1476
 Query Match: 84.4%; Score 27; DB 1; Length 465;
 Best Local Similarity: 80.0%; Pred. No. 2,80002;
 Matches: 4; Conservative 1; Mismatches 0; Indels 9; Gaps 0;
 QY 3 GYRN 7
 DB 270 GYRN 274
 RESULT 44
 A41706
 triphosphan-tRNA ligase (EC 6.1.1.2) [similarity] human
 A:Alternate names: interferon-inducible protein IFP53; peptidic-chain release factor homolog
 C:Species: Homo sapiens (man)
 C:Date: 16-May-2000 #sequence_revision 16 May 2000 #text_change 02 Jan 2002
 C:Accession: A41633; A41706; S19246; J00676; J00533; S26287
 R:Floekner, J.; Rasmussen, H.B.; Justesen, J.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11524, 1991
 A:Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma
 A:Reference number: A41633; M010:92107982; PMID:1763065
 A:Accession: A41633
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-471-5PLE>
 A:Cross-references: GB:X52892; EMBL:330623; FIDN:CAA12545.1; FID:g33821
 R:Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.
 J. Biol. Chem. 265, 24245-24248, 1991
 A:Title: Interferon induces triphosphan-tRNA synthetase expression in human fibroblasts
 A:Reference number: A41706; M010:92105071; PMID:1761529
 A:Accession: A41706
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-471-40R<
 A:Cross-references: GB:J077804; NID:g164656; FIDN:AAA67424.1; FID:g1844657
 R:Kawitt, O.; Flohr, T.; Boettger, E.O.
 EMBO J. 11, 440-466, 1992
 A:Title: Molecular cloning and characterization of an interferon induced human cDNA with
 A:Reference number: S19246; M010:92104646; PMID:1557792
 A:Accession: S19246
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-423-767-425-471-1RW>
 A:Cross-references: EMBL:X62579; NID:g42709; FIDN:CAA44450.1; FID:g42709
 A:Note: 213 Ser and 214 Tyr were also found
 R:Prolova, L.Y.; Gikotova, A.Y.; Subbotina, M.A.; Kissilev, L.L.
 Gene 128, 247-245, 1993
 A:Title: The human gene encoding triphosphan-tRNA synthetase: Interferon-response element
 A:Reference number: J00676; M010:94292992; PMID:7595728
 A:Accession: J00676
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-141-182-471-5PRO1>
 A:Cross-references: GB:X67919; GB:S62847; NID:g37968; GB:X67919; NID:g37969; GB:X67920;
 4; NID:g47974; GB:X67925; GB:S62855; FID:g27775; FID:g27776; GB:S62856; NID:g37976; GB:X6
 A:Note: the authors translated the cDNA GGG for residue 55 as Cys and GAG for residue 4
 R:Prolova, L.Y.; Gikotova, A.Y.; Subbotina, M.A.; Kissilev, L.L.
 Gene 109, 291-296, 1991
 A:Title: Cloning and nucleotide sequence of the structural gene encoding for human triphosphan
 A:Reference number: J00533; M010:92112058; PMID:1765274
 A:Accession: J00533
 A:Molecule type: mRNA
 A:Residues: 1-212-7067-215-471-5PRO2>

A:Cross-references: GB:M61715; NID:g41063; FIDN:AAA61298.1; FID:g44068
 A:Experimental source: fibroblast
 C:Genetics:
 A:Gene: GDB:WARS; IFP53
 A:Cross-references: GDB:119642; OMIM:191050
 A:Map position: 14q23-14q31
 A:Residues: 45, 416, 441, 461, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 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1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 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107	78.1	965	1	AMEN_MOUSE	P97419 mus musculus	180	24	75.0	209	1	HEF_MYCIB	P43949 mycoplasma
108	78.1	965	1	AMEN_FABAT	P15541 erythrolabus	181	24	75.0	209	1	Y622_SUSEC	G9416 sulfobobus
109	78.1	966	1	AMEN_FELCA	P79171 felis silve	182	24	75.0	210	1	KRT1_ABBED	G28841 archaeobadi
110	78.1	966	1	AMEN_HUMAR	P1544 homo sapien	183	24	75.0	210	1	MYG5_ABBED	G3628 camptobadi
111	78.1	985	1	AMEN_PZARV	P1451 human spina	184	24	75.0	211	1	HEH1_CCHIF	P7954 schizosach
112	78.1	990	1	AMEN_MANDUC	Q11001 manduca sex	185	24	75.0	211	1	EMD4_BASUS	P69788 bacillus su
113	78.1	1009	1	BNS2_HSVSA	P24907 herpesvirus	186	24	75.0	211	1	EXOR_MERCE	P95476 metacocci
114	78.1	1029	1	C177_HUMAH	G14709 hofe, adicu	187	24	75.0	221	1	Y279_AEYAT	G5944 archaeobadi
115	78.1	1055	1	EMC2_PZDNC	P77917 pedicoccus	188	24	75.0	225	1	Y618_MELIA	G58250 methanococ
116	78.1	1182	1	EMC2_TFRHC	P15594 trypanosoma	189	24	75.0	226	1	HAPE_RAT	P65972 rattus norv
117	78.1	1194	1	EMC2_HDHAR	Q1574 homo sapien	190	24	75.0	226	1	Y112_AEYAT	G52438 schizosach
118	78.1	1319	1	YAP2_SCHIF	G09884 schizosach	191	24	75.0	232	1	APMX_LARCE	G19724 larva ascos
119	78.1	4695	1	LMAS_HUMAN	G15240 homo sapien	192	24	75.0	236	1	APMX_MERCE	G59544 methanococ
120	75.0	26	1	STP1_RPT4	P19788 bacterioph	193	24	75.0	236	1	LYR1_HUMVI	P62874 escherichia
121	75.0	50	1	TRG_PZDNC	P01341 procthinys	194	24	75.0	236	1	KACH_HAMNI	G94122 baculovirus
122	75.0	51	1	TRG_MYCIB	P1130 myocaster v	195	24	75.0	236	1	YAH1_LACIA	G94122 baculovirus
123	75.0	54	1	RE42_PSEAR	G82119 yersinia pe	196	24	75.0	236	1	YH76_AQUAR	G67652 aquifex aro
124	75.0	59	1	RE42_PSEAR	G96844 pseudomon	197	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
125	75.0	61	1	RE42_TREDA	G83795 treponema p	198	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
126	75.0	73	1	UPKX_SVITU	P43475 escherichia	199	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
127	75.0	73	1	YH76_HUMAR	P43475 escherichia	200	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
128	75.0	77	1	YH76_HUMAR	P43475 escherichia	201	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
129	75.0	75	1	YH76_HUMAR	P43475 escherichia	202	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
130	75.0	75	1	YH76_HUMAR	P43475 escherichia	203	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
131	75.0	88	1	YH76_HUMAR	P43475 escherichia	204	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
132	75.0	89	1	YH76_HUMAR	P43475 escherichia	205	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
133	75.0	100	1	YH76_HUMAR	P43475 escherichia	206	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
134	75.0	101	1	YH76_HUMAR	P43475 escherichia	207	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
135	75.0	105	1	YH76_HUMAR	P43475 escherichia	208	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
136	75.0	107	1	YH76_HUMAR	P43475 escherichia	209	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
137	75.0	109	1	YH76_HUMAR	P43475 escherichia	210	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
138	75.0	119	1	YH76_HUMAR	P43475 escherichia	211	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
139	75.0	121	1	YH76_HUMAR	P43475 escherichia	212	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
140	75.0	122	1	YH76_HUMAR	P43475 escherichia	213	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
141	75.0	125	1	YH76_HUMAR	P43475 escherichia	214	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
142	75.0	131	1	YH76_HUMAR	P43475 escherichia	215	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
143	75.0	132	1	YH76_HUMAR	P43475 escherichia	216	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
144	75.0	137	1	YH76_HUMAR	P43475 escherichia	217	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
145	75.0	138	1	YH76_HUMAR	P43475 escherichia	218	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
146	75.0	138	1	YH76_HUMAR	P43475 escherichia	219	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
147	75.0	142	1	YH76_HUMAR	P43475 escherichia	220	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
148	75.0	154	1	YH76_HUMAR	P43475 escherichia	221	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
149	75.0	156	1	YH76_HUMAR	P43475 escherichia	222	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
150	75.0	156	1	YH76_HUMAR	P43475 escherichia	223	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
151	75.0	160	1	YH76_HUMAR	P43475 escherichia	224	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
152	75.0	161	1	YH76_HUMAR	P43475 escherichia	225	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
153	75.0	162	1	YH76_HUMAR	P43475 escherichia	226	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
154	75.0	162	1	YH76_HUMAR	P43475 escherichia	227	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
155	75.0	162	1	YH76_HUMAR	P43475 escherichia	228	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
156	75.0	167	1	YH76_HUMAR	P43475 escherichia	229	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
157	75.0	167	1	YH76_HUMAR	P43475 escherichia	230	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
158	75.0	168	1	YH76_HUMAR	P43475 escherichia	231	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
159	75.0	170	1	YH76_HUMAR	P43475 escherichia	232	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
160	75.0	170	1	YH76_HUMAR	P43475 escherichia	233	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
161	75.0	171	1	YH76_HUMAR	P43475 escherichia	234	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
162	75.0	172	1	YH76_HUMAR	P43475 escherichia	235	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
163	75.0	174	1	YH76_HUMAR	P43475 escherichia	236	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
164	75.0	177	1	YH76_HUMAR	P43475 escherichia	237	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
165	75.0	185	1	YH76_HUMAR	P43475 escherichia	238	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
166	75.0	189	1	YH76_HUMAR	P43475 escherichia	239	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
167	75.0	190	1	YH76_HUMAR	P43475 escherichia	240	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
168	75.0	190	1	YH76_HUMAR	P43475 escherichia	241	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
169	75.0	194	1	YH76_HUMAR	P43475 escherichia	242	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
170	75.0	196	1	YH76_HUMAR	P43475 escherichia	243	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
171	75.0	201	1	YH76_HUMAR	P43475 escherichia	244	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
172	75.0	202	1	YH76_HUMAR	P43475 escherichia	245	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
173	75.0	202	1	YH76_HUMAR	P43475 escherichia	246	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
174	75.0	202	1	YH76_HUMAR	P43475 escherichia	247	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
175	75.0	203	1	YH76_HUMAR	P43475 escherichia	248	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
176	75.0	207	1	YH76_HUMAR	P43475 escherichia	249	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
177	75.0	207	1	YH76_HUMAR	P43475 escherichia	250	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
178	75.0	208	1	YH76_HUMAR	P43475 escherichia	251	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus
179	75.0	208	1	YH76_HUMAR	P43475 escherichia	252	24	75.0	237	1	YH76_HUMAR	G94122 baculovirus

252	24	75.0	320	1	FLAI_TREHY	P26520	carpenteria	126	24	75.0	407	1	ENC_SALTY	P26479	salmonella
253	24	75.0	320	1	TRAB_ECOLI	P09625	escherichia	127	24	75.0	410	1	TRIP_TREHY	P29129	pseudotub
254	24	75.0	320	1	YIH7_YEAST	P40508	saccharomye	128	24	75.0	410	1	YAG2_BIFID	P06559	bacterioph
255	24	75.0	322	1	CHIC_LYCIS	Q05038	lysozyme	129	24	75.0	412	1	YAG7_SCHIF	Q06271	schistosom
256	24	75.0	322	1	GC6_FAT	P16261	rattus norv	130	24	75.0	413	1	EX1_P22AI	P07240	lactococci
257	24	75.0	323	1	YECB_ECOLI	P76482	escherichia	131	24	75.0	416	1	TPXL_RHIF	F42726	rhizobium
258	24	75.0	323	1	CHIC2_TGAC	P24091	avoxiana	132	24	75.0	416	1	TR75_W258	Q91114	mus musculu
259	24	75.0	324	1	CHUI_SOLIU	P05315	solanum tub	133	24	75.0	417	1	Q6YA_DROME	P02982	drosophila
260	24	75.0	324	1	CHUI_TGAC	P06252	biobolus	134	24	75.0	421	1	TRP2_STRIP	Q04177	streptococ
261	24	75.0	325	1	CHUI_TGAC	Q01982	tes latus	135	24	75.0	421	1	V32_HUMAN	P04660	bacterioph
262	24	75.0	326	1	CHUI_TGAC	P75435	myxoglasma	136	24	75.0	423	1	TRP4_HUMAN	Q06568	homo sapien
263	24	75.0	326	1	TRSD_MYCPN	Q05061	homo sapien	137	24	75.0	423	1	Q6EL_RAC3U	P14792	bacillus su
264	24	75.0	326	1	Y272_HUMAN	P07197	spirochaeta	138	24	75.0	423	1	ACFA_BACCH	P14940	bacillus su
265	24	75.0	326	1	Y343_SVHY4	Q06553	homo sapien	139	24	75.0	427	1	PURE_GABER	Q04412	caulobacter
266	24	75.0	326	1	Y291_PAI60	P16263	homo sapien	140	24	75.0	428	1	ACFA_MF310	P07752	mycobacteri
267	24	75.0	326	1	CDG_HUMAN	P16172	homo sapien	141	24	75.0	428	1	SY25_TGAC	P05689	staphylococ
268	24	75.0	326	1	SPG3_PAPPI	Q01112	chlamydia m	142	24	75.0	431	1	AF7A_ACHAE	P07751	apicomplex
269	24	75.0	326	1	HLM1_CHLMP	P29959	nicotiana t	143	24	75.0	432	1	EX46_HUMAN	P14929	homo sapien
270	24	75.0	334	1	CH13_TOBAC	Q82374	escherichia	144	24	75.0	433	1	EX46_MCHUB	P21558	mus musculu
271	24	75.0	334	1	YELV_F0057	P76342	escherichia	145	24	75.0	433	1	EX46_BAI	P15129	rattus norv
272	24	75.0	334	1	YFIV_F0021	Q82374	escherichia	146	24	75.0	433	1	TRAI_A3K10	P54917	autobacteri
273	24	75.0	334	1	YEDY_SALTY	Q82374	salmonella	147	24	75.0	433	1	ACFA_SAG11	Q04066	salmonella
274	24	75.0	334	1	ASB1_HUMAN	Q04066	chlamydia t	148	24	75.0	434	1	TRX7_DROME	Q04066	drosophila
275	24	75.0	335	1	HPH1_CHITF	Q02000	lactococci	149	24	75.0	439	1	FRY4_HUMAN	P04066	homo sapien
276	24	75.0	335	1	TRPD_LACLA	Q04066	homo sapien	150	24	75.0	447	1	FRY4_HUMAN	P04066	homo sapien
277	24	75.0	336	1	PSIA_YEAST	Q04066	homo sapien	151	24	75.0	447	1	FRY4_HUMAN	P04066	homo sapien
278	24	75.0	337	1	RI92_HSV23	P02174	herpes simp	152	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
279	24	75.0	337	1	Y413_PSFAP	Q04066	pseudomonas	153	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
280	24	75.0	337	1	YK01_PACSC	Q04066	homo sapien	154	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
281	24	75.0	337	1	YK01_PACSC	Q04066	homo sapien	155	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
282	24	75.0	344	1	HEMA_TAHAF	P02174	herpes simp	156	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
283	24	75.0	344	1	HEMA_TAHAF	P02174	herpes simp	157	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
284	24	75.0	344	1	HEMA_TAHAF	P02174	herpes simp	158	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
285	24	75.0	344	1	HEMA_TAHAF	P02174	herpes simp	159	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
286	24	75.0	346	1	H10M_CHICK	Q04066	homo sapien	160	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
287	24	75.0	349	1	PGCA_ACOV1	P02174	herpes simp	161	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
288	24	75.0	352	1	APG1_NUTEL	P02174	herpes simp	162	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
289	24	75.0	352	1	APG1_NUTEL	P02174	herpes simp	163	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
290	24	75.0	360	1	PPVA_PSEUD	P02174	herpes simp	164	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
291	24	75.0	361	1	SEPC_PASMO	P02174	herpes simp	165	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
292	24	75.0	361	1	SEPC_PASMO	P02174	herpes simp	166	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
293	24	75.0	361	1	SEPC_PASMO	P02174	herpes simp	167	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
294	24	75.0	361	1	SEPC_PASMO	P02174	herpes simp	168	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
295	24	75.0	362	1	SEPC_PASMO	P02174	herpes simp	169	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
296	24	75.0	362	1	SEPC_PASMO	P02174	herpes simp	170	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
297	24	75.0	363	1	AP13_MHUCP	P02174	herpes simp	171	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
298	24	75.0	363	1	AP13_MHUCP	P02174	herpes simp	172	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
299	24	75.0	364	1	TRSD_MYCPN	P02174	herpes simp	173	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
300	24	75.0	364	1	TRSD_MYCPN	P02174	herpes simp	174	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
301	24	75.0	366	1	MX11_MOUSE	Q04066	homo sapien	175	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
302	24	75.0	366	1	MX11_MOUSE	Q04066	homo sapien	176	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
303	24	75.0	366	1	MX11_MOUSE	Q04066	homo sapien	177	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
304	24	75.0	367	1	MX11_MOUSE	Q04066	homo sapien	178	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
305	24	75.0	367	1	MX11_MOUSE	Q04066	homo sapien	179	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
306	24	75.0	367	1	MX11_MOUSE	Q04066	homo sapien	180	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
307	24	75.0	367	1	MX11_MOUSE	Q04066	homo sapien	181	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
308	24	75.0	367	1	MX11_MOUSE	Q04066	homo sapien	182	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
309	24	75.0	370	1	Y413_HIFLY	P02174	herpes simp	183	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
310	24	75.0	370	1	Y413_HIFLY	P02174	herpes simp	184	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
311	24	75.0	372	1	MX11_HUMAN	P02174	herpes simp	185	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
312	24	75.0	372	1	MX11_HUMAN	P02174	herpes simp	186	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
313	24	75.0	372	1	MX11_HUMAN	P02174	herpes simp	187	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
314	24	75.0	377	1	POQ_EKWHK	Q04066	homo sapien	188	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
315	24	75.0	380	1	POQ_EKWHK	Q04066	homo sapien	189	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
316	24	75.0	384	1	POQ_EKWHK	Q04066	homo sapien	190	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
317	24	75.0	385	1	BLAR_XENLA	P02174	herpes simp	191	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
318	24	75.0	385	1	BLAR_XENLA	P02174	herpes simp	192	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
319	24	75.0	389	1	LE2_APOEC	P02174	herpes simp	193	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
320	24	75.0	396	1	APG1_NUTEL	P02174	herpes simp	194	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
321	24	75.0	401	1	GLTS_ECOLI	P02174	herpes simp	195	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
322	24	75.0	402	1	DCX_HUMAN	P02174	herpes simp	196	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
323	24	75.0	402	1	DCX_HUMAN	P02174	herpes simp	197	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
324	24	75.0	404	1	ECOL_MOCSE	P02174	herpes simp	198	24	75.0	449	1	RI92_HSV23	P02174	herpes simp
325	24	75.0	405	1	ENTM_BACIF	P02174	herpes simp	199	24	75.0	449	1	RI92_HSV23	P02174	herpes simp

399	24	75.0	574	1	HEAL_MOUSE	Q66758 mus musculus	472	24	75.0	675	1	HEAL_MOUSE	Q47374 acanthamoeba
400	24	75.0	538	1	HEL_HELA	P01125 meleagris g	473	24	75.0	706	1	HEAL_MOUSE	Q06110 homo sapien
401	24	75.0	548	1	HISE_HUMAN	P02961 homo sapien	474	24	75.0	707	1	HEAL_MOUSE	Q06113 homo sapien
402	24	75.0	549	1	HIRE_HUMAN	P02961 homo sapien	475	24	75.0	710	1	HEAL_MOUSE	P26827 thetinomate
403	24	75.0	550	1	SYM_GHLM	Q06107 chlamydia m	476	24	75.0	719	1	HEAL_MOUSE	Q01565 chlamydia m
404	24	75.0	550	1	SYM_GHLM	Q06107 chlamydia m	477	24	75.0	711	1	HEAL_MOUSE	P41797 bacillus st
405	24	75.0	551	1	HASE_XENLA	P57452 xenopus lae	478	24	75.0	721	1	HEAL_MOUSE	P46044 saccharomye
406	24	75.0	551	1	TYPE_HUMAN	P56180 homo sapien	479	24	75.0	711	1	HEAL_MOUSE	Q06905 saccharomye
407	24	75.0	551	1	Y028_HUMAN	Q06186 bacteriophage	480	24	75.0	712	1	HEAL_MOUSE	Q06905 saccharomye
408	24	75.0	552	1	HAS2_BOVIN	Q07711 bos taurus	481	24	75.0	713	1	HEAL_MOUSE	P47000 crotalaria chi
409	24	75.0	552	1	HAS2_CHICK	Q07424 gallus galli	482	24	75.0	719	1	HEAL_MOUSE	P47000 crotalaria chi
410	24	75.0	552	1	HAS2_HUMAN	Q02819 homo sapien	483	24	75.0	720	1	HEAL_MOUSE	Q06574 homo sapien
411	24	75.0	552	1	HAS2_MOUSE	P02312 mus musculus	484	24	75.0	729	1	HEAL_MOUSE	Q06574 homo sapien
412	24	75.0	552	1	HAS2_PAT	Q05776 rattus norv	485	24	75.0	729	1	HEAL_MOUSE	Q06574 homo sapien
413	24	75.0	553	1	HAS3_HUMAN	Q08219 homo sapien	486	24	75.0	724	1	HEAL_MOUSE	P11971 pseudomona
414	24	75.0	554	1	HAS3_MOUSE	Q08659 mus musculus	487	24	75.0	731	1	HEAL_MOUSE	Q08409 treponema p
415	24	75.0	557	1	A032_SHEEP	P45457 glycyline max	488	24	75.0	749	1	HEAL_MOUSE	Q015075 homo sapien
416	24	75.0	559	1	A031_SHEEP	P45456 glycyline max	489	24	75.0	743	1	HEAL_MOUSE	P27069 thetinomate
417	24	75.0	565	1	HEMA_IAGHA	P13101 influenza a	490	24	75.0	756	1	HEAL_MOUSE	Q01106 mus musculus
418	24	75.0	565	1	HEMA_IATKO	P16060 influenza a	491	24	75.0	759	1	HEAL_MOUSE	P42784 saccharomye
419	24	75.0	565	1	HEMA_IATIL	P02454 influenza a	492	24	75.0	761	1	HEAL_MOUSE	Q08762 mus musculus
420	24	75.0	565	1	HEMA_IATIL	P18159 bacillus su	493	24	75.0	773	1	HEAL_MOUSE	P47354 mycobacteri
421	24	75.0	566	1	HEMA_IATIL	P25562 influenza a	494	24	75.0	775	1	HEAL_MOUSE	Q06713 mycobacteri
422	24	75.0	566	1	HEMA_IATIL	P13103 influenza a	495	24	75.0	775	1	HEAL_MOUSE	P17440 turnip crin
423	24	75.0	566	1	HEMA_IATIL	P18875 influenza a	496	24	75.0	778	1	HEAL_MOUSE	P47354 mycobacteri
424	24	75.0	566	1	HEMA_IATIL	P18876 influenza a	497	24	75.0	778	1	HEAL_MOUSE	P22763 escherichia
425	24	75.0	566	1	HEMA_IATIL	P13102 influenza a	498	24	75.0	779	1	HEAL_MOUSE	Q07416 thetinomate
426	24	75.0	566	1	HEMA_IATIL	P02452 influenza a	499	24	75.0	780	1	HEAL_MOUSE	Q0655 thetinomate
427	24	75.0	566	1	HEMA_IATIL	P03448 influenza a	500	24	75.0	781	1	HEAL_MOUSE	Q07416 thetinomate
428	24	75.0	566	1	HEMA_IATIL	P03453 influenza a	501	24	75.0	783	1	HEAL_MOUSE	Q07416 thetinomate
429	24	75.0	566	1	HEMA_IATIL	P25140 influenza a	502	24	75.0	783	1	HEAL_MOUSE	Q07416 thetinomate
430	24	75.0	566	1	HEMA_IATIL	P03455 influenza a	503	24	75.0	784	1	HEAL_MOUSE	Q07416 thetinomate
431	24	75.0	566	1	HEMA_IATIL	P04283 borrelia bu	504	24	75.0	785	1	HEAL_MOUSE	Q07416 thetinomate
432	24	75.0	571	1	HEMA_IATIL	Q02698 brassica ca	505	24	75.0	785	1	HEAL_MOUSE	P05928 sulfobactam
433	24	75.0	574	1	HEMA_IATIL	Q08266 dendrobium	506	24	75.0	786	1	HEAL_MOUSE	Q06113 sulfobactam
434	24	75.0	575	1	HEMA_IATIL	P45273 lycopersicon	507	24	75.0	786	1	HEAL_MOUSE	Q06113 sulfobactam
435	24	75.0	575	1	HEMA_IATIL	P58131 astasia lon	508	24	75.0	817	1	HEAL_MOUSE	Q06113 sulfobactam
436	24	75.0	576	1	HEMA_IATIL	P02927 arabisidopsis	509	24	75.0	824	1	HEAL_MOUSE	Q06113 sulfobactam
437	24	75.0	576	1	HEMA_IATIL	P25248 brassica na	510	24	75.0	830	1	HEAL_MOUSE	Q06113 sulfobactam
438	24	75.0	576	1	HEMA_IATIL	P03110 escherichia	511	24	75.0	832	1	HEAL_MOUSE	Q06113 sulfobactam
439	24	75.0	576	1	HEMA_IATIL	P49296 cucumis sat	512	24	75.0	832	1	HEAL_MOUSE	Q06113 sulfobactam
440	24	75.0	576	1	HEMA_IATIL	P17069 gossypium h	513	24	75.0	836	1	HEAL_MOUSE	Q06113 sulfobactam
441	24	75.0	576	1	HEMA_IATIL	P45479 ricinus com	514	24	75.0	842	1	HEAL_MOUSE	Q06113 sulfobactam
442	24	75.0	577	1	HEMA_IATIL	P2884 ricinus com	515	24	75.0	844	1	HEAL_MOUSE	Q06113 sulfobactam
443	24	75.0	577	1	HEMA_IATIL	P12554 newcastle d	516	24	75.0	847	1	HEAL_MOUSE	Q06113 sulfobactam
444	24	75.0	577	1	HEMA_IATIL	P12573 newcastle d	517	24	75.0	856	1	HEAL_MOUSE	Q06113 sulfobactam
445	24	75.0	577	1	HEMA_IATIL	P12554 newcastle d	518	24	75.0	864	1	HEAL_MOUSE	Q06113 sulfobactam
446	24	75.0	578	1	HEMA_IATIL	P1071 escherichia	519	24	75.0	867	1	HEAL_MOUSE	Q06113 sulfobactam
447	24	75.0	578	1	HEMA_IATIL	Q02839 homo sapien	520	24	75.0	906	1	HEAL_MOUSE	Q06113 sulfobactam
448	24	75.0	578	1	HEMA_IATIL	Q04975 salmoneilla	521	24	75.0	917	1	HEAL_MOUSE	Q06113 sulfobactam
449	24	75.0	580	1	HEMA_IATIL	P1097 salmoneilla	522	24	75.0	925	1	HEAL_MOUSE	Q06113 sulfobactam
450	24	75.0	583	1	HEMA_IATIL	Q01647 mus musculus	523	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
451	24	75.0	583	1	HEMA_IATIL	Q01647 mus musculus	524	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
452	24	75.0	583	1	HEMA_IATIL	Q01647 mus musculus	525	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
453	24	75.0	584	1	HEMA_IATIL	Q01647 mus musculus	526	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
454	24	75.0	584	1	HEMA_IATIL	Q01647 mus musculus	527	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
455	24	75.0	584	1	HEMA_IATIL	Q01647 mus musculus	528	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
456	24	75.0	588	1	HEMA_IATIL	Q01647 mus musculus	529	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
457	24	75.0	595	1	HEMA_IATIL	Q01647 mus musculus	530	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
458	24	75.0	598	1	HEMA_IATIL	Q01647 mus musculus	531	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
459	24	75.0	604	1	HEMA_IATIL	Q01647 mus musculus	532	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
460	24	75.0	609	1	HEMA_IATIL	Q01647 mus musculus	533	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
461	24	75.0	609	1	HEMA_IATIL	Q01647 mus musculus	534	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
462	24	75.0	616	1	HEMA_IATIL	Q01647 mus musculus	535	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
463	24	75.0	616	1	HEMA_IATIL	Q01647 mus musculus	536	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
464	24	75.0	616	1	HEMA_IATIL	Q01647 mus musculus	537	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
465	24	75.0	617	1	HEMA_IATIL	Q01647 mus musculus	538	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
466	24	75.0	621	1	HEMA_IATIL	Q01647 mus musculus	539	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
467	24	75.0	628	1	HEMA_IATIL	Q01647 mus musculus	540	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
468	24	75.0	639	1	HEMA_IATIL	Q01647 mus musculus	541	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
469	24	75.0	663	1	HEMA_IATIL	Q01647 mus musculus	542	24	75.0	933	1	HEAL_MOUSE	Q06113 sulfobactam
470	24	75.0	672	1	HEMA_IATIL	Q01647 mus musculus	543	24	75.0	1005	1	HEAL_MOUSE	Q06113 sulfobactam
471	24	75.0	675	1	HEMA_IATIL	Q01647 mus musculus	544	24	75.0	1006	1	HEAL_MOUSE	Q06113 sulfobactam

545	24	75.0	1009	1	AMBN_HUMAN	G11008	heliophilus	618	23	71.9	314	1	KEFE_ECOLI	09046	sulfobus
546	24	75.0	1009	1	M2P2_HUMAN	C92405	homo sapiens	619	23	71.9	329	1	Y155_HUMAN	04479	ureaplasma
547	24	75.0	1013	1	M2B1_MOUSE	C99159	mus musculus	620	23	71.9	329	1	KEFE_ECOLI	09046	sulfobus
548	24	75.0	1013	1	PRM1_DROME	R82295	triosophila	621	23	71.9	336	1	KAD1_HUMAN	04479	ureaplasma
549	24	75.0	1014	1	EPB4_MOUSE	008644	mus musculus	622	23	71.9	336	1	KEFE_ECOLI	09046	sulfobus
550	24	75.0	1019	1	Y3B4_TPTFA	C82324	triosophila	623	23	71.9	354	1	Q336_HUMAN	04479	ureaplasma
551	24	75.0	1063	1	PRPH_CAPIU	C82373	triosophila	624	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
552	24	75.0	1072	1	PRPH_APATH	R59545	triosophila	625	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
553	24	75.0	1077	1	YBK1_YEAST	R39167	saccharomyces	626	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
554	24	75.0	1077	1	PRPH_SINAL	P45818	homo sapiens	627	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
555	24	75.0	1084	1	PRPH_CPMV	C95025	guinea pig	628	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
556	24	75.0	1088	1	TSU1_YEAST	R38427	saccharomyces	629	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
557	24	75.0	1124	1	PRVA_LAIISA	R38427	saccharomyces	630	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
558	24	75.0	1124	1	PRVA_PFA	R15201	gusum sativ	631	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
559	24	75.0	1125	1	PRVA_PCFM	R15201	gusum sativ	632	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
560	24	75.0	1142	1	ENAM_FIG	C97034	epididymis	633	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
561	24	75.0	1147	1	AC15_HUMAN	R38427	saccharomyces	634	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
562	24	75.0	1148	1	AT1A_APAHE	R38427	saccharomyces	635	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
563	24	75.0	1181	1	CIAP_PACFI	C97034	epididymis	636	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
564	24	75.0	1196	1	AMVH_PAEPO	P21543	paenibacillus	637	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
565	24	75.0	1241	1	AT14_HUMAN	R38427	saccharomyces	638	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
566	24	75.0	1318	1	VE14_EBV	R38427	saccharomyces	639	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
567	24	75.0	1321	1	AB11_MOUSE	C97034	epididymis	640	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
568	24	75.0	1321	1	AB11_MOUSE	C97034	epididymis	641	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
569	24	75.0	1331	1	YDH_POVIN	R60157	bos taurus	642	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
570	24	75.0	1332	1	XDH_HUMAN	P47989	homo sapiens	643	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
571	24	75.0	1245	1	YH90_YEAST	R38427	saccharomyces	644	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
572	24	75.0	1252	1	XDH_GALV1	R38427	saccharomyces	645	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
573	24	75.0	1255	1	Y246_BSV11	C97034	epididymis	646	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
574	24	75.0	1258	1	XDH_CHICK	P47990	gallus gall	647	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
575	24	75.0	1349	1	HE_F1_SCHFC	C97034	epididymis	648	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
576	24	75.0	1372	1	CAN1_PAT	R60157	bos taurus	649	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
577	24	75.0	1443	1	NEO1_CHICK	R60157	bos taurus	650	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
578	24	75.0	1447	1	YH90_YEAST	R38427	saccharomyces	651	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
579	24	75.0	1501	1	CD93_CANAL	C97034	epididymis	652	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
580	24	75.0	1511	1	PD95_YEAST	R38427	saccharomyces	653	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
581	24	75.0	1515	1	CI1R_ACEFP	C97034	epididymis	654	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
582	24	75.0	1521	1	EMF5_GAEEL	R38427	saccharomyces	655	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
583	24	75.0	1523	1	DP01_THPFM	P47990	gallus gall	656	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
584	24	75.0	1529	1	PC9F_YEAST	R38427	saccharomyces	657	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
585	24	75.0	1584	1	XJ90_YEAST	P47170	saccharomyces	658	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
586	24	75.0	1584	1	XJ90_YEAST	P47170	saccharomyces	659	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
587	24	75.0	1648	1	YJ90_YEAST	P47170	saccharomyces	660	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
588	24	75.0	1671	1	DP01_THPFM	P47990	gallus gall	661	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
589	24	75.0	1746	1	TENA_FIG	C97034	epididymis	662	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
590	24	75.0	1750	1	Y872_METJA	C97034	epididymis	663	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
591	24	75.0	1808	1	TENA_CHICK	R60157	bos taurus	664	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
592	24	75.0	1809	1	PM1_MOUSE	C97034	epididymis	665	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
593	24	75.0	1857	1	Y282_YEAST	R38427	saccharomyces	666	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
594	24	75.0	1812	1	RE1A_TPCFM	C97034	epididymis	667	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
595	24	75.0	1831	1	RE1A_TPCFM	C97034	epididymis	668	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
596	24	75.0	1831	1	PRF1_MARVP	R38427	saccharomyces	669	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
597	24	75.0	1747	1	CAF_DROME	R55824	triosophila	670	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
598	24	75.0	1756	1	THV1_MOUSE	C97034	epididymis	671	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
599	24	75.0	1768	1	THV1_MOUSE	C97034	epididymis	672	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
600	24	75.0	1806	1	TM22_MOUSE	C97034	epididymis	673	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
601	24	75.0	1810	1	TM22_MOUSE	C97034	epididymis	674	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
602	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	675	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
603	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	676	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
604	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	677	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
605	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	678	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
606	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	679	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
607	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	680	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
608	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	681	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
609	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	682	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
610	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	683	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
611	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	684	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
612	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	685	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
613	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	686	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
614	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	687	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
615	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	688	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
616	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	689	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma
617	24	75.0	1843	1	Y307_GAEEL	R38427	saccharomyces	690	23	71.9	370	1	Y359_HUMAN	04479	ureaplasma

847	22	68.9	511	1	LYN_MOUSE	Q25911 mus musculus	917	22	68.8	1224	1	SL160_YEAST	P06165 saccharomyces
848	22	68.9	511	1	LYN_RAT	Q02914 rattus norvegicus	911	22	68.8	1227	1	FLUX_CAMEL	P44466 camorhabdalis
849	22	68.9	514	1	MA3_CAMEL	Q19969 camorhabdalis	912	22	68.8	1230	1	SL160_YEAST	P06165 saccharomyces
850	22	68.8	524	1	YV11_CAMEL	P25012 camorhabdalis	913	22	68.8	1233	1	SL160_YEAST	P06165 saccharomyces
851	22	68.8	531	1	YV20_MOUSE	Q09786 schistosoma	914	22	68.8	1236	1	YV18_MOUSE	P21499 schistosoma
852	22	68.8	535	1	YV20_MOUSE	Q09786 schistosoma	915	22	68.8	1239	1	YV18_MOUSE	P21499 schistosoma
853	22	68.8	539	1	YV20_MOUSE	Q09786 schistosoma	916	22	68.8	1242	1	YV18_MOUSE	P21499 schistosoma
854	22	68.8	547	1	PKS1_BACCU	P40806 bacillus subtilis	917	22	68.8	1245	1	YV18_MOUSE	P21499 schistosoma
855	22	68.9	558	1	KS01_FOULI	Q02961 escherichia	918	22	68.8	1248	1	YV18_MOUSE	P21499 schistosoma
856	22	68.9	558	1	KS01_FOULI	P42217 escherichia	919	22	68.8	1251	1	YV18_MOUSE	P21499 schistosoma
857	22	68.9	574	1	YV18_MOUSE	P42217 escherichia	920	22	68.8	1254	1	YV18_MOUSE	P21499 schistosoma
858	22	68.8	569	1	YV18_MOUSE	P42217 escherichia	921	22	68.8	1257	1	YV18_MOUSE	P21499 schistosoma
859	22	68.8	579	1	YV18_MOUSE	Q58128 methanobrevibacter	922	22	68.8	1260	1	YV18_MOUSE	P21499 schistosoma
860	22	68.8	579	1	YV18_MOUSE	Q58128 methanobrevibacter	923	22	68.8	1263	1	YV18_MOUSE	P21499 schistosoma
861	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	924	22	68.8	1266	1	YV18_MOUSE	P21499 schistosoma
862	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	925	22	68.8	1269	1	YV18_MOUSE	P21499 schistosoma
863	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	926	22	68.8	1272	1	YV18_MOUSE	P21499 schistosoma
864	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	927	22	68.8	1275	1	YV18_MOUSE	P21499 schistosoma
865	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	928	22	68.8	1278	1	YV18_MOUSE	P21499 schistosoma
866	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	929	22	68.8	1281	1	YV18_MOUSE	P21499 schistosoma
867	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	930	22	68.8	1284	1	YV18_MOUSE	P21499 schistosoma
868	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	931	22	68.8	1287	1	YV18_MOUSE	P21499 schistosoma
869	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	932	22	68.8	1290	1	YV18_MOUSE	P21499 schistosoma
870	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	933	22	68.8	1293	1	YV18_MOUSE	P21499 schistosoma
871	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	934	22	68.8	1296	1	YV18_MOUSE	P21499 schistosoma
872	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	935	22	68.8	1299	1	YV18_MOUSE	P21499 schistosoma
873	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	936	22	68.8	1302	1	YV18_MOUSE	P21499 schistosoma
874	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	937	22	68.8	1305	1	YV18_MOUSE	P21499 schistosoma
875	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	938	22	68.8	1308	1	YV18_MOUSE	P21499 schistosoma
876	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	939	22	68.8	1311	1	YV18_MOUSE	P21499 schistosoma
877	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	940	22	68.8	1314	1	YV18_MOUSE	P21499 schistosoma
878	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	941	22	68.8	1317	1	YV18_MOUSE	P21499 schistosoma
879	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	942	22	68.8	1320	1	YV18_MOUSE	P21499 schistosoma
880	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	943	22	68.8	1323	1	YV18_MOUSE	P21499 schistosoma
881	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	944	22	68.8	1326	1	YV18_MOUSE	P21499 schistosoma
882	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	945	22	68.8	1329	1	YV18_MOUSE	P21499 schistosoma
883	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	946	22	68.8	1332	1	YV18_MOUSE	P21499 schistosoma
884	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	947	22	68.8	1335	1	YV18_MOUSE	P21499 schistosoma
885	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	948	22	68.8	1338	1	YV18_MOUSE	P21499 schistosoma
886	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	949	22	68.8	1341	1	YV18_MOUSE	P21499 schistosoma
887	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	950	22	68.8	1344	1	YV18_MOUSE	P21499 schistosoma
888	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	951	22	68.8	1347	1	YV18_MOUSE	P21499 schistosoma
889	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	952	22	68.8	1350	1	YV18_MOUSE	P21499 schistosoma
890	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	953	22	68.8	1353	1	YV18_MOUSE	P21499 schistosoma
891	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	954	22	68.8	1356	1	YV18_MOUSE	P21499 schistosoma
892	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	955	22	68.8	1359	1	YV18_MOUSE	P21499 schistosoma
893	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	956	22	68.8	1362	1	YV18_MOUSE	P21499 schistosoma
894	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	957	22	68.8	1365	1	YV18_MOUSE	P21499 schistosoma
895	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	958	22	68.8	1368	1	YV18_MOUSE	P21499 schistosoma
896	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	959	22	68.8	1371	1	YV18_MOUSE	P21499 schistosoma
897	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	960	22	68.8	1374	1	YV18_MOUSE	P21499 schistosoma
898	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	961	22	68.8	1377	1	YV18_MOUSE	P21499 schistosoma
899	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	962	22	68.8	1380	1	YV18_MOUSE	P21499 schistosoma
900	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	963	22	68.8	1383	1	YV18_MOUSE	P21499 schistosoma
901	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	964	22	68.8	1386	1	YV18_MOUSE	P21499 schistosoma
902	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	965	22	68.8	1389	1	YV18_MOUSE	P21499 schistosoma
903	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	966	22	68.8	1392	1	YV18_MOUSE	P21499 schistosoma
904	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	967	22	68.8	1395	1	YV18_MOUSE	P21499 schistosoma
905	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	968	22	68.8	1398	1	YV18_MOUSE	P21499 schistosoma
906	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	969	22	68.8	1401	1	YV18_MOUSE	P21499 schistosoma
907	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	970	22	68.8	1404	1	YV18_MOUSE	P21499 schistosoma
908	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	971	22	68.8	1407	1	YV18_MOUSE	P21499 schistosoma
909	22	68.8	583	1	YV18_MOUSE	Q58128 methanobrevibacter	972	22	68.8	1410	1	YV18_MOUSE	P21499 schistosoma

983 21 65.6 126 1 ACHE1_BOZAI
984 21 65.6 126 1 YP61_XYLFA
985 21 65.6 128 1 AR21_ENTHI
986 21 65.6 129 1 KAP1_IACSU
987 21 65.6 132 1 C563_XYACA
988 21 65.6 132 1 EAT3_MOSU
989 21 65.6 144 1 RE15_HUMAN
990 21 65.6 149 1 MAB1_SCHJA
991 21 65.6 149 1 MAB1_SCHJA
992 21 65.6 149 1 ZG29_XENLA
993 21 65.6 142 1 CYPR1_EGCVI
994 21 65.6 143 1 R135_MOTVA
995 21 65.6 145 1 YJAR_SALIV
996 21 65.6 146 1 HARG_VITSI
997 21 65.6 146 1 RPR1_YEAST
998 21 65.6 147 1 YJAR_EGCVI
999 21 65.6 149 1 RL9_HAEIN
1000 21 65.6 149 1 RL9_PASMI

ALIGNMENTS

RESULT 1
MIR3_MOUSE STANDARD: PR1: 121 AA.
AC G42210;
DT 16-OCT-2001 (Ref.: 40, Created)
DT 16-OCT-2001 (Ref.: 40, Last sequence update)
DT 16-OCT-2001 (Ref.: 40, Last annotation update)
DE Myotubularin-related protein 3 (Fragment).
GN MIR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=100960;
RN 111
RP MEDLINE 98409499; PubMed 9746772;
RA Laporte J., Blondeau F., Bu-Bello A., Tentler D., Kretz C., Dahl N.,
RA Model J.-L.;
RI "Characterization of the myotubularin dual specificity phosphatase
RI gene family from yeast to human."
RL Hum. Mol. Genet. 7:1703-1712(1998).
CC -1- FUNCTION: NOT KNOWN. COULD BE A TYROSINE-PROSPHATASE.
CC -1- SIMILARITY: PUTATIVE TO THE MYOTUBULARIN-1-PT FAMILY.
CC
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CC
EMBL: AF074881; AA080003.1;
DR InterPro: IPR000387; TYR-phosphatase.
DR PROSITE: PS00484; TYR-PROSPHATASE_1; PARTIAL
DR PROSITE: PS00056; TYR-PROSPHATASE_2; PARTIAL.
KW Hydrolase.
FT NON_TER 1 1
SQ SEQUENCE 121 AA: 14292 MW: 097A0749-ABAB9B CACCA,
Query Match 94.8%; Score 30; DB 1; Length 121;
Best Local Similarity 100.0%; Pref. No. 6.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
CY 3 GYRN 7
DB 105 GYRN 109
RESULT 2

HPTL_MYCE
ID HPTL_MYCE STANDARD: PR1: 175 AA.
AC P47696;
DT 01 FEB 1996 (Ref.: 33, Created)
DT 01 FEB 1996 (Ref.: 33, Last sequence update)
DT 15 JUN 2002 (Ref.: 41, Last annotation update)
DE Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)
DE (HGPRTase).
DR HPT OR M458.
GN Mycoplasma genitalium.
OS Bacteria; Firmicutes; Mollicutes; Mycoplasmales; Mycoplasma.
OX NCBI_taxid=2047;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 35030 / G-37;
EX MEDLINE 96026446; PubMed 7569993;
FA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
FA Fleischman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
FA Fritchman J.L., Weidman J.F., Small K.V., Sandusky C.A., Fritchman J.M.,
RA Rayon E.T., Osterback I.K., Sankak D.M., Phillips C.A., Patrick J.M.,
RA Tomb J.F., Dougherty B.A., Bolt K.F., Hu P.-C., Lister T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RI "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN 121
RP SEQUENCE OF 9-98 FROM N.A.
RC STRAIN ATCC 35030 / G-37;
EX MEDLINE 94075240; PubMed 8253680;
FA Peterson S.N., Hu P.-C., Bolt K.F., Hutchison C.A. III;
RI "A survey of the Mycoplasma genitalium genome by using random
RI sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- CATALYTIC ACTIVITY: IMP + PYROPHOSPHATE -> HYPOXANTHINE +
CC 5-PYRISIBO-ALPHA-D-RIBOSE 1-PYRISIBO-ALPHA-D-RIBOSE
CC HYPOXANTHINE TO PRODUCE GMP.
CC
CC -1- PATHWAY: Purine salvage.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PPKIN/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC
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CC
EMBL: U49727; AA72478.1;
DR EMBL: 002193; AAD12474.1;
DR DSSP: P51900; IIRX.
DR TIGR: M458;
DR InterPro: IPR000836; PRTransferase.
DR InterPro: IPR002875; Pp/py-tp_transf.
DR Pfam: PF00156; PRibosyltranf_1.
DR TIGREMS: TIGR01203; HGPRTase; 1.
DR PROSITE: PS00104; PPR-PYR-PP-TRANSFER; 1.
KW Transferase, glycosyltransferase, Purine salvage, Mammalian
KW Complete proteome.
FT METAL 96 96 MAGNESIUM (BY SIMILARITY).
FT METAL 97 97 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 175 AA: 19759 MW: 9647332FFFF43BED CACCA;
Query Match 94.8%; Score 30; DB 1; Length 175;
Best Local Similarity 100.0%; Pref. No. 9.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
CY 3 GYRN 7
DB 159 GYRN 163
RESULT 3

```

HPRT_MYCPN
ID HPRT_MYCPN STANDARD: PRT: 175 AA.
AC P51119;
DI 01-NOV-1997 (Ref. 35, Created)
DI 01-NOV-1997 (Ref. 35, Last sequence update)
DI 15-JUN-2002 (Ref. 41, Last annotation update)
DE Hyperantigen-like phosphatidyltransferase (EC 2.3.1.3) (G3957)
DE (G3957ase).
GN HPT OR MPN672 OR MP170.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatidae; Mycoplasma.
OX NCBI_TaxID: 2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / 8129.
RX MEDLINE=97105985; PubMed=8948633;
RA Hammelreich P., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
PL Nucleic Acids Res. 24:4420-4449(1996)
CC -1- CATALYTIC ACTIVITY: IMP + PYRROPHOSPHATE -> HYDANTHINE +
CC 5-PYRROPHOSPHATE + D-RIBOSE 1-DIPHOSPHATE (GUANINE CAN REPLACE
CC HYDANTHINE TO PRODUCE GMP).
CC -1- PATHWAY: Purine salvage.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PURINE PYRROPHOSPHATE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
CC EMBL: AE006018; AAR95818.1; -
CC HSSP: P00492; 1IMP.
CC InterPro: IPR000846; PPRtransferase.
CC InterPro: IPR002475; PTPase_transf.
CC Pfam: P00156; Pribosyltransf.1.
CC TIGRfams: TIGR01203; HSPasease.1.
CC PROSITE: PS00103; PHF_PYP_PP_IPANSFFP; 1.
CC Transferrase, Glycosyltransferase, Phosphatase, Nucleoside, Nucleotide,
CC Complete proteome.
CC METAL 96 96 MAGNESIUM (BY SIMILARITY).
CC METAL 97 97 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 175 AA. 19620 MW. 25912AAID59854 CR524;
Query Match 91.8%; Score 30; DA 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QV 3 GPVFN 7
DB 159 GPVFN 163
RESULT 4
END_MYCTU
ID END_MYCTU STANDARD: PRT: 245 AA.
AC G59642;
DI 30-MAY-2000 (Ref. 39, Created)
DI 16-JUL-2001 (Ref. 40, Last sequence update)
DI 16-JUL-2001 (Ref. 40, Last annotation update)
DE Endonuclease III (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site)
DE lyase).
GN ERI OR ERI74C OR ERI74 OR M'W025.122C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID: 1773;

```

```

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=H37Rv;
RC MEDLINE=98295957; PubMed=9571240;
RA Cole S.L., Broese K., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Baker S.V., Eickbush J., Karp P., Barlow P., White O.,
RA Rhee K.K., Barton D., Brown D., Chillingworth J., Connor R.,
RA Davies K., Devlin K., Pettwell E., Gentles S., Hamlin N., Holroyd S.,
RA Hornby T., Jacobs K., Krogh A., McLean J., Meale S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rabinovitch M.A., Rogers J.,
RA Sanger H., Seak R., Skellern S., Squares S., Rogers K.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett R.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence";
RL Nature 393:537-543(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DC 1551 / GskKush;
RA Fleischmann R.L., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy K., Dodson K., Gwinn M.L., Haft D., Hickey E.,
RA Kolony J.E., Nelson W.C., Osoyan L.A., Smolke L., Tarr P., White A.,
RA Salzberg A., Venter L., Wilson R., Adams J., Adams M.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL Laboratory 1241(2001);
CC -1- FUNCTION: HAS BOTH AN ESTERASE AND A MYKININ-LIKE-ADENYLASE
CC ACTIVITY AND A DNA 5-GLUCOSYLASE ACTIVITY. INDICES DAMAGED DNA AT
CC CYTOSINES, THYMINE AND GUANINES. ACTS ON A DAMAGED STRAND, 5'
CC FROM THE DAMAGED SITE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: The C-5' bond 3' to the apurinic or
CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
CC leaving a 3' terminal unsaturated sugar and a product with a
CC terminal 5'-phosphate.
CC : CHARGE: NEG 4.8; 4.8 CLEVER WHICH IS NOT PROBABLY FOR THE
CC CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER
CC POSITIONING OF THE ENZYME ALONG THE DNA STRAND (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NTH/FAMLY FAMILY.
CC -----
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CC license@sib.ch).
CC -----
CC EMBL: AL023121; CAAT1996.1; AUT_INIT.
CC EMBL: AF507175; AAK48142.1; AUT_INIT.
CC HSSP: P20625; 2ABK.
CC TIGR: M13775; -
CC Tuberculin; R34674C; -
CC InterPro: IPR004035; EndoIII_FOL.
CC InterPro: IPR004036; EndoIII_HHR.
CC InterPro: IPR003265; Endo_3.
CC InterPro: IPR003651; Pcs_bind.
CC InterPro: IPR003583; HHR_1.
CC Pfam: PF00730; HHR-GH1; 1.
CC SMART: SM00478; ENDOac; 1.
CC SMART: SM00525; PES; 1.
CC SMART: SM00278; HHR1; 1.
CC TIGRfams: TIGR0.083; ntr; 1.
CC PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
CC PROSITE: PS01155; ENDONUCLEASE_III_2; 1.
KW Hydrolyase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair;
KW glycosylase; 1773; 1773; 1773; 1773; 1773; 1773; 1773; 1773; 1773; 1773;
IT METAL 196 196 189H SULFUR (4FE 4S) complete proteome.
FT METAL 205 205 189H SULFUR (4FE 4S) (BY SIMILARITY).
FT METAL 212 212 189H SULFUR (4FE 4S) (BY SIMILARITY).
FT METAL 214 214 189H SULFUR (4FE 4S) (BY SIMILARITY).
SQ SEQUENCE 245 AA. 27030 MW. 28601619400400 CR664;
Query Match 93.8%; Score 30; DA 1; Length 245;

```


DI 01-OCT-1992 (Rel. 27, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (tryptophanyl-trna synthetase (EC 6.1.1.2) (tryptophan: tRNA ligase)
 DF (TrpS).
 GN WAYS ON WPS
 OS Mus musculus (Mouse).
 OC Euryarchaea; Metazoa; Chordata; Vertebrata; Euteleostomi,
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
 EX MEDLINE 9019236; PubMed 733716;
 FA Pajot B., Sarger G., Bonnet J., Garnet M.;
 RT "An alternative splicing modifies the C-terminal end of tryptophanyl-
 trna synthetase in murine embryonic stem cells.";
 RL J. Mol. Biol. 247:559-563(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) -> AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: the short isoform is widely expressed, the
 CC long form is found only in embryonic stem cells.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
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 CC -----
 DR EMBL: X69656; CAA49347.1; 1;
 DE EMBL: X69657; CAA49348.1; 1;
 DR FIR: S31461; S31461.
 DR PIR: S31462; S31462.
 DR MGD: MGI:104630; WARS
 DR InterPro: IP000706; Trp.Trna-synt_lb
 DR InterPro: IP000738; WHEP-TRS.
 DR InterPro: IP000205; tRNA-synt_lb.
 DR InterPro: IP001412; tRNA-synt_1.
 DR Pfam: PF00458; WHEP-TRS; 1.
 DR Pfam: PF00579; tRNA-synt_lb; 1.
 DR PRINTS: PK01039; TRNASYNTHRP.
 DR TIGRFAMs: TIGR00233; TrpS; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE_I; 1.
 DR PROSITE: PS00762; WHEP-TRS; 1.
 FW Aminoacyl-tRNA synthetase; Protein biosynthesis, Ligation, ATP binding,
 KW Alternative splicing.
 FT DOMAIN 23 68
 FT SITE 168 177 WHEP-TRS.
 FT SITE 353 357 "HIGH" REGION.
 FT VARSPLIC 476 481 "KMSKS" REGION.
 SQ SEQUENCE 481 AA: 54292 MW: 805445208074152 CRG64;
 Query Match 93.88; Score 30; DB 1; Length 481;
 Best Local Similarity 100.00; Pred. Rel. 27.
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GYRN 7
 DI 1111
 DI 250 GYRN 254
 RESULT 8
 TYRO-MOUSE
 ID TYRO_MOUSE STANDARD; PFI: 533 AA.
 AC P11344;
 DI 01-JUL-1989 (Rel. 11, Created)
 DI 01-AUG-1990 (Rel. 15, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tyrosinase precursor (EC 1.14.16.1) (Monophenol monooxygenase)
 DE (Albino locus protein).
 GN TYR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 EX STRAIN DBA/2J; PubMed 3141000;
 FA Kuo B., Wajsborth M., Hall A.P., Ballantyne R., Resler D.;
 RT "Sequence analysis of mouse tyrosinase cDNA and the effect of
 melanotropin on its gene expression.";
 RL Biochem. Biophys. Res. Commun. 153:1301-1409(1988).
 CC [2]
 CC SEQUENCE FROM N.A.
 EX STRAIN-Himalayan;
 FA Kwon B.S., Balaban K., Chintamaneni C.;
 RT "Molecular basis of mouse Himalayan mutation.";
 RL Biochem. Biophys. Res. Commun. 161:252-260(1989).
 CC [3]
 CC SEQUENCE FROM N.A.
 EX MEDLINE 89030616; PubMed=3141148;
 FA Mueller G., Ruppert S., Schmid E., Schuetz G.;
 RT "Functional analysis of alternatively spliced tyrosinase gene
 transcripts.";
 RL EMBO J. 7:2723-2730(1988).
 CC [4]
 CC SEQUENCE FROM N.A.
 EX MEDLINE 90000000; PubMed=1444947;
 FA Terao M., Take H., Garattini E., Sartori D., Stader M., Mintz B.;
 RT "Isolation and characterization of variant cDNAs encoding mouse
 tyrosinase.";
 RL Biochem. Biophys. Res. Commun. 159:848-853(1989).
 CC [5]
 CC SEQUENCE FROM N.A.
 EX STRAIN=557B/60;
 FA Yamaoka H., Takeda H., Takeda T., Takeda A., Shinoda T.;
 RT "Isolation and sequencing of mouse tyrosinase cDNA.";
 RL Jpn. J. Genet. 62:271-274(1987).
 CC [6]
 CC SEQUENCE OF 1-273 FROM N.A.
 EX MEDLINE 9012094; PubMed=2517317;
 FA Yamaoka H., Takeda H., Takeda T., Takeda A., Takeda H.;
 RT "Melanin production in cultured albino melanocytes transfected with
 mouse tyrosinase cDNA.";
 RL Jpn. J. Genet. 64:121-135(1989).
 CC [7]
 CC VARIANT ALBINO.
 EX STRAIN-BALB/c;
 EX MEDLINE 9024949; PubMed 2110899;
 FA Takeda H., Takeda H., Takeda T., Takeda A., Takeda H.;
 RT "A point mutation in the tyrosinase gene of BALB/c albino mouse
 causes the cysteine residue substitution at position 85.";
 RL Jpn. J. Biochem. 139:455-461(1990).
 CC [8]
 CC VARIANT CHINCHILLA MICE.
 EX MEDLINE 90360993; PubMed=2118105;
 FA Boermann F., Ruppert S., Hummel E., Hoesch F.X., Mueller G.,
 FA Koether G., Schuetz G.;
 RT "Rescue of the albino phenotype by introduction of a functional
 tyrosinase gene into mice.";
 RL EMBO J. 9:2819-2825(1990).
 CC [9]
 CC FUNCTION: THIS IS A G-PCR CONTAINING KINASE THAT FUNCTIONS IN
 CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
 CC COMPOUNDS. CATALYZES THE RATE LIMITING CONVERSIONS OF TYROSINE TO
 CC DOPA, DOPA TO DOPA QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
 CC INDOLE-5,6-DOLINE.
 CC [10]
 CC CATALYTIC ACTIVITY: L-tyrosine + L-DOPA -> DOPA + L-DOPA

RP SEQUENCE FROM N.A.
 RX MEDLINE-96184849; PubMed-8604333;
 RA Li L., Peterson C., Leverski R.;
 RT "Sequence of the mouse XPC cDNA and genomic structure of the human
 RT XPC gene.";
 RL Nucleic Acids Res. 24:1026-1029(1996);
 RN [2];
 RP SEQUENCE OF 28-587 FROM N.A.
 RX STRAIN-129622;
 RA MEDLINE-95405469; PubMed-7675984;
 RA Sands A.T., Abuin A., Sanchez A., Conti C., Bradley A.;
 RT "High susceptibility to ultraviolet-induced carcinogenesis in mice
 RT lacking XPC.";
 RL Nature 377:162-165(1995);
 RN [1];
 CC [1-] FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
 CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE IN
 CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.
 CC [1-] SUBUNIT: HETERODIMER OF A 125 KDA SUBUNIT (P125) AND OF A
 CC 58 KDA SUBUNIT (P58).
 CC [1-] SUBCELLULAR LOCATION: Nuclear. (Probable).
 CC [1-] SIMILARITY: SOME, TO YEAST RAD4.
 CC -----
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 CC -----
 DR EMBL: U27398; AAC52500.1; .
 DR EMBL: U40006; AAA92720.1; .
 DR MGD: MGI:103557; Xpc
 DR InterPro: IPR004583; Rad4.
 DR TIGRfam: TIGR00605; rad4; 1.
 KW DNA repair; DNA-binding; rad4; 1.
 FT DNA REPAIR: DNA-BINDING. Nuclear protein.
 FT AVN -S GSD (IN REF. 2).
 FT CONFLICT 28 30 S -> L (IN REF. 2).
 FT CONFLICT 53 53 S -> L (IN REF. 2).
 FT CONFLICT 57 67 L -> F (IN REF. 2).
 FT CONFLICT 70 70 F -> S (IN REF. 2).
 FT CONFLICT 134 125 R3 -> STP (IN REF. 2).
 FT CONFLICT 165 170 INVQNM -> GVETT (IN REF. 2).
 FT CONFLICT 181 181 S -> N (IN REF. 2).
 FT CONFLICT 187 187 S -> N (IN REF. 2).
 FT CONFLICT 190 190 P -> S (IN REF. 2).
 FT CONFLICT 192 192 P -> L (IN REF. 2).
 FT CONFLICT 342 342 GSKA -> AKT (IN REF. 2).
 FT CONFLICT 367 367 P -> L (IN REF. 2).
 FT CONFLICT 429 428 R -> C (IN REF. 2).
 FT CONFLICT 467 467 C -> C (IN REF. 2).
 FT CONFLICT 584 594 K -> E (IN REF. 2).
 SQ SEQUENCE 900 AA; 100873 MW; 95737FCB36DC15DD CRC64;

Query Match 93.8%; Score 30; DR 1; Length 900;
 Best Local Similarity 100.0%; Pred.No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

Db 182 GFYRN 186

RESULT 11

XPC_HUMAN

1D XP-HUMAN

AC Q01831

DT 01-JUL-1994 (Ref. 26; Created)

DT 01-OCT-1996 (Ref. 34; Last sequence update)

DT 15-JUN-2002 (Ref. 41; Last annotation update)

DE DNA-repair protein complementing XPC cells (Xeroderma pigmentosum

DE group C complementing protein) (P125).

GN XPC (XPC).

OS Homo sapiens (Human).

CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 CC Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
 CC NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-54.
 RX MEDLINE-94222000; PubMed-9168492;
 RA Mastani C., Sasasawa K., Yamada S., Sonoyama T., Uji M.,
 RA Tometsu T., Takai F., Tanaka F., et al. (1994) Katsma D.,
 RA Kishimoto T., et al. (1994) Katsma D.,
 RA "Purification and cloning of a nucleotide excision repair complex
 RT involving the Xeroderma pigmentosum group C protein and a human
 RT homolog of yeast XPC.";
 RL EMBO J. 13:1841-1843(1994);
 RN [2]
 KI Szelembi L.M., H.A.
 KI From Szelembi L.M., Flanagan K.H.;
 KI "Defining abnormalities in the xeroderma pigmentosum group C (XPC)
 RT gene.";
 RL submitted (May 2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 118-949 FROM N.A.
 RX MEDLINE-92296219; PubMed-1522891;
 RA Ledwinski K.J., Peterson C.A.;
 RT "Expression cloning of a human DNA repair gene involved in Xeroderma
 RT pigmentosum group C.";
 RL Nature 359:70-73(1992);
 RN [4]
 KI REV.LW - H VAF-ADLER, X.C.
 KI MEDLINE-9474920; PubMed-1047254;
 RA Cleaver J.E., Thompson L.H., Richardson A.S., States J.C.;
 RT "A summary of mutations in the UV-sensitive disorders: Xeroderma
 RT pigmentosum, Cockayne's syndrome, and trichothiodystrophy.";
 RL Hum. Mutat. 14:9-22(1999);
 RN [5]
 RP VARIANTS XP-C H15 243, VAL 556 TRS AND GLN-948.
 RX MEDLINE-94139623; PubMed-2498653;
 RA Li L., Bates E.S., Peterson C.A., Ledwinski K.J.;
 RT "Characterization of molecular defects in Xeroderma pigmentosum group
 RT C.";
 RL Nat. Genet. 5:413-417(1993);
 CC [1-] FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
 CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO
 CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.
 CC [1-] SUBUNIT: HETERODIMER OF A 125 KDA SUBUNIT (P125) AND OF A
 CC 58 KDA SUBUNIT (P58).
 CC [1-] SUBCELLULAR LOCATION: Nuclear. (Probable).
 CC [1-] DISEASE: DEFECTS IN XPC ARE A CAUSE OF ALXANDRIA FIBROSIS, A
 CC FAIR HUMAN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY SOLAR
 CC SENSITIVITY, HIGH FREQUENCIES FOR DEVELOPING CANCER, AND ABNOR-
 CC MALTY EXPRESSION OF XPC mRNA AND, IN SOME CASES, NEUROLOGICAL
 CC ABNORMALITIES.
 CC [1-] SIMILARITY: SOME, TO YEAST RAD4.
 CC -----
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 CC OR SEND AN EMAIL TO license@sisb.ebi.ac.uk).
 CC -----
 DR EMBL: D21089; BAA04651.1; .
 DR EMBL: AF261501; AAF87574.1; .
 DR EMBL: AF261892; AAF87574.1; JOINED.
 DR EMBL: AF261894; AAF87574.1; JOINED.
 DR EMBL: AF261894; AAF87574.1; JOINED.
 DR EMBL: AF261896; AAF87574.1; JOINED.
 DR EMBL: AF261896; AAF87574.1; JOINED.
 DR EMBL: AF261897; AAF87574.1; JOINED.
 DR EMBL: AF261898; AAF87574.1; JOINED.
 DR EMBL: AF261899; AAF87574.1; JOINED.
 DR EMBL: AF261900; AAF87574.1; JOINED.
 DR EMBL: X55924; CAA6158.1; .

DR Genbank: BCNC12816; XP01.
 DR MIM: 278720;
 DR InterPro: IPR004583; Rad4.
 DR 11GFAMS: IPR00005; Rad4.
 DR PRA repeat: PRA binding. Rad4 protein. Xeroderma pigmentosum.
 KW disease mutation.
 FT INITIATION 0 0
 FT DOMAIN 29 176 OLD RICH (ACIDIC).
 FT DOMAIN 308 394 LYS-RICH (BASIC).
 FT DOMAIN 389 494 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 407 430 ARG/LYS-RICH (BASIC).
 FT DOMAIN 441 460 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 465 492 ARG/LYS-RICH (BASIC).
 FT DOMAIN 29 33 POLY-GLU.
 FT DOMAIN 123 129 POLY-GLU.
 FT DOMAIN 506 506 POLY-SER.
 FT VARIANT 333 333 P -> H (IN XP-C; SEVERE).
 FT VARIANT 656 656 /FTID-VAR_005846.
 FT VARIANT 938 938 V -> VV (IN XP-C; MILD).
 FT VARIANT 938 938 K -> Q (IN XP-C; MILD).
 FT VARIANT 938 938 /FTID-VAR_005848.
 FT CONFLICT 498 498 V -> A (IN REF. 3).
 SQ SEQUENCE 430 AA: 100049 MW: 25050228.122E3 CREC4.
 Query Match 93.88; Score 30; DP 1; Length 929;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservations 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GYRN 7
 DB 216 GYRN 220
 RESULT 12
 ID PRA_YEAST STANDARD; PRT; 1564 AA.
 AC P51533;
 DT 01-OCT-1996 (Ref. 34, Created)
 DI 01-OCT-1996 (Ref. 34, Last sequence update)
 DF 16-OCT-2001 (Ref. 40, Last annotation update)
 DE ATP-dependent permease PDR10.
 GN PDR10 OR YOR328W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID:4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97051586; PubMed:8894263;
 RA Parle-Rechmatt A.G., Rand N.J., Goulding S.G., Wolfe K.H.;
 RT "Sequence of 26 kb around the PDR10 locus on the right arm of
 Saccharomyces cerevisiae chromosome XV: similarity to part of
 chromosome I.";
 RT Yeast 17:609-1004 (1996)
 RL Yeast 17:609-1004 (1996)
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -2- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY
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 DR EMBL: Z49821; CAA89375.1;
 DR EMBL: Z75246; CAA56649.1;
 DR EMBL: Z75247; CAA99651.1;
 DR SDD: S0005855; PDR10.
 DR InterPro: IPR004593; AAA_ATPase.
 DR InterPro: IPR004439; ABC_Transport
 DR InterPro: IPR005285; PDR.

DR Pfam: PF00005; ABC_tran; 2.
 DR Prodom: PD000006; ABC_Transport; 2.
 DR SMART: SM00482; AAA; 1.
 DR 11GFAMS: IPR00005; Rad4.
 DR PRA repeat: PRA binding. Rad4 protein. Xeroderma pigmentosum.
 KW disease mutation.
 FT INITIATION 0 0
 FT DOMAIN 29 176 OLD RICH (ACIDIC).
 FT DOMAIN 308 394 LYS-RICH (BASIC).
 FT DOMAIN 389 494 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 407 430 ARG/LYS-RICH (BASIC).
 FT DOMAIN 441 460 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 465 492 ARG/LYS-RICH (BASIC).
 FT DOMAIN 29 33 POLY-GLU.
 FT DOMAIN 123 129 POLY-GLU.
 FT DOMAIN 506 506 POLY-SER.
 FT VARIANT 333 333 P -> H (IN XP-C; SEVERE).
 FT VARIANT 656 656 /FTID-VAR_005846.
 FT VARIANT 938 938 V -> VV (IN XP-C; MILD).
 FT VARIANT 938 938 K -> Q (IN XP-C; MILD).
 FT VARIANT 938 938 /FTID-VAR_005848.
 FT CONFLICT 498 498 V -> A (IN REF. 3).
 SQ SEQUENCE 430 AA: 100049 MW: 25050228.122E3 CREC4.
 Query Match 93.88; Score 30; DP 1; Length 1564;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservations 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GYRN 7
 DB 1363 GYRN 1467
 RESULT 13
 ID R132_HORBU STANDARD; PRT; 59 AA.
 AC 051646;
 DT 15-DEC-1998 (Ref. 47, Created)
 DI 15-DEC-1998 (Ref. 47, Last sequence update)
 DF 16-OCT-2001 (Ref. 40, Last annotation update)
 DE 50S ribosomal protein L12.
 GN RPLP0 OR BR0703.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID:119;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97051586; PubMed:8894263;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 EA Lathia C., White O., Ketchum K.A., Badson R., Rhee K., Olson M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.B., Richardson D.,
 SA Anderson J., Kapur N., Adams M.D., Gocayne J.D.,
 RA Utterback L., Wathay L., McDonald L., Artlich P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Borst K., Roberts K., Hatch R.,
 RA Smith R.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochete, Borrelia
 burgdorferi.";
 RT Science 275:39-46 (1997).
 CC -1- SIMILARITY: BELONGS TO THE L247 FAMILY OF RIBOSOMAL PROTEINS.
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Fischer R.D., Helms J., Boettie P.:
Cloning, sequencing, and molecular analysis of the sol operon of
Clostridium acetobutylicum, a chromosomal locus involved in
solventogenesis".
J. Bacteriol. 175:6559-6569(1993).
[2]
SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 702 / VFX B-1787;
MEDLINE-9408497; PubMed-9864345;
Nair R.V., Green E.M., Watson D.F., Bennett G.N., Papoutsakis E.T.:
"Regulation of the sol locus genes for butanol and acetone formation
in Clostridium acetobutylicum ATCC 824 by a putative transcriptional
repressor".
J. Bacteriol. 181:419-430(1999).
[3]
SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 702 / VFX B-1787;
MEDLINE-2135325; PubMed-1456285;
Noellling J., Berton G., Imotohoko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee B.M., Dubois J., Guin J., Hitt J., Wolf Y.L.,
Latusov R.L., Sabathe P., Decoteau-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Kozmin E.V., Smith D.R.:
Genome sequence and comparative analysis of the solvent producing
bacterium Clostridium acetobutylicum".
J. Bacteriol. 183:4824-4838(2001).
[4]
FURTHER TRANSLATION DATA: EMBL: X72831 (AA) (AF013646) (AF013647) (AF013648) (AF013649) (AF013650) (AF013651) (AF013652) (AF013653) (AF013654) (AF013655) (AF013656) (AF013657) (AF013658) (AF013659) (AF013660) (AF013661) (AF013662) (AF013663) (AF013664) (AF013665) (AF013666) (AF013667) (AF013668) (AF013669) (AF013670) (AF013671) (AF013672) (AF013673) (AF013674) (AF013675) (AF013676) (AF013677) (AF013678) (AF013679) (AF013680) (AF013681) (AF013682) (AF013683) (AF013684) (AF013685) (AF013686) (AF013687) (AF013688) (AF013689) (AF013690) (AF013691) (AF013692) (AF013693) (AF013694) (AF013695) (AF013696) (AF013697) (AF013698) (AF013699) (AF013700) (AF013701) (AF013702) (AF013703) (AF013704) (AF013705) (AF013706) (AF013707) (AF013708) (AF013709) (AF013710) (AF013711) (AF013712) (AF013713) (AF013714) (AF013715) (AF013716) (AF013717) (AF013718) (AF013719) (AF013720) (AF013721) (AF013722) (AF013723) (AF013724) (AF013725) (AF013726) (AF013727) (AF013728) (AF013729) (AF013730) (AF013731) (AF013732) (AF013733) (AF013734) (AF013735) (AF013736) (AF013737) (AF013738) (AF013739) (AF013740) (AF013741) (AF013742) (AF013743) (AF013744) (AF013745) (AF013746) (AF013747) (AF013748) (AF013749) (AF013750) (AF013751) (AF013752) (AF013753) (AF013754) (AF013755) (AF013756) (AF013757) (AF013758) (AF013759) (AF013760) (AF013761) (AF013762) (AF013763) (AF013764) (AF013765) (AF013766) (AF013767) (AF013768) (AF013769) (AF013770) (AF013771) (AF013772) (AF013773) (AF013774) (AF013775) (AF013776) (AF013777) (AF013778) (AF013779) (AF013780) (AF013781) (AF013782) (AF013783) (AF013784) (AF013785) (AF013786) (AF013787) (AF013788) (AF013789) (AF013790) (AF013791) (AF013792) (AF013793) (AF013794) (AF013795) (AF013796) (AF013797) (AF013798) (AF013799) (AF013800) (AF013801) (AF013802) (AF013803) (AF013804) (AF013805) (AF013806) (AF013807) (AF013808) (AF013809) (AF013810) (AF013811) (AF013812) (AF013813) (AF013814) (AF013815) (AF013816) (AF013817) (AF013818) (AF013819) (AF013820) (AF013821) (AF013822) (AF013823) (AF013824) (AF013825) (AF013826) (AF013827) (AF013828) (AF013829) (AF013830) (AF013831) (AF013832) (AF013833) (AF013834) (AF013835) (AF013836) (AF013837) (AF013838) (AF013839) (AF013840) (AF013841) (AF013842) (AF013843) (AF013844) (AF013845) (AF013846) (AF013847) (AF013848) (AF013849) (AF013850) (AF013851) (AF013852) (AF013853) (AF013854) (AF013855) (AF013856) (AF013857) (AF013858) (AF013859) (AF013860) (AF013861) (AF013862) (AF013863) (AF013864) (AF013865) (AF013866) (AF013867) (AF013868) (AF013869) (AF013870) (AF013871) (AF013872) (AF013873) (AF013874) (AF013875) (AF013876) (AF013877) (AF013878) (AF013879) (AF013880) (AF013881) (AF013882) (AF013883) (AF013884) (AF013885) (AF013886) (AF013887) (AF013888) (AF013889) (AF013890) (AF013891) (AF013892) (AF013893) (AF013894) (AF013895) (AF013896) (AF013897) (AF013898) (AF013899) (AF013900) (AF013901) (AF013902) (AF013903) (AF013904) (AF013905) (AF013906) (AF013907) (AF013908) (AF013909) (AF013910) (AF013911) (AF013912) (AF013913) (AF013914) (AF013915) (AF013916) (AF013917) (AF013918) (AF013919) (AF013920) (AF013921) (AF013922) (AF013923) (AF013924) (AF013925) (AF013926) (AF013927) (AF013928) (AF013929) (AF013930) (AF013931) (AF013932) (AF013933) (AF013934) (AF013935) (AF013936) (AF013937) (AF013938) (AF013939) (AF013940) (AF013941) (AF013942) (AF013943) (AF013944) (AF013945) (AF013946) (AF013947) (AF013948) (AF013949) (AF013950) (AF013951) (AF013952) (AF013953) (AF013954) (AF013955) (AF013956) (AF013957) (AF013958) (AF013959) (AF013960) (AF013961) (AF013962) (AF013963) (AF013964) (AF013965) (AF013966) (AF013967) (AF013968) (AF013969) (AF013970) (AF013971) (AF013972) (AF013973) (AF013974) (AF013975) (AF013976) (AF013977) (AF013978) (AF013979) (AF013980) (AF013981) (AF013982) (AF013983) (AF013984) (AF013985) (AF013986) (AF013987) (AF013988) (AF013989) (AF013990) (AF013991) (AF013992) (AF013993) (AF013994) (AF013995) (AF013996) (AF013997) (AF013998) (AF013999) (AF014000) (AF014001) (AF014002) (AF014003) (AF014004) (AF014005) (AF014006) (AF014007) (AF014008) (AF014009) (AF014010) (AF014011) (AF014012) (AF014013) (AF014014) (AF014015) (AF014016) (AF014017) (AF014018) (AF014019) (AF014020) (AF014021) (AF014022) (AF014023) (AF014024) (AF014025) (AF014026) (AF014027) (AF014028) (AF014029) (AF014030) (AF014031) (AF014032) (AF014033) (AF014034) (AF014035) (AF014036) (AF014037) (AF014038) (AF014039) (AF014040) (AF014041) (AF014042) (AF014043) (AF014044) (AF0140

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CC or send an email to license@ebi.ac.uk).

DR EMBL: U67509; AAB98606.1; -
DR RSSP: P20625; ZABK.
DR TIGR: M06113; -
DR InterPro: IPR002873; DUF123.
DR InterPro: IPR004035; EndoIII_FCL.
DR InterPro: IPR004046; EndoIII_mh.
DR InterPro: IPR003265; Endo_3c.
DR InterPro: IPR003261; Endo_11c.
DR InterPro: IPR003583; HHH_1.
DR InterPro: IPR000305; nvrC_N
DR Pfam: PF00730; Hbh-GPD; 1.
DR Pfam: PF01986; DUF123; 1.
DR Pfam: PF015467; DUF124; 1.
DR SMART: SM00478; Endo3c; 1.
DR SMART: SM00525; FES; 1.
DR SMART: SM00455; GIVC; 1.
DR SMART: SM00278; HHH1; 1.
DR PROSITE: PS00764; ENDONUCLEASE_III_1; FALSE_NEG.
DR PROSITE: PS01155; ENDONUCLEASE_III_2; 1.
KW Hypothetical protein, Hydrolyase, Glycosidase, Iron sulfur, 4Fe 4S,
KW Complete Proteome.
FT METAL 184 184 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 190 190 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 193 193 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 201 201 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 344 AA; 40567 MW; BC3BEFE1DE778B85 CRC64;

Query Match 84.4%; Score 27; DR 1; Length 344;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYRN 7
DB 77 GFYRN 81
|||||

RESULT 19
ID YCJX_ECOLI STANDARD; EBI; 465 AA.
AC P76046; P77411;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ycjx.
GN YCJX OR B1321.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PubMed 9278503;
RX MEDLINE=97436617; PubMed 9278503;
RA Blattner F.B., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Gillard Vias J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K12.";
RL Science 277:1232-1244(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed 9607030;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isoko K.,
RA Itoh T., Kasai H., Kishimoto K., Kimura S., Kikukawa M.,
RA Kikuchi M., Makino Y., Miki T., Mizubuchi K., Mori H., Mori T.,

EA Matsuzaki F., Kishida S., Nakamura Y., Nishimoto H., Nishio Y.,
EA Oshima T., Saito N., Sempel G., Seki Y., Sivasubraman S.,
EA Yamai H., Yabuta T., Yabuta K., Yabuchi Y., Wada C.,
EA Yamamoto Y., Horiochi T.;
E "A 3.9 kb DNA sequence of the *Escherichia coli* K12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
KL DNA RES. 4:363-377(1996).
CC 1. SIMILARITY: STRCS; To H. INHERITAE H11637.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).

Query Match 84.4%; Score 27; DR 1; Length 465;
Best Local Similarity 80.0%; Pred. No. 12372;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYRN 7
DB 270 GFYRN 274
|||||

RESULT 20
ID SYW_HUMAN STANDARD; EBI; 471 AA.
AC P23811; P78535; Q90014;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE tryptophanyl tRNA synthetase (E.C.2.3.1.2) (tryptophan tRNA idase)
DE (trpS) (trpS) (trpS).
GN WARS.
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE 92106711; PubMed 1761599;
RX Rubin B.Y., Anderson S.L., Xing L., Powell R.J., Tate W.P.;
RA "Interferon induces tryptophanyl tRNA synthetase expression in human
RT fibroblasts.";
KL J. Biol. Chem. 266:24245-24248(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE-92107062; PubMed-1763065;
RX Eickbush J., Eickbush H.H., Gestesen J.;
RT "Human interferon gamma potently induces the synthesis of a 55 kDa
RT protein (gamma 2) highly homologous to rabbit peptide chain release
RT factor and bovine tryptophanyl-tRNA synthetase.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:11523-11524(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE-9210258; PubMed-1762574;
RX Polonsky L., Sedemund H.A., Glickman A.V., Ziegler A.,
RA Kisselov L.L.;
RT "Cloning and nucleotide sequence of the structural gene encoding for
RT human tryptophanyl tRNA synthetase.";
RL Gene 199:291-296(1994).
RN [4]
RP SEQUENCE FROM N.A.

EX MEDLINE 92164636; PubMed 1547432;
 RT Howitt L., Flohr T., Boettger E.C.;
 RT "Molecular cloning and characterization of an interferon induced
 RT human cDNA with sequence homology to a mammalian peptide chain
 RT release factor.";
 RL EMBO J. 11:489-496(1992).
 RN [5]
 RN SEQUENCE OF 1-13 FROM N.A.
 RX MEDLINE 96419994; PubMed 8724762;
 RX Sokolova I.V., Nardolillo-Skiff A.H., Ambekar A.M., Taffan P.T.;
 RT "Alternative splicing of 5'-terminal exons of the human tryptophanyl-
 RT tRNA synthetase gene.";
 RL Mol. Biol. (Mosk) 40:319-329(1996).
 RN [6]
 RN SEQUENCE OF 1-141 AND 182-471 FROM R.A.
 RC TISSUE-SPECIFIC;
 RX MEDLINE 93492992; PubMed 7469289;
 RX Protova I.V., Grigoreva A.V., Sidorova M.A., Kisselev E.I.;
 RT "The human gene encoding tryptophanyl tRNA synthetase: interferon-
 RT response elements and exon-intron organization.";
 RL Gene 128:247-245(1993).
 RN [7]
 RN SEQUENCE OF 245-276; 278-296; 299-317 AND 350-365;
 RC TISSUE:Keratinoctyes;
 RX MEDLINE 94162043; PubMed 1286667;
 RX Kasmussen B., van Veen J., Pijpe M., Jansen R., Gills J.B.;
 RA Vandenkerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [8]
 RN FUNCTION;
 RX MEDLINE 9225128; PubMed 1373391;
 RX Banno F.-C., Flohr T., Howitt L., Boettger E.C.;
 RT "An interferon-induced protein with release factor activity is a
 RT tryptophanyl-tRNA synthetase.";
 RL FEBS Lett. 300:162-166(1992).
 CC -1- CATALYTIC ACTIVITY: AIP + L-tryptophan + tRNA(Trp) -> AMP +
 CC tryptophanyl-tRNA(Trp);
 CC -2- SUBUNIT: HOMODIMER.
 CC -3- INDUCTION: BY INTERFERON GAMMA.
 CC -4- SIMILARITY: HOMOLOGES TO CLASS I AMINOACYL-TRNA SYNTHETASE DOMAIN.
 CC -5- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
 CC [11]
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DR MM: 191050; -;
 DR InterPro: IPR002306; ITP-tRNA-synt_1b;
 DR InterPro: IPR007348; WHEP-TRS;
 DE InterPro: IPR002306; tRNA-synt_1b;
 DR InterPro: IPR001412; tRNA-synt_1;
 DR Pfam: PF00458; WHEP-TRS; 1;
 DR Pfam: PF00579; tRNA-synt_1b; 1;
 DR PRINTS: PR01039; TRNASYNTHRP;
 DR TIGRfams: TIGR00243; Trps; 1;
 DE EC: F.5.1.2.2, AA: tRNA-LIGASE; 1; 1;
 DE PROSITE: PS00762; WHEP-TRS; 1;
 KW Aminoacyl-tRNA synthetase; protein biosynthesis; tRNAse; AIP binding.
 FT DOMAIN 19 64
 FT SLIDE 164 174
 FT SITE 43 453
 FT CONFLICT 213 214
 FT CONFLICT 424 424 A -> R (IN REF. 4).
 EQ SEQUENCE 471 AA: 53166 MW: 5963444795409640964
 Query Match 94.4%; Score 27; E-Val 1e-464th 471;
 Best Local Similarity 80.0%; Prod. No. 1420024;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFVN 7
 EB 245 GFVN 250
 IIII
 RESULT 21
 YAL5_SCHPO
 ID YAL5_SCHPO STANDARD: PRI: 471 AA.
 AC Q09928;
 DT 01-FEB-1996 (rel. 35, Created)
 DT 01-FEB-1996 (rel. 35, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Probable peptidyl-prolyl is-trans isomerase (21E1.050) (EC 5.2.1.8).
 GN SPAC21E1.050;
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota, Euk., Ascomycota, Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 UX NCBI-TaxID:4896;
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN 972;
 RX MEDLINE-21848401; PubMed 11859460;
 RA Wood V., Gwilliam R., Pajandream M.A., Lyse M., Lyne R., Stewart A.,
 RA Brooks R., Brown N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Sgouras J., Paul N., Hays S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor P., Cronin A., Davis P., Bellwell L., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hudson G.,
 RA Holroyd S., Hornsby T., Howarth S., Buckle E.J., Hunt S., Jangals K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA McGeary P., Mould S., Muddall K., Murphy L., Nibbelk D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton T., Simmonds M., Spence P., Spurr S., Staines Z.,
 RA Taylor K., Taylor R.G., Totty A., Walsh S.V., Warren T., Whitthead S.,
 RA Woodward J., Vackarik G., Zerb R., Bork P., Bork J., Bork R.,
 RA Well J., Vasthards E., Richter M., Schuster M., Mordet Auer S.,
 RA Gabal C., Fuchs M., Frilow C., Holzer E., Meisl D., Hilbert H.,
 RA Betz M., Eick J., Bork A., Bork A., Bork R., Bork J., Bork L.H.,
 RA Eder P., Zimmermann W., Wiedler H., Wambert R., Parniske R.,
 RA Goffeau A., Paulsen O., Drouot S., Glock S., Lelander V., Mollner S.,
 RA Galibert F., Aves S.J., Xiang Z., Hart C., Mager K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thodo G.,
 RA Bada R.R., Cruzado L., Jimenez J., Sanchez M., del Roy F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forshurst S.,
 RA Gerbault L., Lowe T., McCombie W.R., Paulsen O., Potashkin J.,
 RA Shklovski G.V., Ossery B., Bartoli R.S., Burso P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega 180) peptidylproline

CC (omega-0).

CC 1. SIMILARITY. BELONGS TO THE CYCLOPHILIN TYPE PPIASE FAMILY.

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DR EMU: 267944; CAA91964 1;

DR HSSP: Q27450; IC5F.

DR InterPro: IPR002130; CSA_PPIase.

DR InterPro: IPR003613; ZnF_MODING.

DR Pfam: PF00160; pro_isomerase_1.

DR PRINTS: PR00153; CSNPISMRASE.

DR SMART: SM00594; Ubox; 1.

DR PROSITE: PS00170; CSA_PPIASE_1; 1.

DR PROSITE: PS00772; CSA_PPIASE_2; 1.

KW Hypothetical protein; Isomerase; Rolamase.

FT DOMAIN 237 383 PPIASE, CYCLOPHILIN-TYPE.

SQ SEQUENCE 471 AA: 53573 MW: 56155620590606 Ck364;

Query Match 84.4%; Score 27; BB 1; Length 471;

Best Local Similarity 80.0%; Pred. No. 126/22;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7

DB 245 GYEN 269

RESULT 22

SVW_BOVIN

ID SVW_BOVIN STANDAPP: PPT: 475 AA.

AC P17248;

DT 01-NOV-1990 (Rel. 15, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)

DE (TPRS).

CN WARS.

OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Cetartiodactyla; Perissodactyla; Bovina; Bovidae;

CC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RX SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Retina;

RX MEDLINE=91329348; PubMed=1907847;

RA Garret M., Pajot B., Trezequet V., Labrousse J., Morle M.,

RA Gaudier J.-C., Benedetto J.-P., Gallatranque M.-L., Alterio J.,

RA Gueguen M., Sarger C., Labrousse B., Boudet J.,

RT "A mammalian tryptophanyl-tRNA synthetase shows high homology to

RT prokaryotic synthetases but near identity with mammalian peptide

RT chain release factor.";

RL Biochemistry 30:7809-7817(1991).

RN [2]

RP SEQUENCE OF 17-475 FROM N.A.

RC TISSUE=Pancreas;

PA Garret M., Trezequet V., Pajot B., Gaudier J.-C., Morle M.,

PA Gueguen M., Benedetto J.-P., Sarger C., Alterio J., La Porcelle P.,

RA Labrousse J., Boudet J.,

RL Submitted (MAP-1990) to the EMBL/Genbank/DDB databases.

CC 1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) -> AMP +

CC diphosphate + L-tryptophanyl-tRNA(Trp).

CC 1- SIMILARITY: HOMODIMER.

CC 1- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.

CC 1- SIMILARITY: CONTAINS 1 WHIP-TRS DOMAIN.

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DR EMP: V52919; CAA47972 1;

DR EMU: A52414; CAA00526 1;

DR PIR: A40279; YNB0.

DR PIR: S14540; S14540.

DR InterPro: IPR002306; TRP-trna_synth_lb.

DR InterPro: IPR00748; WHIP-TRS.

DR InterPro: IPR02305; tRNA_synth_lb.

DR InterPro: IPR01412; tRNA_synth_1.

DR Pfam: PF00458; WHIP-TRS; 1.

DR Pfam: PF00579; tRNA_synth_lb; 1.

DR TRNATS: TRN00233; tRNA_SINTHTRP.

DR TRNATS: TRN00243; TRNATS; 1.

DR PROSITE: PS00178; AA-trna_LIGASE_1; 1.

DR PROSITE: PS00762; WHIP-TRS; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; tRNA; AMP-binding.

FT DOMAIN 24 69 WHIP-TRS.

FT DOMAIN 1 117 DISPENSABLE TO THE CATALYTIC ACTIVITY.

FT SITE 169 178 "HIGH" REGION.

FT SITE 352 353 "KERS" REGION.

FT CONFLICT 17 17 L > M (IR REF. 2).

SQ SEQUENCE 475 AA: 53729 MW: 57531750137E42 CR664;

Query Match 84.4%; Score 27; BB 1; Length 475;

Best Local Similarity 80.0%; Pred. No. 126/22;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7

DB 250 GYEN 254

RESULT 24

SVW_RABIT

ID SVW_RABIT STANDAPP: PPT: 475 AA.

AC P24612; Q28607;

DT 01-NOV-1991 (Rel. 20, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)

DE (TPRS).

CN WARS.

OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RX SEQUENCE FROM N.A.

RC MEDLINE=9025904; PubMed=2185472;

RA Gaudier J.-C., Trezequet V., Morle M.,

RA Gueguen M., Sarger C., Labrousse B., Boudet J.,

RT "Cloning and expression of a mammalian peptide chain release factor

RT with sequence similarity to tryptophanyl tRNA synthetases.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:3598-3602(1990).

RN [2]

RP REVIEWS TO 159 174 AND 227 229; AND FUNCTION.

RC MEDLINE=9409008; PubMed=8404867;

RA Trezequet V., Gaudier J.-C., Sarger C., Morle M.,

RA Gueguen M., Fossecy L.L., Tate W.P., Haeumel A.L.,

RT "Mammalian polypeptide chain release factor and tryptophanyl tRNA

RT synthetase are distinct proteins.";

RL EMBO J. 12:4013-4019(1994).

CC 1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) -> AMP +

CC diphosphate + L-tryptophanyl-tRNA(Trp).

CC 1- SIMILARITY: HOMODIMER.

CC 1- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.

CC 1- SIMILARITY: CONTAINS 1 WHIP-TRS DOMAIN.

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CC
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CC      or send an email to license@ebi-sib.ch).
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the developing articular cartilage of joints in the shoulder,
elbow, wrist, and digits of the embryo.
!- DISAST: Defects in ANKH are the cause of a generalized,
progressive form of arthritis. It is an autosomal recessive
disorder that leads to the development of articular
degeneration in articular surfaces and synovial fluid leading to joint
space narrowing, cartilage erosion, and formation of bony
outgrowths or osteophytes that cause fusion and joint immobility
and destruction.
-!- SIMILARITY: BELONGS TO THE ANKH FAMILY.
CC
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CC      or send an email to license@ebi-sib.ch).
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CC similarity).
CC -1- SUBCELLULAR LOCATION: Membrane protein (By similarity).
CC -2- SIMILARITY: BELONGS TO THE ANKH FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcements/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF393241; AAK73750.1; -.
CC Transport: Phosphate transport; Transmembrane.
CC DOMAIN 1 85
CC TRANSMEM 96 106
CC DOMAIN 107 121
CC TRANSMEM 132 152
CC DOMAIN 153 158
CC TRANSMEM 159 179
CC DOMAIN 180 189
CC TRANSMEM 190 219
CC DOMAIN 211 326
CC TRANSMEM 327 347
CC DOMAIN 349 350
CC TRANSMEM 351 371
CC DOMAIN 372 403
CC TRANSMEM 404 426
CC DOMAIN 427 429
CC TRANSMEM 430 452
CC DOMAIN 453 492
CC TRANSMEM 492 492
CC SEQUENCE 492 AA; 54264 MW; 99CAC27641A1PC8B CRC64.

Query Match: 84.4% Score 27, DP 1, Length 450;
Best Local Similarity: 80.0%; Pred. No. 1,40-02;
Matches 4: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 211 GYRN 215

RESULT 24
PHNL_DRSOI
ID PHNL_DRSOI STANDARD: PRT: 550 AA.
AC P12944;
DT 01-JAN-1999 (Rel. 13, Created)
DI 01-MAY-1991 (Rel. 18, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Periplasmic [NiFe] hydrogenase large subunit precursor (EC 1.19.99.1)
LE (NiFe hydrogenase large chain).
GN HYDB.
OS Desulfovibrio gigas.
OC Bacteria; Proteobacteria; Delta subdivision; Desulfobacteriales;
OC Desulfovibrio.
OC NCML_Daxid-879;
CX [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-30.
RX MEDLINE-88111028; PubMed-3322743;
RA Li C., Peck H.D. Jr., le Gall J., Przybyla A.E.;
RT "Cloning, characterization, and sequencing of the genes encoding the
RT large and small subunits of the periplasmic [NiFe]hydrogenase of
RT Desulfovibrio gigas.";
RL DNA 6:539-551(1987).
RN [2]
RP SEQUENCE FROM N.A., AND REVISIONS.
RX MEDLINE-89213989; PubMed-2651421;
RA Voordouw G., Menon N.K., le Gall J., Choi E.S., Peck H.D. Jr.,
RA Przybyla A.E.;
RT "Analysis and comparison of nucleotide sequences encoding the genes
RT for [NiFe] and [NiFeSe] hydrogenases from Desulfovibrio gigas and
RT Desulfovibrio baculatus.";
RL J. Bacteriol. 171:2994-2999(1989).

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RN [3]
RP SEQUENCE OF 1-29.
RX MEDLINE-88106446; PubMed-332275;
RA PICKRILL B.C., Ho S.H., Li C., Menon N.K., Choi E.S., Przybyla A.E.,
RA Voordouw G., Menon N.K., le Gall J., Przybyla A.E.;
RA Moura I., Moura J.J.G., Patil D., Hoynh H.H.;
RT "Identification of three classes of hydrogenase in the genus,
RT Desulfovibrio.";
RL Biochem. Biophys. Res. Commun. 149:369-377(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS).
RX MEDLINE-95157629; PubMed-7854413;
RA Voiboda A., Charon M.H., Piras G., Hatchikian E.C., Frey M.,
RA Pontecilla-camps J.C.;
RT "Crystal structure of the nickel-iron hydrogenase from Desulfovibrio
RT gigas.";
RL Nature 373:580-587(1995).
CC : CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) -> 2 reduced
CC : ferredoxin + H(2).
CC : COFACTOR: ONE NICKEL ION, TWO SET AS CLUSTERS AND ONE 4FE-4S
CC : CLUSTER. THE LARGE SUBUNIT IS THOUGH TO CONTAIN THE NICKEL ION.
CC : SUBUNIT: DIHETEROMER OF A LARGE AND A SMALL SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -2- SUBCELLULAR LOCATION: Periplasmic.
CC -3- MISCELLANEOUS. FORMER THE LEADER OF THE SMALL SUBUNIT SERVES AS A
CC : TRANSPORT VEHICLE FOR BOTH SUBUNITS.
CC : SIMILARITY: BELONGS TO THE [NiFe]/[NiFeSe] HYDROGENASE LARGE
CC : SUBUNIT FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M18084; AAK33478.1; ALL_SEQ.
CC PIR: R32315; HQDVLD.
CC PIR: D27490; D27480.
CC PDB: 1FRV; 08-NOV-96.
CC InterPro: IP0001501; N1_Hdl.
CC Pfam: PF00374; Nifose_Hases; 1.
CC PROSITE: PS00507; N1_HGENASE_1; 1.
CC PROSITE: PS00508; N1_HGENASE_2; 1.
CC EXPROT: ExproT: Nif_Hase, Nif_H, Nif_H2, Nif_H3, Nif_H4, Nif_H5, Nif_H6, Nif_H7, Nif_H8, Nif_H9, Nif_H10, Nif_H11, Nif_H12, Nif_H13, Nif_H14, Nif_H15, Nif_H16, Nif_H17, Nif_H18, Nif_H19, Nif_H20, Nif_H21, Nif_H22, Nif_H23, Nif_H24, Nif_H25, Nif_H26, Nif_H27, Nif_H28, Nif_H29, Nif_H30, Nif_H31, Nif_H32, Nif_H33, Nif_H34, Nif_H35, Nif_H36, Nif_H37, Nif_H38, Nif_H39, Nif_H40, Nif_H41, Nif_H42, Nif_H43, Nif_H44, Nif_H45, Nif_H46, Nif_H47, Nif_H48, Nif_H49, Nif_H50, Nif_H51, Nif_H52, Nif_H53, Nif_H54, Nif_H55, Nif_H56, Nif_H57, Nif_H58, Nif_H59, Nif_H60, Nif_H61, Nif_H62, Nif_H63, Nif_H64, Nif_H65, Nif_H66, Nif_H67, Nif_H68, Nif_H69, Nif_H70, Nif_H71, Nif_H72, Nif_H73, Nif_H74, Nif_H75, Nif_H76, Nif_H77, Nif_H78, Nif_H79, Nif_H80, Nif_H81, Nif_H82, Nif_H83, Nif_H84, Nif_H85, Nif_H86, Nif_H87, Nif_H88, Nif_H89, Nif_H90, Nif_H91, Nif_H92, Nif_H93, Nif_H94, Nif_H95, Nif_H96, Nif_H97, Nif_H98, Nif_H99, Nif_H100, Nif_H101, Nif_H102, Nif_H103, Nif_H104, Nif_H105, Nif_H106, Nif_H107, Nif_H108, 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OS Giardia lamblia (Giardia intestinalis).
EX Enkaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
RN NCBI_TaxID 5741;
RP SEQUENCE FROM N.A.
RC STRAIN AD-1;
RX MEDLINE:9441470; PubMed 8425510;
RA By P.L., Maythofer G.;
RT "Two genes encoding homologous 70-kDa surface proteins are present within individual trophozoites of the binucleate protozoan parasite Giardia intestinalis."
RI Gene 129:257-262(1993).
CC -1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN; ANCHORED TO THE PLASMA MEMBRANE.
CC -1- DOMAIN: CONTAINS 27 REPEATS OF THE CXX MOTIF.
CC -1- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch) or send an email to license@isb-sib.ch.
CC -----
DR EMBL: M33641; AAA02688.1; -.
DR EMBL: M97488; AAA02581.1; -.
DR PIR: A35502; A35502.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03402; VSP; 2.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00061; EGF_Like; 1.
DR SMART: SM00261; PD; 3.
KW Signal; Antigen; Glycoprotein; Transmembrane; Repeat.
FT SIGNAL 1 17
FT CHAIN 18 713 MAJOR SURFACE LABELLED TROPHOZOITE
FT DOMAIN 18 679 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 680 708 POTENTIAL.
FT DOMAIN 709 713 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAc...) (POTENTIAL).
FT VARIANT 682 682 A -1 (1R STRAIN ADELALDE-1).
FT VARIANT 686 686 A -5 (1R STRAIN ADELALDE-1).
SQ SEQUENCE 713 AA; 72510 MW; 9A07195843E5601 CRC64;

Query Match 84.4%; Score 27; DB 1; Length 667;
Best Local Similarity 80.0%; Pred. No. 1; Pos.0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYKN 7
ID 462 GFYKN 466
ID 414 GFYKN 418

RESULT 24
V179.FOWPV STANDARD; PRO: 91 AA;
AC Q90554;
DI 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Virion envelope protein FV179.
GN FV179.
OS Fowlpox virus (FV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordata; Aves;
OC Avipoxvirus.
GX NCBI_TaxID:10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:20192920; PubMed 10729150;
RA McCafferty M., So M., Gentry D.G.;
RT "Isolation and expression of the gene for a major surface protein of Giardia lamblia."
RL Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990).

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DR EMBL: Z11509; CAA77694.1;
DR EMBL: AL391254; CAC04539.1;
DR EMBL: S20943; R5M019.
DR BSSP: P02417; LDIIV.
DR InterPro: IPR000244; Ribosomal_L9.
DR Pfam: PF01281; Ribosomal_L9; 1.
DR TIGFAMS: TIGR0158; L9; 1.
DR PROSITE: PS00651; RIBOSOMAL_L9; 1.
KW Ribosomal protein; rRNA-binding; chloroplast; Transl. peptide.
FT TRANSIT 1 47 CHLOROPLAST (POTENTIAL).
FT CHAIN 48 197 50S RIBOSOMAL PROTEIN L9.
SQ SEQUENCE 197 AA: 22174 MW: 45509.65111320 CYS44.

Query Match
Best Local Similarity 80.0%; Score 26; DB 1; Length 197;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYRN 7
DB 73 GYRN 77

RESULT 32
YALF_LACIA
ID YALF_LACIA STANDARD: PRT: 218 AA.
AC G9CJH5;
DI 15-JUN-2002 (rel. 41, Created)
DI 15-JUN-2002 (rel. 41, Last sequence update)
DI 15-JUN-2002 (rel. 41, Last annotation update)
DE Hypothetical protein yalF.
GN YalF or L1403.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI TaxID 1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN L11403;
RX M011NP-212c146; bab04-11403;
RA Molini A., Wincker P., Mauget S., Jallion O., Malarne K.,
RA Weissbach J., Philipe S.P., Sorokin A.;
RA "The complete genome sequence of the lactic acid bacterium Lactococcus
R1 lactis ssp. lactis L1403."
R2 Genome Res. 11:740-753(2001).
CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -! SIMILARITY: BELONGS TO THE YALF/YF FAMILY
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (see http://www.isb-sib.ch) or
CC send an email to license@sib-sib.ch).
DR EMBL: AF006247; AAK04180.1;
DR InterPro: IPR004675; Abi.
DR Pfam: PF02517; Abi1; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 124 143 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
SQ SEQUENCE 218 AA: 25414 MW: 9578649397801172 CYS64;

Query Match
Best Local Similarity 80.0%; Score 26; DB 1; Length 218;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYRN 7
DB 67 GYRN 71

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RESULT 33
ENDS_SYNY4
ID ENDS_SYNY4 STANDARD: PRT: 219 AA.
AC P74715;
DI 15-JUN-1998 (rel. 36, Created)
DI 15-JUN-1998 (rel. 36, Last sequence update)
DI 16-OCT-2001 (rel. 40, Last annotation update)
DE Endonuclease III (3'-5' 4,2,99,18) (DNA dependent on pyrimidine site)
DE lyase).
GN NTH OR SLK1822.
OS Synecocystis sp. (strain PC6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI TaxID 1148;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-97061201; PubMed-8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Suda M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuo A., Muraki A., Nakazaki N., Nambu K.,
RA Okumura S., Shimpo S., Takaguchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RI "Sequence analysis of the genome of the unicellular cyanobacterium
RI Synecocystis sp. strain PC6803. II. Sequence determination of the
RI entire genome and assignment of potential protein-coding regions."
R2 DNA Res. 3:109-136(1996).
CC -! FUNCTION: HAS BOTH AN ATP-DEPENDENT 3'-5' EXONUCLEASE
CC ACTIVITY AND A DNA N-GLYCOSYLASE ACTIVITY. INCISES DAMAGED DNA AT
CC CYTOSINES, THYMINES AND GUANINES, AS WELL AS A DAMAGED GUARD, 5'
CC FROM THE DAMAGED SITE (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: The c-c-p bond 3' to the apurinic or
CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
CC leaving a 3'-terminal unsaturated sugar and a product with a
CC terminal 5'-phosphate.
CC -! COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT RELEASED FOR THE
CC CATALYTIC ACTIVITY, BUT WHICH IS PREVIOUSLY INVOLVED IN THE PROPER
CC POSITIONING OF THE ENZYME ALONG THE DNA STRAND (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE RIBREX1 FAMILY.
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CC send an email to license@sib-sib.ch).
DR EMBL: D90908; BAA17762.1;
DR BSSP: P20625; 2ABK.
DR InterPro: IPR004035; EndoIII_FCH.
DR InterPro: IPR004036; EndoIII_HH.
DR PROSITE: PS003265; Endo_3c.
DR InterPro: IPR003651; FeS_Bind.
DR InterPro: IPR003584; HHH_1.
DR Pfam: PF00740; HHH-GPDS; 1.
DR SMART: SM00478; ENDO3c; 1.
DR SMART: SM00525; FES; 1.
DR SMART: SM0273; HHH1; 1.
DR TIGFAMS: TIGR01084; ntl; 1.
DR PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
DR PROSITE: PS01155; ENDONUCLEASE_III_2; 1.
KW Hydrolyase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair;
KW Glycosylase; Lyase; Iron sulfur; 4FE-4S; Complete proteome.
FT METAL 197 197 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 204 204 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 207 207 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 213 213 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 219 AA: 24377 MW: 48449268109949 CYS64;

Query Match
Best Local Similarity 80.0%; Score 26; DB 1; Length 219;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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140 198 GFFRN 202
RESULT 46
KRAE_CAREL
ID KRAE_CAREL STANDARD: PFI: 813 AA.
AC 007292; Q9N4E4;
DI 01-OCT-1994 (Rel. 40, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rat hemolysin Serine/threonine protein kinase (EC 2.7.1.1).
DS LIN 45 OR RAP-1 OR Y74B6A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID 6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 94247635; PubMed 8484477;
RA Han M., Golden A., Han Y., Sternberg P.W.;
RT "C. elegans lin-45 raf gene participates in let-60 ras stimulated
RT vulval differentiation.",
RL Nature 363:133-140(1995);
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN Bristol N2;
RA Becker M., Graess T., Shater S.;
BL Submitted (MAR-2000) to the EMBL database.
RN [3]
RP REVISIONS.
RA Waterston R.C.
RL Submitted (JUN-2001) to the EMBL database.
CC -! FUNCTION: PROTEIN KINASE THAT PARTICIPATES IN THE REGULATION OF
CC C-CELLS. PHENVA ACTS DOWNSTREAM OF THE RAS PROTEIN LET-60
CC -! SIMILARITY: BELONGS TO THE SPK/THP FAMILY OF PROTEIN KINASES
CC MIL/SAP SUBFAMILY.
CC -! SIMILARITY: CONTAINS 1 SHC-INTERACTING PEPTIDE ESTERASE AND 1 AG
CC BINDING DOMAIN.
CC
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CC
CC EMBL: L15447; AAA28142.1;
CC EMBL: AC024264; AAF16042.1;
CC PIR: S33261; S33261.
CC WormPep: Y74B6A.5; CE25555
CC BSSP: P04049; TP4R.
CC InterPro: IPR002219; RAT PF Elcd
CC InterPro: IPR000719; Fuk_pkinase.
CC InterPro: IPR003116; RBD.
CC InterPro: IPR004040; STY_pkinase.
CC InterPro: IPR002293; Ser_Thr_pkinase.
CC Pfam: pf00069; pkinase; 1.
CC Pfam: pf00140; DAG_PE-Bind; 1.
CC Pfam: pf02196; RBD; 1.
CC Pfam: pf000001; Fuk_pkinase; 1.
CC SMART: SM00109; CL; 1.
CC SMART: SM00455; RBD; 1.
CC SMART: SM00221; STYPE; 1
CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE: PS03081; DAG_PE_BIND_DOM_2; 1.
CC PROSITE: PS03197; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS04011; PROTEIN_KINASE_DOM_1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP binding; Zinc;
KW Diol-ester binding.
EI DOMAIN 171 217 PEPTID-ESTERASE AND DAG BINDING.
EI DOMAIN 481 748 PROTEIN KINASE.

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FT NP_BIND 487 495 ATP (BY SIMILARITY).
FT BINDING 507 507 ATP (BY SIMILARITY).
FT ACT_SITE 602 602 BY SIMILARITY.
FT CONFLICT 801 801 A -> R (IN REF. 1).
SQ SEQUENCE 813 AA, 90406 MW, 6.924966E+04 kDa, 1149649 CR664;
Query Match 81.2%; Score 26; DP 1; Length 813;
Best Local Similarity 80.0%; Pred. No. 3,4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 GFFRN 7
11111
1b 445 GFFRN 449
RESULT 47
GLND_NEIMA STANDARD: PFI: 852 AA.
AC Q50079;
DI 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE [protein-P11] uridylyltransferase (EC 2.7.7.59) (P11 uridylyl
DE transferase) (Uridylyl removing enzyme) (Urase).
DS GLND OR NMA1874.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID 46699;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN 2291 / Ser. group A / Serotype 4A;
RX MEDLINE 926979; PubMed 10761916;
RA Eickbush S.H., Adams M., Jakes K.B., Bentley S.H., Churcher C.,
RA Klee S.P., Morrell G., Basham D., Brown D., Chillingworth T.,
RA Davies S.M., Davis P., Dingle V., Drenth W., Durbin R.,
RA Eickbush H., Heath S., Meade S., Mouton R., Quail M.A.,
RA Rabadan A., Raftery L., Rupp B., Simmonds M., Skellern J.,
RA Whithead S., Spratt R.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 2291.",
RL Nature 404:502-506(2000).
CC -! FUNCTION: REGULATES HYDXYLATION OR DEHYDXYLATION THE P11
CC (GLND) REGULATORY PROTEIN (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: UDP + [protein-P11] -> diphosphate + uridylyl-
CC [protein-P11].
CC -! SIMILARITY: BELONGS TO THE GLND FAMILY.
CC
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CC
CC EMBL: AL162755; CA884620.1;
CC InterPro: IPR002412; ACT.
CC InterPro: IPR002819; HU.
CC InterPro: IPR008607; ME_Please_HBO.
CC Pfam: pf01842; ACT; 2.
CC Pfam: pf01966; RBD; 1.
CC SMART: SM00471; HBD; 1.
CC SMART: SM00471; HBD; 1.
CC Transferrase; Nucleoside transferase; Complete proteome.
SQ SEQUENCE 852 AA, 97007 MW, 1149676077 kDa, 1149649 CR664;
Query Match 81.2%; Score 26; DP 1; Length 852;
Best Local Similarity 80.0%; Pred. No. 3,4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 GFFRN 7
11111
1b 391 GFFRN 395

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Query Match          81.2%  Score 26; DB 1; Length 1030;
Best Local Similarity 80.9%  Pred. No. 4,400,000;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

99 3 GIVEN 7
10 954 OFFER 950
11 1111
12 954 OFFER 950

RESULT 40
ID ATHA_MOUSE STANDARD: PRT: 1032 AA.
AC G64446; G95CV46;
DT 15-JUN-2002 (Rel. 41, last sequence update)
DI 15-JUN-2002 (Rel. 41, last annotation update)
DE Potassium-transporting ATPase alpha chain 1 (P: 3.5, 1.10) (Proton
GN pump) (Gastric H+/K+ ATPase alpha subunit).
GN ATP4A.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID 10116;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN BALB/c; Tissue: Gastric; Sex: Male.
EX MEDLINE 95282414; PubMed 7762414.
RA Matthews P.M.; Clancy D.; Gaisler P.; Garcia K.; Horikawa J. D.;
RA Kradetzki J. P.; Rossier B. C.;
R1 "Primary structure and functional expression of the mouse and frog
R1 alpha subunit of the gastric H+/K+ ATPase."
R1 Am. J. Physiol. 268:G1207-G1214 (1995).
RN 12
RP SEQUENCE OF 221-1032 FROM N.A.
RC STRAIN C57BL/6J; Tissue: Tongue;
EX MEDLINE 21085660; PubMed 11217851;
RA Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;
RA Arakawa T.; Hara A.; Fukunishi Y.; Konno H.; Adachi J.; Fukuda S.;
RA Aizawa K.; Iwata M.; Nishi K.; Miyasawa H.; Kudo S.; Yamashita T.;
RA Saito T.; Iwaki Y.; Gajdosi T.; Bono H.; Kasukawa T.; Saito R.;
RA Kadota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Casavant T.;
RA Fleischnann W.; Gaasterland T.; Gliss C.; Kling B.; Kochiwa H.;
RA Kuehl P.; Lewis S.; Matsuo Y.; Nikaide I.; Pesole G.; Quackenbush J.;
RA Schriml L.M.; Stachli P.; Suzuki R.; Tomita R.; Wagner L.; Washio T.;
RA Sakai K.; Okido T.; Patino M.; Aono H.; Baldarelli R.; Barish G.;
RA Nakai J.; Boftelli D.; Bojunga R.; Carninci P.; de Bonaldo M.P.;
RA Brownstein M.J.; Bull C.; Fletcher C.; Fujita M.; Gariboldi M.;
RA Gustinech S.; Hill D.; Holman M.; Hume D.A.; Kamiya M.; Lee N.H.;
RA Lyons P.; Marchionni L.; Mashima H.; Marzulli J.; Mombaerts P.;
RA Rardone P.; Ring B.; Rinehart M.; Rodriguez L.; Sakaguchi N.;
RA Sasaki H.; Sato K.; Schenkebach C.; Soga T.; Shibata Y.; Storch K.-P.;
RA Suzuki H.; Toyosaka K.; Wast K.R.; Wolff C.; Whitlaker G.; Wilming L.;
RA Wynshaw Boris A.; Yoshida K.; Yasenawa Y.; Kawaji H.; Katsuki S.;
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
R1 Nature 409:685-690 (2001).
CC 1-1 FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE
CC EXCHANGE OF H(+) AND K(+) IONS ACROSS THE PLASMA MEMBRANE.
CC RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
CC 1-1 CATALYTIC ACTIVITY: ATP + H2O + H+(+) -> K(+) + ADP +
CC phosphate + H+(out) + K+(in).
CC 1-1 SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
CC 1-1 SUBCELLULAR LOCATION: Integral membrane protein.
CC 1-1 SIMILARITY: BELONGS TO THE GATION TRANSPORTER ATPASES FAMILY
CC (EL-E2 ATPASES). SUBFAMILY 11C.
CC
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CC
CC EMBL: U17282; AAA79514.1; -.
CC EMBL: AK009674; PAP26432.1; -.
CC DR HSSD: P04191; 1E0L.
CC DR MGD: M01:88113; Alp4a.
CC DR InterPro: IPR004014; ATPase_E1-E2.
CC DR InterPro: IPR000661; H+/K+ATPase.
CC DR InterPro: IPR001454; Hydrolase/hydrolase.
CC DR Pfam: PF00122; E1-E2_ATPase; 1.
CC DR Pfam: PF00689; Cation_ATPase_G; 2.
CC DR Pfam: PF00690; Cation_ATPase_N; 1.
CC DR Pfam: PF00702; Hydrolase; 1.
CC DR TIGRfam: TIGR01106; X_K_ATPase_alp; 1.
CC DR PROSITE: PS00154; ATPase_E1-E2; 1.
CC DR Hydrolase, Potassium Transport; Hydrolase Ion Transport; Transmembrane;
CC KW Phosphorylation; ATP-Binding; Matheium; Metal-binding.
CC BY SIMILARITY.
CC INIT MET 0 0
CC FT DOMAIN 1 95
CC FT TRANSMEM 96 116
CC FT DERAIN 117 129
CC FT TRANSMEM 140 160
CC FT DERAIN 161 296
CC FT TRANSMEM 297 316
CC FT DOMAIN 317 328
CC FT TRANSMEM 329 346
CC FT DERAIN 347 780
CC FT TRANSMEM 781 800
CC FT DOMAIN 801 841
CC FT TRANSMEM 842 851
CC FT DERAIN 852 874
CC FT TRANSMEM 875 926
CC FT DOMAIN 927 946
CC FT TRANSMEM 947 960
CC FT DERAIN 961 979
CC FT TRANSMEM 980 994
CC FT TRANSMEM 995 1015
CC FT DOMAIN 1016 1032
CC FT MOD_RES 384 384
CC FT MOD_RES 951 951
CC FT METAL 725 725
CC FT METAL 729 729
CC FT CONFLICT 927 927
CC FT CONFLICT 1029 1029
CC FT SEQUENCE 1032 AA; 114894 MW; 0661B6474F0376D0 SR664;
CC
CC Query Match          81.2%  Score 26; DB 1; Length 1032;
CC Best Local Similarity 80.9%  Pred. No. 4,400,000;
CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC 27 3 GIVEN 7
CC 10 954 OFFER 950
CC 11 1111
CC 12 954 OFFER 950
CC
CC RESULT 41
CC ID ATHA_RAT STANDARD: PRT: 1032 AA.
CC AC P09426; P70511; G63253; P97992;
CC DI 01-MAR-1989 (Rel. 10, Created)
CC DT 15-JUN-2002 (Rel. 41, last sequence update)
CC DI 15-JUN-2002 (Rel. 41, last annotation update)
CC DE Potassium-transporting ATPase alpha chain 1 (P: 3.5, 1.10) (Proton
CC GN pump) (Gastric H+/K+ ATPase alpha subunit).
CC GN ATP4A OR IKA.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC OX NCBI_TaxID 10116;
CC RN 1
CC RP SEQUENCE FROM N.A.

```

RX MEDLINE=87057483; PubMed=3024364;
 RA Shull G.P., Liggett J.R.;
 RT "Molecular cloning of the rat stomach (H⁺ + K⁺)-ATPase.";
 RL J. Biol. Chem. 261:16788-16794(1986)
 RN [2]
 RP REVISIONS.
 RA Shull G.E.;
 RL Submitted (FEB-1987) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 53-506 FROM N.A.
 RX MEDLINE=95142238; PubMed 7840253;
 RA Ahn K.Y., Kone B.C.;
 RT "Expression and cellular localization of mRNA encoding the 'gastric' isozyme of H⁺-K⁺-ATPase alpha-subunit in rat kidney.";
 RL Am. J. Physiol. 268:F99-F103(1995).
 RN [4]
 RP SEQUENCE OF 1-49 FROM N.A.
 RC ISSUP=Liver;
 RA Song L., Mortell P., Gantz L., Marini L.F., Yamada T.;
 RL Submitted (FEB 1993) to the EMBL/GenBank/DBJ databases
 RN [5]
 RP SEQUENCE OF 176-259 AND 435-465 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=9120294; PubMed=11494840;
 RA Oshima K.-I., Motajima K., Mahmood S., Shimada A., Tamura S., Maeda M., Futai M.;
 RT "Control region and gastric specific transcription of the rat H⁺-K⁺-ATPase alpha subunit gene.";
 RL FEBS Lett. 281:250-254(1991).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF H⁺ AND K⁺ IONS ACROSS THE PLASMA MEMBRANE. RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
 CC -!- CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) + K⁺(Out) = ADP + phosphate + H⁺(Out) + K⁺(In).
 CC -!- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIC
 CC
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 CC
 DR EMBL: J02649; AAA66036.1; ..
 DR EMBL: S74801; .. NOT_ANNOTATED_CDS.
 DR EMBL: L11569; AAA72454.1; ..
 DR EMBL: X61934; CAA43938.1; ..
 DR EMBL: X61935; CAA43939.1; ..
 DR PIR: A25344; A25344
 DR HSSP: P04191; IEUL.
 DR InterPro: IP0001757; ATPase_E1-E2.
 DR InterPro: IP0004014; Cation_ATPase.
 DR InterPro: I0606661; H⁺-K⁺ ATPase.
 DR InterPro: I06091153; H⁺ pump, hydrolase.
 DR Pfam: PF00122; E1-E2_ATPase; 2.
 DR Pfam: PF00689; Cation_ATPase_C; 1.
 DR Pfam: PF00690; Cation_ATPase_N; 2.
 DR Pfam: PF00702; Hydrolase; 1.
 DR TIGRfams: TIGR01106; X_K_ATPase_alp; 1.
 DR PROSITE: PS00154; ATPase_E1_P2; 1.
 KW hydrolase; potassium transport; hydronium ion transport; Transmembrane.
 KW phosphorylation; ATP-binding; Magnesium; Metal binding.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 116 POTENTIAL.
 FT DOMAIN 117 139 LUMENAL (POTENTIAL).
 FT TRANSMEM 140 160 POTENTIAL.
 FT DOMAIN 161 296 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 297 316 POTENTIAL.

FT DOMAIN 317 328 LUMENAL (POTENTIAL).
 FT TRANSMEM 329 345 POTENTIAL.
 FT DOMAIN 347 780 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 781 800 POTENTIAL.
 FT DOMAIN 801 810 LUMENAL (POTENTIAL).
 FT TRANSMEM 811 831 POTENTIAL.
 FT DOMAIN 832 851 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 852 874 POTENTIAL.
 FT DOMAIN 875 926 LUMENAL (POTENTIAL).
 FT TRANSMEM 927 946 POTENTIAL.
 FT DOMAIN 947 990 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 991 979 POTENTIAL.
 FT DOMAIN 980 995 LUMENAL (POTENTIAL).
 FT TRANSMEM 1016 1032 POTENTIAL.
 FT DOMAIN 1033 1032 POTENTIAL.
 FT MOD_RES 384 384
 FT MOD_RES 951 951
 FT METAL 725 725
 FT METAL 729 729
 FT ORGANELLOC 2 2
 SQ SEQUENCE 1032 AA: 113906 MW: 5045914827669876 CWC64;
 Query Match 81.2%; Score 26; DA 1; Length 1042;
 Best Local Similarity 80.0%; Pred. No. 4,4e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 27 3 CYPRN 7
 11111
 10 956 GFFRN 960
 RESULT 42
 ATHA_CANFA
 ID ATHA_CANFA STANDARD; PRI: 1033 AA.
 AC P50996;
 DT 01-JUL-1996 (Ref. 34, Created)
 DT 15-JUN-2002 (Ref. 41, Last sequence update)
 DT 15-JUN-2002 (Ref. 41, Last annotation update)
 DE Potassium-transporting ATPase alpha chain 1 (EC 3.6.4.10) (Proton pump) (Gastric H⁺/K⁺ ATPase alpha subunit).
 GN ATP4A.
 OS Canis familiaris (dog).
 EC Enkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 PY 09-11-1996 0915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RX MEDLINE=94071880; PubMed=8250881;
 RA Song L., Mortell M.P., Gantz L., Brown D.P., Yamada T.;
 RT "Molecular cloning and structural analysis of canine gastric H⁺-K⁺-ATPase.";
 RL Biochem. Biophys. Res. Commun. 196:1240-1247(1993).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF H⁺ AND K⁺ IONS ACROSS THE PLASMA MEMBRANE. RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
 CC -!- CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) + K⁺(Out) = ADP + phosphate + H⁺(Out) + K⁺(In).
 CC -!- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIC.
 CC
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 CC
 DR EMBL: L11569; AAA40848.1; ..
 DR HSSP: P04191; IEUL.

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DR InterPro: IPR001757; ATPase_E1_E2.
DR InterPro: IPR004014; Cation_ATPase.
DR InterPro: IPR006661; H+/K+_ATPase.
DR InterPro: IPR001454; Hlgase/hydrlase.
DR Pfam: PF00122; E1_E2_ATPase_1.
DR Pfam: PF00689; Cation_ATPase_C_1.
DR Pfam: PF00690; Cation_ATPase_N_1.
DR Pfam: PF00702; Hydrolase_1.
DR TIGRams: TIGR01106; X_K_ATPase_alp_1.
DR ProSITE: PS00154; ATPase_E1_E2_1.
KW Hydrolase; Potassium transport; Hydrogen ion transport; Transmembrane.
KW Phosphorylation; ATP-binding; Magnesium; Metal-binding
FT INIT_MET 0 0 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 96 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
FT DOMAIN 118 140 LUMENAL (POTENTIAL).
FT TRANSMEM 141 161 POTENTIAL.
FT DOMAIN 162 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 317 POTENTIAL.
FT DOMAIN 318 329 LUMENAL (POTENTIAL).
FT TRANSMEM 330 347 POTENTIAL.
FT DOMAIN 348 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 801 POTENTIAL.
FT DOMAIN 802 811 LUMENAL (POTENTIAL).
FT TRANSMEM 812 842 POTENTIAL.
FT DOMAIN 843 852 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 853 875 POTENTIAL.
FT DOMAIN 876 928 LUMENAL (POTENTIAL).
FT TRANSMEM 928 947 POTENTIAL.
FT DOMAIN 948 961 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 962 980 POTENTIAL.
FT DOMAIN 981 995 LUMENAL (POTENTIAL).
FT TRANSMEM 996 1016 POTENTIAL.
FT DOMAIN 1017 1033 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 552 552 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT METAL 726 726 MAGNESIUM (BY SIMILARITY).
FT METAL 730 730 MAGNESIUM (BY SIMILARITY).
DR SEQUENCE: 1033 AA; 113974 MW; 4525278C4E2658E8 CRC64;

Query Match: 81.2%; Score 26; DP 1; Length 1033;
Best local Similarity: 80.0%; Pred. No. 4.4e-02;
Matches 4; Conservation 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QYFN 7
Db 957 QYFN 961

RESULT 43
ATHA_P03 STANDARD; PRT: 1033 AA.
Ac P19156;
Dr 01-NOV-1999 (Rel. 16, Created)
Dr 15-JUN-2002 (Rel. 41, Last sequence update)
Dr 15-JUN-2002 (Rel. 41, Last annotation update)
Dr Potassium transporting ATPase alpha chain 1 (EC 3.6.3.10) (Proton pump) (Gastric H+/K+ ATPase alpha subunit).
CN ATHA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID 9823;
LN 111
RP SEQUENCE FROM N.A.
RX MEDLINE 89061712; PubMed 2848518;
RA Maeda M., Ishizaki J., Futai M.
RT "CDNA cloning and sequence determination of pig gastric H+-K+ ATPase."
RL Biochem. Biophys. Res. Commun. 157:204-209(1988).
RN 121
RP SEQUENCE OF 1-17.
RX MEDLINE 8625667; PubMed 4017415;

RA Lane L.K., Kirley T.L., Ball W.J., Jr.:
RT "Structural studies on H+/K+-ATPase: determination of the NH2-terminal amino acid sequences and immunoblotting reactivity with Na+/K+-ATPase."
RL Biochem. Biophys. Res. Commun. 138:185-192(1986).
RN 143
RX SEQUENCE of 1-10, AND PHOSPHORYLATION OF SER-26.
RX MEDLINE-97040701; PubMed-8886014;
RA Itoawa K., Kaya S., Shimada A., Imaizawa T., Maardh S., Corbin J.C.
RA Kikkawa U., Taniuchi K.:
RT "Ser-27, Tyr-10 and Tyr-7 in the alpha chain of pig stomach H+/K+ ATPase as Ca(2+)-dependent phosphorylatable sites by intrinsic and extrinsic protein kinases."
RL Biochem. Biophys. Res. Commun. 227:810-815(1996).
RN 144
RX PHOSPHORYLATION OF TYR-6 AND TYR-9.
RX MEDLINE-95318126; PubMed-7797549;
RA Itoawa K., Ishiguro T., Kaya S., Shimada A., Imaizawa T., Taniuchi K.:
RT "Reversible phosphorylation of both Tyr7 and Tyr10 in the alpha-chain of pig stomach H+/K+ ATPase by a membrane bound kinase and a phosphatase."
RL J. Biol. Chem. 270:15475-15478(1995).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF H(+) AND K(+) IONS ACROSS THE PLASMA MEMBRANE. RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
CC -1- CATALYTIC ACTIVITY: ATP + H(2O) + K(+)(in) + K(+)(out) ADP + phosphate + H(+)(out) + K(+)(in).
CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY 1IC.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/amboss/ or send an email to license@isb-sib.ch)
CC -----
DR EMBL, M22724; AAA1004.1; -.
DR PIR: A31671; A31671.
DR PIR: A34238; A34238.
DR HSSP: P04191; 1EHL.
DR InterPro: IPR001757; ATPase_E1_E2.
DR InterPro: IPR004014; Cation_ATPase.
DR InterPro: IPR006661; H+/K+_ATPase.
DR InterPro: IPR001454; Hlgase/hydrlase.
DR Pfam: PF00122; E1_E2_ATPase_1.
DR Pfam: PF00689; Cation_ATPase_C_1.
DR Pfam: PF00690; Cation_ATPase_N_1.
DR Pfam: PF00702; Hydrolase_1.
DR TIGRams: TIGR01106; X_K_ATPase_alp_1.
DR ProSITE: PS00154; ATPase_E1_E2_1.
KW Hydrolase; Potassium transport; Hydrogen ion transport; Transmembrane;
KW Phosphorylation; ATP-binding; Magnesium; Metal-binding.
FT INIT_MET 0 0 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 96 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
FT DOMAIN 118 140 LUMENAL (POTENTIAL).
FT TRANSMEM 141 161 POTENTIAL.
FT DOMAIN 162 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 317 POTENTIAL.
FT DOMAIN 318 329 LUMENAL (POTENTIAL).
FT TRANSMEM 330 347 POTENTIAL.
FT DOMAIN 348 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 801 POTENTIAL.
FT DOMAIN 802 811 LUMENAL (POTENTIAL).
FT TRANSMEM 812 842 POTENTIAL.
FT DOMAIN 843 852 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 853 875 POTENTIAL.
FT DOMAIN 876 928 LUMENAL (POTENTIAL).
FT TRANSMEM 928 947 POTENTIAL.

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GenCore version 5.1.4_p5_4578
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COM protein - protein search, using sw model.

Run on: April 30, 2003, 13:21:59 | Search time 66.1819 seconds
(without alignments)
21.797 Million cell updates/sec

Title: US-09-498-5560-79
Perfect score: 32
Sequence: 1XXCFYRN 7

Scoring table: BLOSUM62
Gapop 10 0 , Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Database :
SPTRMBL_21:*
1: sp_arched:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_recomb:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	30	93	8	77	16	Q9XK01	Q9XK01 escherichia
2	30	93	8	91	5	Q16948	Q16948 bacillostoma
3	30	93	9	102	5	Q963V9	Q963V9 bacillostoma
4	30	93	8	110	16	Q9KXV9	Q9KXV9 streptococcus
5	30	93	8	134	16	P74345	P74345 streptococcus
6	30	93	8	158	2	Q44390	Q44390 bacillus tu
7	30	93	8	172	14	Q9A2A6	Q9A2A6 bacillostoma
8	30	93	8	178	8	Q9TAJ9	Q9TAJ9 bacillostoma
9	30	93	8	184	5	Q96793	Q96793 bacillostoma
10	30	93	9	184	5	Q57312	Q57312 bacillus tu
11	30	93	9	216	17	Q8TNC2	Q8TNC2 metakansara
12	30	93	8	232	16	Q9X365	Q9X365 bacillus tu
13	30	93	8	230	12	Q903P4	Q903P4 bacillostoma
14	30	93	8	237	17	Q9HIV4	Q9HIV4 bacillostoma
15	30	93	8	256	17	Q92319	Q92319 bacillus tu
16	30	93	8	325	5	Q9KRX3	Q9KRX3 bacillus tu

90	27	81.4	593	10	Q8W410	Q8W410 arabidopsis	163	26	81.2	215	16	Q8W814	Q8W814 fusobacteri
91	27	84.4	596	2	Q46079	Q46079 pedobacter	164	26	81.2	234	16	Q8W512	Q8W512 aphid sal
92	27	84.4	597	2	Q61771	Q61771 caenorhabdi	165	26	81.2	239	16	Q8W512	Q8W512 brachydanio
93	27	84.4	524	16	Q8W837	Q8W837 deltamorus	166	26	81.2	249	4	Q8W809	Q8W809 homo sapien
94	27	84.4	530	1	Q66W60	Q66W60 homo sapien	167	26	81.2	249	11	Q8W811	Q8W811 mus muscula
95	27	84.4	530	11	Q8W118	Q8W118 mus muscula	168	26	81.2	252	16	Q8W819	Q8W819 rhizobium l
96	27	84.4	530	11	Q8W112	Q8W112 mus muscula	169	26	81.2	255	4	Q8W812	Q8W812 candida gla
97	27	84.4	530	1	Q6W872	Q6W872 drosophila	170	26	81.2	270	4	Q8W862	Q8W862 homo sapien
98	27	84.4	545	4	Q6W812	Q6W812 homo sapien	171	26	81.2	289	16	Q8W821	Q8W821 yersinia pe
99	27	84.4	545	5	Q6W183	Q6W183 drosophila	172	26	81.2	281	16	Q8W819	Q8W819 brachydanio
100	27	84.4	545	17	Q8W8012	Q8W8012 salicobas	173	26	81.2	282	16	Q8W806	Q8W806 streptococ
101	27	84.4	549	16	Q6W807	Q6W807 rhizobium m	174	26	81.2	292	6	Q8W836	Q8W836 marica fase
102	27	81.4	559	5	Q8W802	Q8W802 drosophila	175	26	81.2	298	5	Q8W114	Q8W114 caenorhabdi
103	27	84.4	564	11	Q8W116	Q8W116 mus muscula	176	26	81.2	309	11	Q8W214	Q8W214 mus muscula
104	27	84.4	589	11	Q8W117	Q8W117 mus muscula	177	26	81.2	322	13	Q8W217	Q8W217 arabidopsis
105	27	84.4	589	11	Q8W431	Q8W431 mus muscula	178	26	81.2	324	10	Q8W8X1	Q8W8X1 rhodospirill
106	27	84.4	592	16	Q8W112	Q8W112 clostridium	179	26	81.2	324	10	Q8W818	Q8W818 arabidopsis
107	27	84.4	596	5	Q8W184	Q8W184 drosophila	180	26	81.2	325	10	Q8W822	Q8W822 arabidopsis
108	27	84.4	599	17	Q8W874	Q8W874 fibrobacter	181	26	81.2	342	11	Q8W4107	Q8W4107 mus muscula
109	27	84.4	599	16	Q8W873	Q8W873 caenorhabdi	182	26	81.2	342	16	Q8W8X18	Q8W8X18 clostridium
110	27	84.4	564	5	Q8W813	Q8W813 electrothid	183	26	81.2	341	5	Q8W824	Q8W824 marica fase
111	27	84.4	567	5	Q8W113	Q8W113 giardia lam	184	26	81.2	349	5	Q8W876	Q8W876 streptomyces
112	27	84.4	570	6	Q8W875	Q8W875 elena cavia	185	26	81.2	349	5	Q8W806	Q8W806 thermomacet
113	27	84.4	677	10	Q8W129	Q8W129 arabidopsis	186	26	81.2	349	16	Q8W805	Q8W805 acetabularia
114	27	84.4	700	5	Q8W875	Q8W875 icistmania	187	26	81.2	349	17	Q8W874	Q8W874 halobacteri
115	27	84.4	704	5	Q8W8048	Q8W8048 giardia lam	188	26	81.2	369	17	Q8W8019	Q8W8019 streptomyces
116	27	84.4	709	5	Q8W117	Q8W117 giardia lam	189	26	81.2	373	16	Q8W113	Q8W113 yersinia pe
117	27	84.4	709	5	Q8W444	Q8W444 giardia lam	190	26	81.2	383	10	Q8W1056	Q8W1056 arabidopsis
118	27	84.4	725	5	Q8W872	Q8W872 drosophila	191	26	81.2	393	17	Q8W877	Q8W877 halobacteri
119	27	84.4	761	16	Q8W806	Q8W806 thermomacet	192	26	81.2	425	11	Q8W1045	Q8W1045 mus muscula
120	27	84.4	768	5	Q8W112	Q8W112 drosophila	193	26	81.2	437	16	Q8W142	Q8W142 yersinia pe
121	27	84.4	785	16	Q8W878	Q8W878 thermomacet	194	26	81.2	437	16	Q8W142	Q8W142 yersinia pe
122	27	84.4	804	5	Q8W877	Q8W877 drosophila	195	26	81.2	445	17	Q8W876	Q8W876 elena cavia
123	27	84.4	804	5	Q8W901	Q8W901 drosophila	196	26	81.2	451	17	Q8W871	Q8W871 yersinia pe
124	27	84.4	818	4	Q8W518	Q8W518 homo sapien	197	26	81.2	451	10	Q8W875	Q8W875 arabidopsis
125	27	84.4	818	10	Q8W827	Q8W827 arabidopsis	198	26	81.2	455	10	Q8W8N5	Q8W8N5 salt hydropis
126	27	84.4	818	11	Q8W897	Q8W897 rattus norv	199	26	81.2	477	16	Q8W8A9	Q8W8A9 rhizobium
127	27	84.4	839	5	Q8W870	Q8W870 caenorhabdi	200	26	81.2	484	5	Q8W1426	Q8W1426 caenorhabdi
128	27	84.4	944	4	Q8W504	Q8W504 arabidopsis	201	26	81.2	456	5	Q8W1426	Q8W1426 caenorhabdi
129	27	84.4	964	4	Q8W877	Q8W877 homo sapien	202	26	81.2	456	17	Q8W877	Q8W877 pseudomonas
130	27	84.4	965	10	Q8W115	Q8W115 arabidopsis	203	26	81.2	530	16	Q8W119	Q8W119 pseudomonas
131	27	84.4	1945	4	Q8W8W1	Q8W8W1 homo sapien	204	26	81.2	537	16	Q8W205	Q8W205 arabidoma sp
132	27	84.4	1113	5	Q8W8X1	Q8W8X1 caenorhabdi	205	26	81.2	560	5	Q8W013	Q8W013 giardia lam
133	27	84.4	1176	4	Q8W875	Q8W875 homo sapien	206	26	81.2	561	5	Q8W145	Q8W145 homo sapien
134	27	84.4	1199	5	Q8W141	Q8W141 caenorhabdi	207	26	81.2	519	5	Q8W146	Q8W146 homo sapien
135	27	84.4	1221	5	Q8W876	Q8W876 caenorhabdi	208	26	81.2	519	3	Q8W148	Q8W148 candida gla
136	27	84.4	1259	10	Q8W876	Q8W876 caenorhabdi	209	26	81.2	639	16	Q8W219	Q8W219 rhizobium m
137	27	84.4	1265	10	Q8W876	Q8W876 oryza sativ	210	26	81.2	662	8	Q8W1462	Q8W1462 phacelia ca
138	27	84.4	1346	5	Q8W876	Q8W876 caenorhabdi	211	26	81.2	719	16	Q8W8A4	Q8W8A4 salmonella
139	27	84.4	1364	4	Q8W891	Q8W891 homo sapien	212	26	81.2	719	16	Q8W8A6	Q8W8A6 salmonella
140	27	84.4	1766	4	Q8W874	Q8W874 homo sapien	213	26	81.2	812	5	Q8W4E3	Q8W4E3 caenorhabdi
141	27	84.4	1746	11	Q8W121	Q8W121 mus muscula	214	26	81.2	854	16	Q8W014	Q8W014 arabidoma sp
142	27	84.4	3599	13	Q8W874	Q8W874 brachydanio	215	26	81.2	895	16	Q8W259	Q8W259 synecocyst
143	27	84.4	3705	13	Q8W874	Q8W874 brachydanio	216	26	81.2	895	16	Q8W259	Q8W259 synecocyst
144	27	84.4	3715	11	Q8W876	Q8W876 salicobas	217	26	81.2	895	16	Q8W142	Q8W142 caenorhabdi
145	27	84.4	3715	11	Q8W876	Q8W876 mus muscula	218	26	81.2	949	11	Q8W811	Q8W811 rattus norv
146	27	84.4	3731	11	Q8W874	Q8W874 homo sapien	219	26	81.2	1025	11	Q8W1462	Q8W1462 mus muscula
147	27	84.4	3771	11	Q8W874	Q8W874 mus muscula	220	26	81.2	1025	16	Q8W878	Q8W878 arabidoma sp
148	27	84.4	3824	13	Q8W873	Q8W873 mus muscula	221	26	81.2	1242	5	Q8W8X3	Q8W8X3 drosophila
149	27	84.4	3825	11	Q8W145	Q8W145 brachydanio	222	26	81.2	1256	5	Q8W8A9	Q8W8A9 caenorhabdi
150	27	84.4	3087	5	Q8W802	Q8W802 mus muscula	223	26	81.2	1763	5	Q8W113	Q8W113 drosophila
151	26	81.2	43	4	Q8W876	Q8W876 plasmodium	224	26	81.2	1893	5	Q8W279	Q8W279 drosophila
152	26	81.2	81	4	Q8W116	Q8W116 starhybacter	225	26	81.2	1951	5	Q8W832	Q8W832 drosophila
153	26	81.2	106	11	Q8W822	Q8W822 mus muscula	226	26	81.2	2051	6	Q8W115	Q8W115 drosophila
154	26	81.2	122	11	Q8W116	Q8W116 mus muscula	227	26	81.2	28	6	Q8W449	Q8W449 bos taurus
155	26	81.2	124	13	Q8W876	Q8W876 rhodospirill	228	26	78.1	65	10	Q8W184	Q8W184 zea mays (m
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157	26	81.2	155	5	Q8W146	Q8W146 homo sapien	230	26	78.1	71	7	Q8W1361	Q8W1361 brachydanio
158	26	81.2	159	2	Q8W147	Q8W147 caenorhabdi	231	26	78.1	71	3	Q8W1369	Q8W1369 brachydanio
159	26	81.2	185	16	Q8W874	Q8W874 bacillus ps	232	26	78.1	72	16	Q8W8X4	Q8W8X4 brachydanio
160	26	81.2	185	16	Q8W146	Q8W146 neisseria m	233	26	78.1	72	16	Q8W8X4	Q8W8X4 brachydanio
161	26	81.2	209	17	Q8W8A9	Q8W8A9 salicobas	234	26	78.1	72	16	Q8W8X4	Q8W8X4 brachydanio
162	26	81.2	209	16	Q8W875	Q8W875 fusobacteri	235	26	78.1	91	5	Q8W877	Q8W877 mus postoma

236	25	79.1	91	16	Q91644	Q91641 myoblasts	300	25	76.1	94	15	Q91641
237	25	78.1	95	5	Q91644	Q91644 myoblasts	311	25	79.1	94	15	Q91644
238	25	78.1	96	5	Q91646	Q91646 myoblasts	311	25	79.1	94	15	Q91646
239	25	79.1	98	6	Q91647	Q91647 myoblasts	311	25	79.1	94	15	Q91647
240	25	79.1	100	5	Q91648	Q91648 myoblasts	311	25	79.1	94	15	Q91648
241	25	79.1	102	5	Q91649	Q91649 myoblasts	311	25	79.1	94	15	Q91649
242	25	79.1	104	12	Q91650	Q91650 myoblasts	311	25	79.1	94	15	Q91650
243	25	79.1	106	12	Q91651	Q91651 myoblasts	311	25	79.1	94	15	Q91651
244	25	79.1	108	12	Q91652	Q91652 myoblasts	311	25	79.1	94	15	Q91652
245	25	78.1	124	16	Q91658	Q91658 myoblasts	311	25	79.1	94	15	Q91658
246	25	78.1	124	16	Q91658	Q91658 myoblasts	311	25	79.1	94	15	Q91658
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248	25	79.1	143	16	Q91666	Q91666 myoblasts	311	25	79.1	94	15	Q91666
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261	25	79.1	176	14	Q91677	Q91677 myoblasts	311	25	79.1	94	15	Q91677
262	25	79.1	180	5	Q91675	Q91675 myoblasts	311	25	79.1	94	15	Q91675
263	25	78.1	181	5	Q91678	Q91678 myoblasts	311	25	79.1	94	15	Q91678
264	25	78.1	182	11	Q91682	Q91682 myoblasts	311	25	79.1	94	15	Q91682
265	25	78.1	188	11	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
266	25	79.1	190	16	Q91677	Q91677 myoblasts	311	25	79.1	94	15	Q91677
267	25	78.1	191	16	Q91677	Q91677 myoblasts	311	25	79.1	94	15	Q91677
268	25	78.1	194	3	Q91680	Q91680 myoblasts	311	25	79.1	94	15	Q91680
269	25	78.1	194	13	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
270	25	78.1	200	16	Q91687	Q91687 myoblasts	311	25	79.1	94	15	Q91687
271	25	78.1	204	11	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
272	25	78.1	204	16	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
273	25	78.1	204	16	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
274	25	78.1	210	17	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
275	25	78.1	213	17	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
276	25	78.1	215	15	Q91686	Q91686 myoblasts	311	25	79.1	94	15	Q91686
277	25	78.1	215	16	Q91686	Q91686 myoblasts	311	25	79.1	94	15	Q91686
278	25	78.1	216	5	Q91686	Q91686 myoblasts	311	25	79.1	94	15	Q91686
279	25	78.1	218	7	Q91686	Q91686 myoblasts	311	25	79.1	94	15	Q91686
280	25	78.1	227	10	Q91680	Q91680 myoblasts	311	25	79.1	94	15	Q91680
281	25	78.1	227	10	Q91680	Q91680 myoblasts	311	25	79.1	94	15	Q91680
282	25	78.1	227	10	Q91680	Q91680 myoblasts	311	25	79.1	94	15	Q91680
283	25	78.1	236	4	Q91683	Q91683 myoblasts	311	25	79.1	94	15	Q91683
284	25	78.1	236	7	Q91685	Q91685 myoblasts	311	25	79.1	94	15	Q91685
285	25	78.1	239	16	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
286	25	78.1	239	16	Q91681	Q91681 myoblasts	311	25	79.1	94	15	Q91681
287	25	78.1	244	16	Q91688	Q91688 myoblasts	311	25	79.1	94	15	Q91688
288	25	78.1	257	16	Q91684	Q91684 myoblasts	311	25	79.1	94	15	Q91684
289	25	78.1	265	5	Q91689	Q91689 myoblasts	311	25	79.1	94	15	Q91689
290	25	79.1	267	10	Q91689	Q91689 myoblasts	311	25	79.1	94	15	Q91689
291	25	79.1	270	5	Q91686	Q91686 myoblasts	311	25	79.1	94	15	Q91686
292	25	79.1	277	11	Q91697	Q91697 myoblasts	311	25	79.1	94	15	Q91697
293	25	79.1	280	16	Q91697	Q91697 myoblasts	311	25	79.1	94	15	Q91697
294	25	78.1	280	16	Q91697	Q91697 myoblasts	311	25	79.1	94	15	Q91697
295	25	78.1	290	12	Q91698	Q91698 myoblasts	311	25	79.1	94	15	Q91698
296	25	78.1	290	17	Q91698	Q91698 myoblasts	311	25	79.1	94	15	Q91698
297	25	78.1	294	17	Q91696	Q91696 myoblasts	311	25	79.1	94	15	Q91696
298	25	78.1	297	16	Q91691	Q91691 myoblasts	311	25	79.1	94	15	Q91691
299	25	78.1	299	16	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
300	25	78.1	300	16	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
301	25	78.1	300	16	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
302	25	78.1	303	16	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
303	25	78.1	307	10	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
304	25	78.1	307	10	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
305	25	78.1	307	10	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
306	25	78.1	308	11	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
307	25	78.1	311	11	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695
308	25	78.1	311	16	Q91695	Q91695 myoblasts	311	25	79.1	94	15	Q91695

382	25	78.1	498	16	Q8XV31	Q8XV31 raietania s	455	25	78.1	689	10	Q8W411	Q8W411 oryza sativ
383	25	78.1	499	16	Q8XV32	Q8XV32 rhizobium l	456	25	78.1	689	5	Q8W258	Q8W258 plasmodium
384	25	78.1	500	16	Q8XV33	Q8XV33 caenorhabdi	457	25	78.1	692	16	Q8W259	Q8W259 myobacteri
385	25	78.1	501	16	Q8XV34	Q8XV34 caenorhabdi	458	25	78.1	701	5	Q8W384	Q8W384 caenorhabdi
386	25	78.1	502	16	Q8XV35	Q8XV35 spiranthus	459	25	78.1	703	5	Q8W387	Q8W387 caenorhabdi
387	25	78.1	503	16	Q8XV36	Q8XV36 homo sapien	460	25	78.1	710	10	Q8W389	Q8W389 arabidopsis
388	25	78.1	504	16	Q8XV37	Q8XV37 homo sapien	461	25	78.1	729	16	Q8W390	Q8W390 myobacteri
389	25	78.1	505	16	Q8XV38	Q8XV38 homo sapien	462	25	78.1	735	16	Q8W391	Q8W391 myobacteri
390	25	78.1	506	16	Q8XV39	Q8XV39 homo sapien	463	25	78.1	745	16	Q8W392	Q8W392 myobacteri
391	25	78.1	507	16	Q8XV40	Q8XV40 mekela vira	464	25	78.1	747	10	Q8W393	Q8W393 arabidopsis
392	25	78.1	508	16	Q8XV41	Q8XV41 mekela vira	465	25	78.1	748	8	Q8W394	Q8W394 arabidopsis
393	25	78.1	509	16	Q8XV42	Q8XV42 caenorhabdi	466	25	78.1	754	8	Q8W395	Q8W395 arabidopsis
394	25	78.1	510	16	Q8XV43	Q8XV43 caenorhabdi	467	25	78.1	779	16	Q8W396	Q8W396 arabidopsis
395	25	78.1	511	16	Q8XV44	Q8XV44 caenorhabdi	468	25	78.1	801	17	Q8W397	Q8W397 arabidopsis
396	25	78.1	512	16	Q8XV45	Q8XV45 caenorhabdi	469	25	78.1	802	4	Q8W398	Q8W398 arabidopsis
397	25	78.1	513	16	Q8XV46	Q8XV46 caenorhabdi	470	25	78.1	902	16	Q8W399	Q8W399 arabidopsis
398	25	78.1	514	16	Q8XV47	Q8XV47 caenorhabdi	471	25	78.1	903	16	Q8W400	Q8W400 arabidopsis
399	25	78.1	515	16	Q8XV48	Q8XV48 caenorhabdi	472	25	78.1	917	16	Q8W401	Q8W401 arabidopsis
400	25	78.1	516	16	Q8XV49	Q8XV49 caenorhabdi	473	25	78.1	924	16	Q8W402	Q8W402 arabidopsis
401	25	78.1	517	16	Q8XV50	Q8XV50 caenorhabdi	474	25	78.1	861	4	Q8W403	Q8W403 arabidopsis
402	25	78.1	518	16	Q8XV51	Q8XV51 caenorhabdi	475	25	78.1	866	5	Q8W404	Q8W404 arabidopsis
403	25	78.1	519	16	Q8XV52	Q8XV52 caenorhabdi	476	25	78.1	866	5	Q8W405	Q8W405 arabidopsis
404	25	78.1	520	16	Q8XV53	Q8XV53 caenorhabdi	477	25	78.1	873	10	Q8W406	Q8W406 arabidopsis
405	25	78.1	521	16	Q8XV54	Q8XV54 caenorhabdi	478	25	78.1	979	10	Q8W407	Q8W407 arabidopsis
406	25	78.1	522	16	Q8XV55	Q8XV55 caenorhabdi	479	25	78.1	991	3	Q8W408	Q8W408 arabidopsis
407	25	78.1	523	16	Q8XV56	Q8XV56 caenorhabdi	480	25	78.1	992	3	Q8W409	Q8W409 arabidopsis
408	25	78.1	524	16	Q8XV57	Q8XV57 caenorhabdi	481	25	78.1	992	3	Q8W410	Q8W410 arabidopsis
409	25	78.1	525	16	Q8XV58	Q8XV58 caenorhabdi	482	25	78.1	992	3	Q8W411	Q8W411 arabidopsis
410	25	78.1	526	16	Q8XV59	Q8XV59 caenorhabdi	483	25	78.1	992	3	Q8W412	Q8W412 arabidopsis
411	25	78.1	527	16	Q8XV60	Q8XV60 caenorhabdi	484	25	78.1	992	3	Q8W413	Q8W413 arabidopsis
412	25	78.1	528	16	Q8XV61	Q8XV61 caenorhabdi	485	25	78.1	992	3	Q8W414	Q8W414 arabidopsis
413	25	78.1	529	16	Q8XV62	Q8XV62 caenorhabdi	486	25	78.1	992	3	Q8W415	Q8W415 arabidopsis
414	25	78.1	530	16	Q8XV63	Q8XV63 caenorhabdi	487	25	78.1	992	3	Q8W416	Q8W416 arabidopsis
415	25	78.1	531	16	Q8XV64	Q8XV64 caenorhabdi	488	25	78.1	992	3	Q8W417	Q8W417 arabidopsis
416	25	78.1	532	16	Q8XV65	Q8XV65 caenorhabdi	489	25	78.1	992	3	Q8W418	Q8W418 arabidopsis
417	25	78.1	533	16	Q8XV66	Q8XV66 caenorhabdi	490	25	78.1	992	3	Q8W419	Q8W419 arabidopsis
418	25	78.1	534	16	Q8XV67	Q8XV67 caenorhabdi	491	25	78.1	992	3	Q8W420	Q8W420 arabidopsis
419	25	78.1	535	16	Q8XV68	Q8XV68 caenorhabdi	492	25	78.1	992	3	Q8W421	Q8W421 arabidopsis
420	25	78.1	536	16	Q8XV69	Q8XV69 caenorhabdi	493	25	78.1	992	3	Q8W422	Q8W422 arabidopsis
421	25	78.1	537	16	Q8XV70	Q8XV70 caenorhabdi	494	25	78.1	992	3	Q8W423	Q8W423 arabidopsis
422	25	78.1	538	16	Q8XV71	Q8XV71 caenorhabdi	495	25	78.1	992	3	Q8W424	Q8W424 arabidopsis
423	25	78.1	539	16	Q8XV72	Q8XV72 caenorhabdi	496	25	78.1	992	3	Q8W425	Q8W425 arabidopsis
424	25	78.1	540	16	Q8XV73	Q8XV73 caenorhabdi	497	25	78.1	992	3	Q8W426	Q8W426 arabidopsis
425	25	78.1	541	16	Q8XV74	Q8XV74 caenorhabdi	498	25	78.1	992	3	Q8W427	Q8W427 arabidopsis
426	25	78.1	542	16	Q8XV75	Q8XV75 caenorhabdi	499	25	78.1	992	3	Q8W428	Q8W428 arabidopsis
427	25	78.1	543	16	Q8XV76	Q8XV76 caenorhabdi	500	25	78.1	992	3	Q8W429	Q8W429 arabidopsis
428	25	78.1	544	16	Q8XV77	Q8XV77 caenorhabdi	501	25	78.1	992	3	Q8W430	Q8W430 arabidopsis
429	25	78.1	545	16	Q8XV78	Q8XV78 caenorhabdi	502	25	78.1	992	3	Q8W431	Q8W431 arabidopsis
430	25	78.1	546	16	Q8XV79	Q8XV79 caenorhabdi	503	25	78.1	992	3	Q8W432	Q8W432 arabidopsis
431	25	78.1	547	16	Q8XV80	Q8XV80 caenorhabdi	504	25	78.1	992	3	Q8W433	Q8W433 arabidopsis
432	25	78.1	548	16	Q8XV81	Q8XV81 caenorhabdi	505	25	78.1	992	3	Q8W434	Q8W434 arabidopsis
433	25	78.1	549	16	Q8XV82	Q8XV82 caenorhabdi	506	25	78.1	992	3	Q8W435	Q8W435 arabidopsis
434	25	78.1	550	16	Q8XV83	Q8XV83 caenorhabdi	507	25	78.1	992	3	Q8W436	Q8W436 arabidopsis
435	25	78.1	551	16	Q8XV84	Q8XV84 caenorhabdi	508	25	78.1	992	3	Q8W437	Q8W437 arabidopsis
436	25	78.1	552	16	Q8XV85	Q8XV85 caenorhabdi	509	25	78.1	992	3	Q8W438	Q8W438 arabidopsis
437	25	78.1	553	16	Q8XV86	Q8XV86 caenorhabdi	510	25	78.1	992	3	Q8W439	Q8W439 arabidopsis
438	25	78.1	554	16	Q8XV87	Q8XV87 caenorhabdi	511	25	78.1	992	3	Q8W440	Q8W440 arabidopsis
439	25	78.1	555	16	Q8XV88	Q8XV88 caenorhabdi	512	25	78.1	992	3	Q8W441	Q8W441 arabidopsis
440	25	78.1	556	16	Q8XV89	Q8XV89 caenorhabdi	513	25	78.1	992	3	Q8W442	Q8W442 arabidopsis
441	25	78.1	557	16	Q8XV90	Q8XV90 caenorhabdi	514	25	78.1	992	3	Q8W443	Q8W443 arabidopsis
442	25	78.1	558	16	Q8XV91	Q8XV91 caenorhabdi	515	25	78.1	992	3	Q8W444	Q8W444 arabidopsis
443	25	78.1	559	16	Q8XV92	Q8XV92 caenorhabdi	516	25	78.1	992	3	Q8W445	Q8W445 arabidopsis
444	25	78.1	560	16	Q8XV93	Q8XV93 caenorhabdi	517	25	78.1	992	3	Q8W446	Q8W446 arabidopsis
445	25	78.1	561	16	Q8XV94	Q8XV94 caenorhabdi	518	25	78.1	992	3	Q8W447	Q8W447 arabidopsis
446	25	78.1	562	16	Q8XV95	Q8XV95 caenorhabdi	519	25	78.1	992	3	Q8W448	Q8W448 arabidopsis
447	25	78.1	563	16	Q8XV96	Q8XV96 caenorhabdi	520	25	78.1	992	3	Q8W449	Q8W449 arabidopsis
448	25	78.1	564	16	Q8XV97	Q8XV97 caenorhabdi	521	25	78.1	992	3	Q8W450	Q8W450 arabidopsis
449	25	78.1	565	16	Q8XV98	Q8XV98 caenorhabdi	522	25	78.1	992	3	Q8W451	Q8W451 arabidopsis
450	25	78.1	566	16	Q8XV99	Q8XV99 caenorhabdi	523	25	78.1	992	3	Q8W452	Q8W452 arabidopsis
451	25	78.1	567	16	Q8XV00	Q8XV00 caenorhabdi	524	25	78.1	992	3	Q8W453	Q8W453 arabidopsis
452	25	78.1	568	16	Q8XV01	Q8XV01 caenorhabdi	525	25	78.1	992	3	Q8W454	Q8W454 arabidopsis
453	25	78.1	569	16	Q8XV02	Q8XV02 caenorhabdi	526	25	78.1	992	3	Q8W455	Q8W455 arabidopsis
454	25	78.1	570	16	Q8XV03	Q8XV03 caenorhabdi	527	25	78.1	992	3	Q8W456	Q8W456 arabidopsis

528	25	78.1	1233	16	Q9P122	Q9P122 streptococcus	601	34	75.0	100	10	Q9P122	Q9P122 rhizobium m
529	25	78.1	1294	5	Q9P126	Q9P126 gram-negative	602	34	75.0	100	10	Q9P126	Q9P126 gram-negative
530	25	78.1	1336	5	Q9P126	Q9P126 gram-negative	603	34	75.0	100	10	Q9P126	Q9P126 gram-negative
531	25	78.1	1511	5	Q9P126	Q9P126 gram-negative	604	34	75.0	100	10	Q9P126	Q9P126 gram-negative
532	25	78.1	1522	2	Q9P126	Q9P126 gram-negative	605	34	75.0	100	10	Q9P126	Q9P126 gram-negative
533	25	78.1	1525	3	Q9P126	Q9P126 gram-negative	606	34	75.0	100	10	Q9P126	Q9P126 gram-negative
534	25	78.1	1526	16	Q9P126	Q9P126 gram-negative	607	34	75.0	100	10	Q9P126	Q9P126 gram-negative
535	25	78.1	1646	5	Q9P126	Q9P126 gram-negative	608	34	75.0	100	10	Q9P126	Q9P126 gram-negative
536	25	78.1	1808	2	Q9P126	Q9P126 gram-negative	609	34	75.0	100	10	Q9P126	Q9P126 gram-negative
537	25	78.1	2035	2	Q9P126	Q9P126 gram-negative	610	34	75.0	100	10	Q9P126	Q9P126 gram-negative
538	25	78.1	2039	16	Q9P126	Q9P126 gram-negative	611	34	75.0	100	10	Q9P126	Q9P126 gram-negative
539	25	78.1	2161	10	Q9P126	Q9P126 gram-negative	612	34	75.0	100	10	Q9P126	Q9P126 gram-negative
540	25	78.1	2164	12	Q9P126	Q9P126 gram-negative	613	34	75.0	100	10	Q9P126	Q9P126 gram-negative
541	25	78.1	3695	4	Q9P126	Q9P126 gram-negative	614	34	75.0	100	10	Q9P126	Q9P126 gram-negative
542	25	78.1	6077	12	Q9P126	Q9P126 gram-negative	615	34	75.0	100	10	Q9P126	Q9P126 gram-negative
543	25	78.1	6077	12	Q9P126	Q9P126 gram-negative	616	34	75.0	100	10	Q9P126	Q9P126 gram-negative
544	25	78.1	6077	12	Q9P126	Q9P126 gram-negative	617	34	75.0	100	10	Q9P126	Q9P126 gram-negative
545	25	78.1	6077	12	Q9P126	Q9P126 gram-negative	618	34	75.0	100	10	Q9P126	Q9P126 gram-negative
546	24	75.0	36	9	Q9P126	Q9P126 gram-negative	619	34	75.0	100	10	Q9P126	Q9P126 gram-negative
547	24	75.0	36	9	Q9P126	Q9P126 gram-negative	620	34	75.0	100	10	Q9P126	Q9P126 gram-negative
548	24	75.0	36	9	Q9P126	Q9P126 gram-negative	621	34	75.0	100	10	Q9P126	Q9P126 gram-negative
549	24	75.0	36	9	Q9P126	Q9P126 gram-negative	622	34	75.0	100	10	Q9P126	Q9P126 gram-negative
550	24	75.0	36	9	Q9P126	Q9P126 gram-negative	623	34	75.0	100	10	Q9P126	Q9P126 gram-negative
551	24	75.0	36	9	Q9P126	Q9P126 gram-negative	624	34	75.0	100	10	Q9P126	Q9P126 gram-negative
552	24	75.0	36	9	Q9P126	Q9P126 gram-negative	625	34	75.0	100	10	Q9P126	Q9P126 gram-negative
553	24	75.0	36	9	Q9P126	Q9P126 gram-negative	626	34	75.0	100	10	Q9P126	Q9P126 gram-negative
554	24	75.0	36	9	Q9P126	Q9P126 gram-negative	627	34	75.0	100	10	Q9P126	Q9P126 gram-negative
555	24	75.0	36	9	Q9P126	Q9P126 gram-negative	628	34	75.0	100	10	Q9P126	Q9P126 gram-negative
556	24	75.0	36	9	Q9P126	Q9P126 gram-negative	629	34	75.0	100	10	Q9P126	Q9P126 gram-negative
557	24	75.0	36	9	Q9P126	Q9P126 gram-negative	630	34	75.0	100	10	Q9P126	Q9P126 gram-negative
558	24	75.0	36	9	Q9P126	Q9P126 gram-negative	631	34	75.0	100	10	Q9P126	Q9P126 gram-negative
559	24	75.0	36	9	Q9P126	Q9P126 gram-negative	632	34	75.0	100	10	Q9P126	Q9P126 gram-negative
560	24	75.0	36	9	Q9P126	Q9P126 gram-negative	633	34	75.0	100	10	Q9P126	Q9P126 gram-negative
561	24	75.0	36	9	Q9P126	Q9P126 gram-negative	634	34	75.0	100	10	Q9P126	Q9P126 gram-negative
562	24	75.0	36	9	Q9P126	Q9P126 gram-negative	635	34	75.0	100	10	Q9P126	Q9P126 gram-negative
563	24	75.0	36	9	Q9P126	Q9P126 gram-negative	636	34	75.0	100	10	Q9P126	Q9P126 gram-negative
564	24	75.0	36	9	Q9P126	Q9P126 gram-negative	637	34	75.0	100	10	Q9P126	Q9P126 gram-negative
565	24	75.0	36	9	Q9P126	Q9P126 gram-negative	638	34	75.0	100	10	Q9P126	Q9P126 gram-negative
566	24	75.0	36	9	Q9P126	Q9P126 gram-negative	639	34	75.0	100	10	Q9P126	Q9P126 gram-negative
567	24	75.0	36	9	Q9P126	Q9P126 gram-negative	640	34	75.0	100	10	Q9P126	Q9P126 gram-negative
568	24	75.0	36	9	Q9P126	Q9P126 gram-negative	641	34	75.0	100	10	Q9P126	Q9P126 gram-negative
569	24	75.0	36	9	Q9P126	Q9P126 gram-negative	642	34	75.0	100	10	Q9P126	Q9P126 gram-negative
570	24	75.0	36	9	Q9P126	Q9P126 gram-negative	643	34	75.0	100	10	Q9P126	Q9P126 gram-negative
571	24	75.0	36	9	Q9P126	Q9P126 gram-negative	644	34	75.0	100	10	Q9P126	Q9P126 gram-negative
572	24	75.0	36	9	Q9P126	Q9P126 gram-negative	645	34	75.0	100	10	Q9P126	Q9P126 gram-negative
573	24	75.0	36	9	Q9P126	Q9P126 gram-negative	646	34	75.0	100	10	Q9P126	Q9P126 gram-negative
574	24	75.0	36	9	Q9P126	Q9P126 gram-negative	647	34	75.0	100	10	Q9P126	Q9P126 gram-negative
575	24	75.0	36	9	Q9P126	Q9P126 gram-negative	648	34	75.0	100	10	Q9P126	Q9P126 gram-negative
576	24	75.0	36	9	Q9P126	Q9P126 gram-negative	649	34	75.0	100	10	Q9P126	Q9P126 gram-negative
577	24	75.0	36	9	Q9P126	Q9P126 gram-negative	650	34	75.0	100	10	Q9P126	Q9P126 gram-negative
578	24	75.0	36	9	Q9P126	Q9P126 gram-negative	651	34	75.0	100	10	Q9P126	Q9P126 gram-negative
579	24	75.0	36	9	Q9P126	Q9P126 gram-negative	652	34	75.0	100	10	Q9P126	Q9P126 gram-negative
580	24	75.0	36	9	Q9P126	Q9P126 gram-negative	653	34	75.0	100	10	Q9P126	Q9P126 gram-negative
581	24	75.0	36	9	Q9P126	Q9P126 gram-negative	654	34	75.0	100	10	Q9P126	Q9P126 gram-negative
582	24	75.0	36	9	Q9P126	Q9P126 gram-negative	655	34	75.0	100	10	Q9P126	Q9P126 gram-negative
583	24	75.0	36	9	Q9P126	Q9P126 gram-negative	656	34	75.0	100	10	Q9P126	Q9P126 gram-negative
584	24	75.0	36	9	Q9P126	Q9P126 gram-negative	657	34	75.0	100	10	Q9P126	Q9P126 gram-negative
585	24	75.0	36	9	Q9P126	Q9P126 gram-negative	658	34	75.0	100	10	Q9P126	Q9P126 gram-negative
586	24	75.0	36	9	Q9P126	Q9P126 gram-negative	659	34	75.0	100	10	Q9P126	Q9P126 gram-negative
587	24	75.0	36	9	Q9P126	Q9P126 gram-negative	660	34	75.0	100	10	Q9P126	Q9P126 gram-negative
588	24	75.0	36	9	Q9P126	Q9P126 gram-negative	661	34	75.0	100	10	Q9P126	Q9P126 gram-negative
589	24	75.0	36	9	Q9P126	Q9P126 gram-negative	662	34	75.0	100	10	Q9P126	Q9P126 gram-negative
590	24	75.0	36	9	Q9P126	Q9P126 gram-negative	663	34	75.0	100	10	Q9P126	Q9P126 gram-negative
591	24	75.0	36	9	Q9P126	Q9P126 gram-negative	664	34	75.0	100	10	Q9P126	Q9P126 gram-negative
592	24	75.0	36	9	Q9P126	Q9P126 gram-negative	665	34	75.0	100	10	Q9P126	Q9P126 gram-negative
593	24	75.0	36	9	Q9P126	Q9P126 gram-negative	666	34	75.0	100	10	Q9P126	Q9P126 gram-negative
594	24	75.0	36	9	Q9P126	Q9P126 gram-negative	667	34	75.0	100	10	Q9P126	Q9P126 gram-negative
595	24	75.0	36	9	Q9P126	Q9P126 gram-negative	668	34	75.0	100	10	Q9P126	Q9P126 gram-negative
596	24	75.0	36	9	Q9P126	Q9P126 gram-negative	669	34	75.0	100	10	Q9P126	Q9P126 gram-negative
597	24	75.0	36	9	Q9P126	Q9P126 gram-negative	670	34	75.0	100	10	Q9P126	Q9P126 gram-negative
598	24	75.0	36	9	Q9P126	Q9P126 gram-negative	671	34	75.0	100	10	Q9P126	Q9P126 gram-negative
599	24	75.0	36	9	Q9P126	Q9P126 gram-negative	672	34	75.0	100	10	Q9P126	Q9P126 gram-negative
600	24	75.0	36	9	Q9P126	Q9P126 gram-negative	673	34	75.0	100	10	Q9P126	Q9P126 gram-negative

674	24	75.0	158	15	098XV3	098XV2 human, immun	747	24	75.0	175	17	09V9M1	098M1 streptococcus
675	24	75.0	158	16	091408	091408 pseudomonas	748	24	75.0	176	16	09CFP7	09CF17 lactococcus
676	24	75.0	158	16	090EL5	090EL5 pasteurella	749	24	75.0	177	12	09QV-2	09QV2 cyath virus
677	24	75.0	158	16	091167	091167 human immun	750	24	75.0	177	12	09QV-1	09QV1 cyath virus
678	24	75.0	160	16	09Y116	09Y116 raistonia s	751	24	75.0	178	5	09USG0	09US0 schizosacch
679	24	75.0	160	17	090216	090216 archaeglob	752	24	75.0	178	5	091101	091101 caenorhabdi
680	24	75.0	161	16	090594	090592 rhicobium i	753	24	75.0	178	5	090519	090519 human, immun
681	24	75.0	161	16	0909K1	0909K1 thermomac	754	24	75.0	179	15	090086	090086 variola vir
682	24	75.0	161	16	090956	090956 poliovirus r	755	24	75.0	179	15	090086	090086 variola vir
683	24	75.0	163	16	090952	090952 poliovirus m	756	24	75.0	179	15	090086	090086 variola vir
684	24	75.0	163	16	090952	090952 poliovirus m	757	24	75.0	180	1	090952	090952 variola vir
685	24	75.0	163	17	090957	090957 pyrobaculum	758	24	75.0	180	1	090957	090957 metabiosare
686	24	75.0	163	17	090958	090958 pyrobaculum	759	24	75.0	190	34	090957	090957 streptococ
687	24	75.0	163	17	090958	090958 pyrobaculum	760	24	75.0	190	34	090957	090957 streptococ
688	24	75.0	164	11	090958	090958 pyrobaculum	761	24	75.0	191	5	090958	090958 caenorhabdi
689	24	75.0	164	11	090958	090958 pyrobaculum	762	24	75.0	191	5	090958	090958 caenorhabdi
690	24	75.0	164	11	090958	090958 pyrobaculum	763	24	75.0	191	5	090958	090958 caenorhabdi
691	24	75.0	164	11	090958	090958 pyrobaculum	764	24	75.0	191	5	090958	090958 caenorhabdi
692	24	75.0	165	16	090958	090958 pyrobaculum	765	24	75.0	191	5	090958	090958 caenorhabdi
693	24	75.0	165	16	090958	090958 pyrobaculum	766	24	75.0	191	5	090958	090958 caenorhabdi
694	24	75.0	166	16	090958	090958 pyrobaculum	767	24	75.0	191	5	090958	090958 caenorhabdi
695	24	75.0	166	16	090958	090958 pyrobaculum	768	24	75.0	191	5	090958	090958 caenorhabdi
696	24	75.0	167	2	090958	090958 pyrobaculum	769	24	75.0	191	5	090958	090958 caenorhabdi
697	24	75.0	167	2	090958	090958 pyrobaculum	770	24	75.0	191	5	090958	090958 caenorhabdi
698	24	75.0	167	2	090958	090958 pyrobaculum	771	24	75.0	191	5	090958	090958 caenorhabdi
699	24	75.0	167	2	090958	090958 pyrobaculum	772	24	75.0	191	5	090958	090958 caenorhabdi
700	24	75.0	168	16	090958	090958 pyrobaculum	773	24	75.0	191	5	090958	090958 caenorhabdi
701	24	75.0	168	17	090958	090958 pyrobaculum	774	24	75.0	191	5	090958	090958 caenorhabdi
702	24	75.0	168	17	090958	090958 pyrobaculum	775	24	75.0	191	5	090958	090958 caenorhabdi
703	24	75.0	169	5	090958	090958 pyrobaculum	776	24	75.0	191	5	090958	090958 caenorhabdi
704	24	75.0	169	12	090958	090958 pyrobaculum	777	24	75.0	191	5	090958	090958 caenorhabdi
705	24	75.0	169	12	090958	090958 pyrobaculum	778	24	75.0	191	5	090958	090958 caenorhabdi
706	24	75.0	169	12	090958	090958 pyrobaculum	779	24	75.0	191	5	090958	090958 caenorhabdi
707	24	75.0	169	12	090958	090958 pyrobaculum	780	24	75.0	191	5	090958	090958 caenorhabdi
708	24	75.0	169	12	090958	090958 pyrobaculum	781	24	75.0	191	5	090958	090958 caenorhabdi
709	24	75.0	169	12	090958	090958 pyrobaculum	782	24	75.0	191	5	090958	090958 caenorhabdi
710	24	75.0	169	12	090958	090958 pyrobaculum	783	24	75.0	191	5	090958	090958 caenorhabdi
711	24	75.0	169	12	090958	090958 pyrobaculum	784	24	75.0	191	5	090958	090958 caenorhabdi
712	24	75.0	169	12	090958	090958 pyrobaculum	785	24	75.0	191	5	090958	090958 caenorhabdi
713	24	75.0	169	12	090958	090958 pyrobaculum	786	24	75.0	191	5	090958	090958 caenorhabdi
714	24	75.0	169	12	090958	090958 pyrobaculum	787	24	75.0	191	5	090958	090958 caenorhabdi
715	24	75.0	169	12	090958	090958 pyrobaculum	788	24	75.0	191	5	090958	090958 caenorhabdi
716	24	75.0	169	12	090958	090958 pyrobaculum	789	24	75.0	191	5	090958	090958 caenorhabdi
717	24	75.0	169	12	090958	090958 pyrobaculum	790	24	75.0	191	5	090958	090958 caenorhabdi
718	24	75.0	169	12	090958	090958 pyrobaculum	791	24	75.0	191	5	090958	090958 caenorhabdi
719	24	75.0	169	12	090958	090958 pyrobaculum	792	24	75.0	191	5	090958	090958 caenorhabdi
720	24	75.0	169	12	090958	090958 pyrobaculum	793	24	75.0	191	5	090958	090958 caenorhabdi
721	24	75.0	169	12	090958	090958 pyrobaculum	794	24	75.0	191	5	090958	090958 caenorhabdi
722	24	75.0	169	12	090958	090958 pyrobaculum	795	24	75.0	191	5	090958	090958 caenorhabdi
723	24	75.0	169	12	090958	090958 pyrobaculum	796	24	75.0	191	5	090958	090958 caenorhabdi
724	24	75.0	169	12	090958	090958 pyrobaculum	797	24	75.0	191	5	090958	090958 caenorhabdi
725	24	75.0	169	12	090958	090958 pyrobaculum	798	24	75.0	191	5	090958	090958 caenorhabdi
726	24	75.0	169	12	090958	090958 pyrobaculum	799	24	75.0	191	5	090958	090958 caenorhabdi
727	24	75.0	169	12	090958	090958 pyrobaculum	800	24	75.0	191	5	090958	090958 caenorhabdi
728	24	75.0	169	12	090958	090958 pyrobaculum	801	24	75.0	191	5	090958	090958 caenorhabdi
729	24	75.0	169	12	090958	090958 pyrobaculum	802	24	75.0	191	5	090958	090958 caenorhabdi
730	24	75.0	169	12	090958	090958 pyrobaculum	803	24	75.0	191	5	090958	090958 caenorhabdi
731	24	75.0	169	12	090958	090958 pyrobaculum	804	24	75.0	191	5	090958	090958 caenorhabdi
732	24	75.0	169	12	090958	090958 pyrobaculum	805	24	75.0	191	5	090958	090958 caenorhabdi
733	24	75.0	169	12	090958	090958 pyrobaculum	806	24	75.0	191	5	090958	090958 caenorhabdi
734	24	75.0	169	12	090958	090958 pyrobaculum	807	24	75.0	191	5	090958	090958 caenorhabdi
735	24	75.0	169	12	090958	090958 pyrobaculum	808	24	75.0	191	5	090958	090958 caenorhabdi
736	24	75.0	169	12	090958	090958 pyrobaculum	809	24	75.0	191	5	090958	090958 caenorhabdi
737	24	75.0	169	12	090958	090958 pyrobaculum	810	24	75.0	191	5	090958	090958 caenorhabdi
738	24	75.0	169	12	090958	090958 pyrobaculum	811	24	75.0	191	5	090958	090958 caenorhabdi
739	24	75.0	169	12	090958	090958 pyrobaculum	812	24	75.0	191	5	090958	090958 caenorhabdi
740	24	75.0	169	12	090958	090958 pyrobaculum	813	24	75.0	191	5	090958	090958 caenorhabdi
741	24	75.0	169	12	090958	090958 pyrobaculum	814	24	75.0	191	5	090958	090958 caenorhabdi
742	24	75.0	169	12	090958	090958 pyrobaculum	815	24	75.0	191	5	090958	090958 caenorhabdi
743	24	75.0	169	12	090958	090958 pyrobaculum	816	24	75.0	191	5	090958	090958 caenorhabdi
744	24	75.0	169	12	090958	090958 pyrobaculum	817	24	75.0	191	5	090958	090958 caenorhabdi
745	24	75.0	169	12	090958	090958 pyrobaculum	818	24	75.0	191	5	090958	090958 caenorhabdi
746	24	75.0	169	12	090958	090958 pyrobaculum	819	24	75.0	191	5	090958	090958 caenorhabdi
747	24	75.0	169	12	090958	090958 pyrobaculum	820	24	75.0	191	5	090958	090958 caenorhabdi

820	24	75.0	17	16	Q836D5	Q83455 fusobacteri	854	24	75.0	223	11	Q769V5	Q83455 mus musculu
821	24	75.0	199	5	Q836S3	Q83723 drosophila	894	24	75.0	223	17	Q769V5	Q83455 metabact
822	24	75.0	193	3	Q836V6	Q83655 pseudomonas	895	24	75.0	223	3	Q769V5	Q83455 pseudobacilli
823	24	75.0	194	3	Q836V7	Q83672 pseudomonas	896	24	75.0	224	16	Q836X2	Q83455 escherichia
824	24	75.0	194	3	Q836V7	Q83672 pseudomonas	897	24	75.0	224	16	Q836X2	Q83455 escherichia
825	24	75.0	194	3	Q836V7	Q83672 pseudomonas	898	24	75.0	225	12	Q836V7	Q83455 san muel
826	24	75.0	194	16	Q836N10	Q83610 salmonella	899	24	75.0	225	12	Q836V7	Q83455 salmonella
827	24	75.0	203	2	Q836V7	Q83677 streptococ	900	24	75.0	225	12	Q836V7	Q83455 streptococ
828	24	75.0	203	4	Q836V8	Q83678 streptococ	901	24	75.0	225	12	Q836V7	Q83455 streptococ
829	24	75.0	203	16	Q836V4	Q83631 human immun	902	24	75.0	226	2	Q836V8	Q83455 versinia pe
830	24	75.0	203	13	Q836V4	Q83631 human immun	903	24	75.0	226	2	Q836V8	Q83455 pseudomonas
831	24	75.0	203	13	Q836V4	Q83631 human immun	904	24	75.0	226	2	Q836V8	Q83455 pseudomonas
832	24	75.0	201	15	Q836V6	Q83635 human immun	905	24	75.0	226	2	Q836V8	Q83455 pseudomonas
833	24	75.0	202	8	Q836V6	Q83635 human immun	906	24	75.0	227	2	Q836V8	Q83455 drosophila
834	24	75.0	202	15	Q836V4	Q83631 human immun	907	24	75.0	227	16	Q836V8	Q83455 drosophila
835	24	75.0	202	15	Q836V4	Q83631 human immun	908	24	75.0	227	16	Q836V8	Q83455 drosophila
836	24	75.0	202	15	Q836V4	Q83631 human immun	909	24	75.0	228	16	Q836V8	Q83455 streptococ
837	24	75.0	203	15	Q836V6	Q83636 human immun	910	24	75.0	228	16	Q836V8	Q83455 streptococ
838	24	75.0	204	4	Q836V6	Q83636 human immun	911	24	75.0	229	16	Q836V8	Q83455 streptococ
839	24	75.0	204	17	Q836V8	Q83634 salitobus	912	24	75.0	230	5	Q836V8	Q83455 caenobact
840	24	75.0	206	5	Q836V8	Q83634 salitobus	913	24	75.0	231	5	Q836V8	Q83455 caenobact
841	24	75.0	205	11	Q836V8	Q83634 salitobus	914	24	75.0	231	5	Q836V8	Q83455 caenobact
842	24	75.0	205	15	Q836V8	Q83634 salitobus	915	24	75.0	232	11	Q836V8	Q83455 caenobact
843	24	75.0	206	15	Q836V8	Q83634 salitobus	916	24	75.0	233	11	Q836V8	Q83455 caenobact
844	24	75.0	207	16	Q836V4	Q83634 salitobus	917	24	75.0	234	16	Q836V4	Q83455 caenobact
845	24	75.0	207	16	Q836V4	Q83634 salitobus	918	24	75.0	235	16	Q836V4	Q83455 caenobact
846	24	75.0	208	16	Q836V4	Q83634 salitobus	919	24	75.0	236	16	Q836V4	Q83455 caenobact
847	24	75.0	209	16	Q836V4	Q83634 salitobus	920	24	75.0	237	16	Q836V4	Q83455 caenobact
848	24	75.0	209	16	Q836V4	Q83634 salitobus	921	24	75.0	238	16	Q836V4	Q83455 caenobact
849	24	75.0	209	15	Q836V8	Q83634 salitobus	922	24	75.0	23	16	Q836V8	Q83455 caenobact
850	24	75.0	209	15	Q836V8	Q83634 salitobus	923	24	75.0	235	11	Q836V8	Q83455 mus musculu
851	24	75.0	209	15	Q836V8	Q83634 salitobus	924	24	75.0	235	15	Q836V8	Q83455 human immun
852	24	75.0	209	16	Q836V4	Q83634 salitobus	925	24	75.0	236	4	Q836V4	Q83455 homo sapien
853	24	75.0	209	16	Q836V4	Q83634 salitobus	926	24	75.0	236	30	Q836V4	Q83455 homo sapien
854	24	75.0	209	16	Q836V4	Q83634 salitobus	927	24	75.0	237	3	Q836V4	Q83455 solanum tub
855	24	75.0	211	4	Q836V8	Q83634 salitobus	928	24	75.0	237	3	Q836V8	Q83455 metsetaria g
856	24	75.0	211	4	Q836V8	Q83634 salitobus	929	24	75.0	237	3	Q836V8	Q83455 salitobus
857	24	75.0	211	5	Q836V8	Q83634 salitobus	930	24	75.0	237	3	Q836V8	Q83455 staphylococ
858	24	75.0	212	5	Q836V8	Q83634 salitobus	931	24	75.0	237	16	Q836V8	Q83455 staphylococ
859	24	75.0	212	11	Q836V8	Q83634 salitobus	932	24	75.0	238	5	Q836V8	Q83455 periplaneta
860	24	75.0	213	5	Q836V8	Q83634 salitobus	933	24	75.0	238	9	Q836V8	Q83455 bacterioph
861	24	75.0	213	5	Q836V8	Q83634 salitobus	934	24	75.0	238	9	Q836V8	Q83455 mus musculu
862	24	75.0	214	16	Q836V8	Q83634 salitobus	935	24	75.0	239	9	Q836V8	Q83455 saliniphila t
863	24	75.0	214	16	Q836V8	Q83634 salitobus	936	24	75.0	240	10	Q836V8	Q83455 solanum tub
864	24	75.0	214	16	Q836V8	Q83634 salitobus	937	24	75.0	240	10	Q836V8	Q83455 solanum tub
865	24	75.0	214	9	Q836V8	Q83634 salitobus	938	24	75.0	241	5	Q836V8	Q83455 drosophila
866	24	75.0	214	17	Q836V8	Q83634 salitobus	939	24	75.0	241	5	Q836V8	Q83455 drosophila
867	24	75.0	215	15	Q836V8	Q83634 salitobus	940	24	75.0	242	17	Q836V8	Q83455 staphylococ
868	24	75.0	215	16	Q836V8	Q83634 salitobus	941	24	75.0	242	17	Q836V8	Q83455 pyrodictus
869	24	75.0	216	2	Q836V8	Q83634 salitobus	942	24	75.0	243	6	Q836V8	Q83455 pyrodictus
870	24	75.0	216	2	Q836V8	Q83634 salitobus	943	24	75.0	243	6	Q836V8	Q83455 saliniphila t
871	24	75.0	216	3	Q836V8	Q83634 salitobus	944	24	75.0	243	16	Q836V8	Q83455 saliniphila t
872	24	75.0	216	11	Q836V8	Q83634 salitobus	945	24	75.0	243	4	Q836V8	Q83455 homo sapien
873	24	75.0	216	17	Q836V8	Q83634 salitobus	946	24	75.0	245	5	Q836V8	Q83455 drosophila
874	24	75.0	217	5	Q836V8	Q83634 salitobus	947	24	75.0	245	5	Q836V8	Q83455 bos taurus
875	24	75.0	217	16	Q836V8	Q83634 salitobus	948	24	75.0	246	8	Q836V8	Q83455 ocellularia
876	24	75.0	217	16	Q836V8	Q83634 salitobus	949	24	75.0	246	16	Q836V8	Q83455 saliniphila t
877	24	75.0	217	16	Q836V8	Q83634 salitobus	950	24	75.0	246	16	Q836V8	Q83455 escherichia
878	24	75.0	219	16	Q836V8	Q83634 salitobus	951	24	75.0	246	16	Q836V8	Q83455 escherichia
879	24	75.0	219	10	Q836V8	Q83634 salitobus	952	24	75.0	246	11	Q836V8	Q83455 mus musculu
880	24	75.0	219	15	Q836V8	Q83634 salitobus	953	24	75.0	246	16	Q836V8	Q83455 versinia pe
881	24	75.0	219	16	Q836V8	Q83634 salitobus	954	24	75.0	246	16	Q836V8	Q83455 heliobacte
882	24	75.0	219	16	Q836V8	Q83634 salitobus	955	24	75.0	246	16	Q836V8	Q83455 heliobacte
883	24	75.0	219	16	Q836V8	Q83634 salitobus	956	24	75.0	246	16	Q836V8	Q83455 heliobacte
884	24	75.0	220	16	Q836V8	Q83634 salitobus	957	24	75.0	246	16	Q836V8	Q83455 heliobacte
885	24	75.0	220	2	Q836V8	Q83634 salitobus	958	24	75.0	247	2	Q836V8	Q83455 escherichia
886	24	75.0	220	4	Q836V8	Q83634 salitobus	959	24	75.0	247	16	Q836V8	Q83455 escherichia
887	24	75.0	220	15	Q836V8	Q83634 salitobus	960	24	75.0	247	16	Q836V8	Q83455 escherichia
888	24	75.0	220	16	Q836V8	Q83634 salitobus	961	24	75.0	248	16	Q836V8	Q83455 kaempferia
889	24	75.0	220	16	Q836V8	Q83634 salitobus	962	24	75.0	248	16	Q836V8	Q83455 kaempferia
890	24	75.0	221	16	Q836V8	Q83634 salitobus	963	24	75.0	248	16	Q836V8	Q83455 kaempferia
891	24	75.0	221	16	Q836V8	Q83634 salitobus	964	24	75.0	249	16	Q836V8	Q83455 kaempferia
892	24	75.0	223	16	Q836V8	Q83634 salitobus	965	24	75.0	249	11	Q836V8	Q83455 mus musculu

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966 24 75.0 249 16 Q98114 rhicobium l
967 24 75.0 249 16 Q83299 treponema p
968 24 75.0 251 5 Q12288 saccharomye
969 24 75.0 251 5 Q8SRW5 encaphalito
970 24 75.0 251 10 Q8SRJ9 solanum tub
971 24 75.0 251 19 Q8SA62 onchrychis
972 24 75.0 252 5 Q90133 leishmania
973 24 75.0 252 10 Q43814 solanum tub
974 24 75.0 252 10 Q46004 hordeum vul
975 24 75.0 253 2 Q91501 arena sativ
976 24 75.0 253 17 Q26841 methanobact
977 24 75.0 254 4 Q63216 homo sapien
978 24 75.0 254 4 Q63206 homo sapien
979 24 75.0 254 5 Q66589 caenorhabdi
980 24 75.0 254 10 Q46004 hordeum vul
981 24 75.0 254 10 Q46004 hordeum vul
982 24 75.0 254 10 Q46004 hordeum vul
983 24 75.0 254 10 Q46004 hordeum vul
984 24 75.0 254 10 Q46004 hordeum vul
985 24 75.0 254 10 Q46004 hordeum vul
986 24 75.0 254 10 Q46004 hordeum vul
987 24 75.0 254 10 Q46004 hordeum vul
988 24 75.0 254 10 Q46004 hordeum vul
989 24 75.0 254 10 Q46004 hordeum vul
990 24 75.0 254 10 Q46004 hordeum vul
991 24 75.0 254 10 Q46004 hordeum vul
992 24 75.0 254 10 Q46004 hordeum vul
993 24 75.0 254 10 Q46004 hordeum vul
994 24 75.0 254 10 Q46004 hordeum vul
995 24 75.0 254 10 Q46004 hordeum vul
996 24 75.0 255 11 Q82A76 yersinia pe
997 24 75.0 256 11 Q40761 yersinia pe
998 24 75.0 257 16 Q91437 pseudomon
999 24 75.0 257 16 Q91437 pseudomon
1000 24 75.0 259 5 Q96K90 drosophila

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ALIGNMENTS

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RESULT 1
Q9X9Q1 PRELIMINARY: PRT: 77 AA.
ID Q9X9Q1
AC Q9X9Q1
DI 01-MAR-2002 (TrEMBLrel. 29, Created)
DI 01-MAR-2002 (TrEMBLrel. 29, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein Z1846.
GN Z1846.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae
OC Escherichia.
OX NCBI_TaxID:8334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN: 75-117 / 11173 / ATCC 25692.
EX MEDLINE: 21074955; PubMed 11206551.
FA Perla N.L., Plunkett G. III, Borland V., Mau B., Glasner J.D.,
FA Rose D.J., Mayhew G.F., Evans P.S., Greer J., Kirkpatrick H.A.,
FA Postel G., Backett J., Klink S., Routh A., Shao Y., Miller L.,
FA Grobeck E. I., Davis N.W., Lim A., Gumbartz E.L., Petracusis K.,
FA Avelar J., Anantharaman T.S., Lin J., Yen G., Schwartz D.S.,
FA Welch R.A., Blattner F.R.
FA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
FA Nature 409:529-533(2001).
DI EMPN: AF095427; Acc55694.1
DR Hypothetical proteins; Complete proteome.
SQ SEQUENCE 77 AA: 6087 MW: F85056712A58545E CR064;
Query Match 94.8%; Score 40; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 GYRN 7
DB 62 GYRN 66
ID Q16938 PRELIMINARY: PRT: 91 AA.
AC Q16938;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant protein C2 precursor (Fragment).
OS Anacylostoma sp. (flatworm).
OC Platyhelminthes; Platyhelminthes; Anacylostomidae; Anacylostoma.
OC Anacylostoma sp. (flatworm).
OX NCBI_TaxID:29470;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 98298719; PubMed 9634780;
EX Bostats J.S., Messersmith R., Le Royset A., Fiechtent D.,
EX van den Brande L., Ganssens M.J., Lauwereys M., Vlasuk G.P.,
EX Staussens P.F.;
EX "Surface expression and lipid based detection of PHAS fused to
EX filamentous phage gene VI."
EX Biotechnology 13:379-382(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE: 96312555; PubMed 8700900;
EX Staussens P., Beraud F.W., Ganssens M., Jaspers L., Laroche Y.,
EX Bostats J.S., Messersmith R., Lauwereys M., Cappelletto M., Botez P.J.,
EX Lasters I., Vlasuk G.P.;
EX "Anticoagulant repertoire of the hookworm Anacylostoma caninum."
EX Proc. Natl. Acad. Sci. U.S.A. 93:2149-2154(1996).
DI EMPN: 240733; Acc47080.1;
DR BSSP: P56682; IDV.
DR InterPro: IPR000561; EXP-like.
DR InterPro: IPR002919; TIL_Ysrich.
DR Pfam: PF01826; TIL1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
KW Signal
FT SIGNAL 1 7
FT CHAIN 8 91
SQ SEQUENCE 91 AA: 10358 MW: E2B13F4597C24DA CR664;
Query Match 93.8%; Score 40; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
Q962V8 PRELIMINARY: PRT: 102 AA.
ID Q962V8
AC Q962V8;
DI 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anticoagulant peptide-1 precursor.
OS Anacylostoma sp.
OC Platyhelminthes; Platyhelminthes; Anacylostomidae; Anacylostoma.
OC Anacylostoma sp.
OX NCBI_TaxID:53426;
RN [1]
RP SEQUENCE FROM N.A.
RC "Cloning of the major factor Xa inhibitor (AcvAP-1) from Anacylostoma
RI Anacylostoma."

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RL Submitted (JUL 2001) to the EMBL/GenBank/TrEMBL databases.
 DB EMBL: A839710; AAK81733.1; ...
 DR InterPro: IPR000561; PIP-1186.
 DE InterPro: IPR000561, PIP-1186.
 DE Pfam: PF01826; TIR1.
 DE PROSITE: PS01186; ERF_2; "IPN"WN_1
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 102 ANTI-COAGULANT PEPTIDE-1.
 SC SEQUENCE 102 AA; 1183 MW; 31572598a9f73d77e7f4.

Query Match 93.9%; Score 30; IP 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7

DB 71 GYRN 75

RESULT 4

Q9KYV8 PRELIMINARY; PRT; 110 AA.
 AC Q9KYV8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein SC03187.
 GN SC03187 OR SC22.04.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacterlia; Actinobacteridae;
 OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces;
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Pabnickel-Sch F., Rajandream M.A., Rothermel K., Butler S.,
 RA Sequer K., Saunders P., Sharp S., Squares P., Squires S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall R.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL355832; CAP09971.1.
 KW Hypothetical protein
 SC SEQUENCE 110 AA; 10931 MW; 09a90f52925a9fa92c64;

Query Match 93.9%; Score 30; IP 16; Length 110;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 51 GYRN 55

RESULT 5

P74345 PRELIMINARY; PRT; 134 AA.
 AC P74345;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein str1528.
 GN SLR1528
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;

KN SEQUENCE FROM N.A.
 RF MEDLINE:9736121; PubMed:9955231;
 FA Hinkel J., Sato S., Fukui H., Iwata A., Asanuma Y., Nakamura Y.,
 FA Miyajima H., Hirosewa M., Shibata M., Saitoh M., Saitoh T.,
 FA Hasegawa T., Watanabe A., Maraki A., Nakagaki Y., Miyake Y., Shimura S.,
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 Tabata S.;
 RA "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC 6803. II. Sequence determination of the
 F1 entire genome and assignment of potential protein coding regions.";
 EL DNA Res. 2:109-134(1995).
 DR EMBL: D50914; BAA18434.1;
 KW Hypothetical protein; Complete proteome.
 SC SEQUENCE 134 AA; 14545 MW; 7E5414E80FH44D10 C8C64;

Query Match 93.8%; Score 30; IP 16; Length 134;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 27 GYRN 31

RESULT 6

Q44490 PRELIMINARY; PRT; 158 AA.
 AC Q44490;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Orf2.
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=1172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29413;
 RA Thiel T., Lyons E.M., Erker J.C., Ernst A.;
 RA "A novel type of protein in the cell wall of the cyst-forming
 cyanobacterium.";
 EL Proc. Natl. Acad. Sci. U.S.A. 92:9458-9462(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29413;
 RA Thiel T., Lyons E.M., Erker J.C.;
 FL Submitted (JUN 1996) to the EMBL/GenBank/TrEMBL databases.
 DR EMBL: U49859; AAU4026.1; ...
 DR EMBL: U49859; AAU4026.1; ...
 DR Pfam: PF03270; D0F269; 1;
 SC SEQUENCE 158 AA; 17791 MW; D157E0F59C364F0B C8C64;

Query Match 93.8%; Score 30; IP 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 45 GYRN 49

RESULT 7

Q9A2A6 PRELIMINARY; PRT; 172 AA.
 AC Q9A2A6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein CC3660.
 GN CC3660.
 OS Caulobacter crescentus.

RA Hallow R.M., Hase A.L., Ravendall J., Raynor-Peterson L., Reddick E.M.,
RA Reesce V., Rios P.V., Roemer R.P., Ruppel D., Ruppel D., Ruppel S.,
RA Rorkova D., Rotchan M.P., Rouck T., Ruckenstein P., Ruffin P.,
RA Butlis K.C., Busam D.A., Butler B., Cadieux E., Center A., Chandra L.,
RA Cherry J.M., Cawley S., Dahlie C., Davenport L.P., Davies P.,
RA de Fabios B., Delcher A., Deng Z., Mays A.B., Dew L., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dupan-Loup S., Dupuy R.C., Dunn T.,
RA Durbin K.J., Evangelista C.C., Ferrara C., Fortner S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gard N.S., Gelhart W.M., Glasser K.,
RA Glodok A., Gou P., Gorrrell D.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman P., Hernandez T., Hough J.,
RA Rostin D., Houston K.A., Howland J.J., Wei M.H., Ibarra-Cu A.,
RA Jafari M., Kalash P., Karpf B.H., Kato T., Zeng L., Kato T., Kato W.A.,
RA Klinec B.L., Kodira G., Klatte J., Klatte J., Klatte J., Klatte J.,
RA Laska P., Liu Y., Lovelace A.A., Li F., Li Z., Liang Y., Lin X.,
RA Lin X., Mattiel P., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mohrly C., Morris J., Moshetti A.,
RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.,
RA Nelson D.F., Nelson P.A., Nye E., Nussbaum J.K., Pacht J.D.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
RA Palmer K., Penington K., Sanders R.D.C., Schofield P., Shen H.,
RA Shaw B., Shih K., Shih K., Shih K., Shih K., Shih K., Shih K.,
RA Shih K., Shih K., Shih K., Shih K., Shih K., Shih K., Shih K.,


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RESULT 20
Q9P819 PRELIMINARY: PRT: 362 AA.
ID Q9P819
AC Q9P819
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phosphoserine aminotransferase.
GN XP2326.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group.
OC Xylella
OX NCBI_TaxID=23371;
KN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 9A5C;
RX MEDLINE 20365717; PubMed 1091047;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarado P., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonavetti E.D., Bordin S., Bove J.M., Briones M.E.S.,
RA Bueco M.R., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Contino J.L., Cristofani M., Dias-Neto E., Decara C., El-Berry H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Figueira I.S., Franco S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.J., Hohlseil J.D., Junqueira M.H., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.F., Lalibert F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miranda E.C., Miyaki G.Y., Monteiro-Vitorello G.B.,
RA Moon B.H., Nadi M.A., Nascimento A.L.T.G., Netto L.P.S.,
RA Nhani A., Nhani M.A., Nunes L.P., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A.T., Pasquero J.R.,
RA Quaggio R.R., Roberto P.G., Rodrigues V., de Rosa A.T.M.,
RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.F., Silva W.A., Jr.,
RA da Silva V.F., Silvestri M.F., Silvestri W.J., de Souza A.A.,
RA de Souza A.P., Torresi M.P., Truffi P., Tsai S.M., Tsubako M.B.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zako M.A., Zatz M., Zeldin J., Zetubal J.C.,
RA "The genome sequence of the plant pathogen Xylella fastidiosa";
RT Nature 406:151-159(2000).
RL EMBL: AF004043; AAF85125.1; -.
DR BSSP: P24721; IRON.
DR InterPro: IPR000192; AminoTransIV.
DR Plan: PF00266; aminoTra_5; 1.
DR Problem: P0001544; Pser_aminTraust; 1.
KW Complete proteome.
SQ SEQUENCE 362 AA; 49615 MW; 10E451A7A6276A4 C99264;

Query Match 93.8%; Score 40; DB 16; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 284 GYRN 288
|||||

RESULT 21
Q9Y020 PRELIMINARY: PRT: 378 AA.
ID Q9Y020
AC Q9Y020
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable phosphoserine aminotransferase (PSAT) protein
DE (EC 2.6.1.52).
GN SERC OR RSC0903 OR R504512.

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OS Kalstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Kalstonia group.
OC Kalstonia
OX NCBI_TaxID 305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GM11000;
RX MEDLINE-21681879; PubMed 11823852;
RA Salendyuk M., Gelin S., Artigalade F., Garry J., Mancuet S.,
RA Ariat M., Billaut A., Brothier P., Camus J.C., Cattolico L.,
FA Chaudier M., Chetoui N., Claude-Robard C., Dumas S., Demange N.,
PA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
PA Squier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Kalstonia solanacearum";
RL Nature 415:457-502(2002).
DR EMBL: AL046061; CAP14605.1; -.
DR InterPro: IPR00192; AminoTransIV.
DE InterPro: IPR00192; Pser_aminTraust.
DE Plan: PF00266; aminoTra_5; 1.
DR Problem: P0001544; Pser_aminTraust; 1.
KW Transferrase; AminoTransferase; Complete proteome.
SQ SEQUENCE 378 AA; 41860 MW; 14CA56B9094E97B C9664;

Query Match 93.8%; Score 40; DB 16; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 300 GYRN 304
|||||

RESULT 22
ID 001482 PRELIMINARY: PRT: 408 AA.
AC 001482;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 46.2 kDa protein.
GN C06A5.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pterodermidae; Caenorhabditis.
OX NCBI_TaxID 6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RX MEDLINE 99066513; PubMed 9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RA Davidson S., Wohldmann P.;
RT "The sequence of C. elegans cosmid C06A5.";
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
EL 2001.11.13(11:13); bioRxiv 1094; bioRxiv 1094;
CC -1- SIMILARITY: CONTAINS 1 KING-TYPE ZINC FINGER.
DS EMBL_097193; AAF52442.1;
DR InterPro: IPR018411; Znf_Fing.
DR Plan: PF000097; ZF_C4HC4; 1.
DR SMART: SM00184; ZINC; 1.
DR PROSITE: PS00519; ZF_RING_1; 1.
KW Hypothetical protein; Zinc finger.

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AC STRAIN CV, COLUMBIA;
RX MEDLINE 21016719; PubMed-11130712;
RA Theodoridis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White G., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buchler E., Chan A., Chao Q., Chen H., Cheuk P.F., Chin C.W.,
RA Chung M.K., Cohen I., Conway A.R., Conway A.F., Cressy T.H., Fawcett F.,
RA Dunn J., Equi P., Feldblum T.V., Feng J.-D., Feng R., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetschka T., Korts D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee T.M., Leng C.A., Li T.H., Li Y.P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti K., Marziani A.,
RA Maltischer J., Miranda M., Nguyen M., Norman W.C., Osborne B.L.,
RA Paj G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tamburra G., Toriumi M.J., Town C.D.,
RA Dittmarck T., Van Aken C., Vayssiere M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Vontor T.C., Davis P.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000);
DR EMBL: AC024261; BAG528.1;
DR DSSP: P42265; ICR3;
DR InterPro: IPR001360; GH_1;
DR Pfam: PF002432; Glyco_hydro_1; 1;
DR PROSITE: PR00141; GHYDROLASE1;
DR PROSITE: ps00650; GH_1; 1;
DR PROSITE: ps00672; GLYCOSYL_HYDROL_F_2; 1;
DR PROSITE: ps00653; GLYCOSYL_HYDROL_F_2; 1;
SQ SEQUENCE 465 AA; 52158 MW; 9E540BA7FB86D492 CAC64;

Query Match 93.8%; Score 40; DB 10; Length 465;
Best local similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 331 GYRN 335

RESULT 26
Q02868 PRELIMINARY; PRI: 472 AA;
AC Q02868;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 01, Last annotation update)
DE 04ES100 (Fragment);
GN DRILO OR YOR428W;
OS Saccharomyces cerevisiae (baker's yeast);
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Fungi; Fungi; Fungi;
OC Saccharomycetes; Saccharomycetes; Saccharomycetes;
OX NCBI_TaxID 4942;
RN [1];
RP SEQUENCE FROM N.A.
RA STRAIN GPRN;
RL Submitted (DEC-1995) to the EMBL/GenBank/Joint Japanese
DR EMBL: D42227; AAA65444.1;
DR SCD: S0005955; DRI10;
SQ SEQUENCE 472 AA; 54409 MW; 4470N229E0C1979 CAC64;

Query Match 93.8%; Score 40; DB 4; Length 472;
Best local similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7
DB 272 GYRN 276

RESULT 27
Q096K0 PRELIMINARY; PRI: 475 AA;
AC Q096K0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-SEP-2001 (TREMBLrel. 19, Last annotation update)
DE Putative involvement in vesicular transport by similarity to yeast
DE SPAC1527.03;
GN SPAC1527.03;
OS Schizosaccharomyces pombe (fission yeast);
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetes; Schizosaccharomycetes;
OX NCBI_TaxID 4896;
RN [1];
RP SEQUENCE FROM N.A.
RA STRAIN 972H;
RA Seeger K., Harris D., Wood V., Fajandreu M.A., Bartoll R.G.;
RA Submitted (MAY-2000) to the EMBL/GenBank/Joint databases;
DR EMBL: AL355653; CAG0798.1; 1;
SQ SEQUENCE 475 AA; 53233 MW; 6767475E8545A78 CAC64;

Query Match 94.8%; Score 40; DB 4; Length 475;
Best local similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 293 GYRN 297

RESULT 28
Q09C65 PRELIMINARY; PRI: 475 AA;
AC Q09C65;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adult male lung cDNA, RIKEN full-length enriched library;
DE clone:1200002c07, full insert sequence;
GN WARS;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID 10090;
RN [1];
RP SEQUENCE FROM N.A.;
RX ST5A2N:55751.62; C1330P 1000;
RX MEDLINE-21085660; PubMed 11217851;
RA Kawai J., Shimadzu A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Asakawa T., Imai A., Imai S., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Akita K., Imai M., Imai K., Imai K., Imai K., Imai K., Imai K.,
RA Saito T., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Kadota K., Matsuda H.A., Ashburner M., Bartoll R., Gussard T.,
RA Fleischmann W., Gussard T., Gussard T., Gussard T., Gussard T.,
RA Kawai J., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Schmitt L.M., Staudt P., Suzuki K., Tomita M., Wadner L., Washio T.,
RA Sakai K., Okada T., Furum M., Aono H., Baldarelli R., Barish G.,
RA Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Brownstein M.J., Rott C., Fletcher C., Fujita M., Gariboli M.,
RA Gustafson S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons K., Karchenko L., Karchenko L., Karchenko L., Karchenko L.,
RA Nordene P., King R., Karchenko L., Karchenko L., Karchenko L.,
RA Sakai K., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Watanabe H., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Watanabe H., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y., Imai Y.,
RA Hayashizaki Y.;
RL "functional annotation of a full length mouse cDNA collection.";
RL Nature 409:645-650(2001);
DR EMBL: AK004541; BAB2057.1;
DR MGD: MGI:104640; WARS;
DR InterPro: IPR002305; tRNA-synt_1b;
DR InterPro: IPR001412; tRNA-synt_1;
DR InterPro: IPR002306; Ttp_tRNA synt 1b;

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DR InterPro: IPR000738: WHEP-TFS
DR Pfam: PF00579: tRNA-synt_1b: 1.
DR Pfam: PF00458: WHEP-TFS: 1.
DR PRINTS: PF01030: TPNASYNTHPTP.
DR TIGRFAMS: TIGR00233: tfs: 1.
DR PROSITE: PS00178: AA_IPNA_LIGASE_I: 1.
DR PROSITE: PS00762: WHEP-TFS: 1.
DR SMART: S00077: 475 AA, 5241 MW, C34E7E18C5210E12 CDS34.

Query Match 93.8%; Score 30; DP 11; Length 481.
Best Local Similarity 100.0%; Prod. No. 1 556c-79.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYRN 7
DB 250 GFYRN 254

RESULT 29
Q99J58 PRELIMINARY: PRT; 481 AA.
AC Q99J58;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TrpTfapfapf; tRNA synthetase.
GN WARS
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
PC TISSUE=MAMMARY TOWP WAP-TAC MODEL 5 MONTHS OLD;
RA Straussberg P.;
EL Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases
DR EMBL: BC000450; AAH04450.1; 5.
DR MGD: MGI:104630; WARS.
DR InterPro: IPR001412: tRNA-synt_1b.
DR InterPro: IPR002306: TP-TRNA-synt_1b.
DR InterPro: IPR000738: WHEP-TFS.
DR Pfam: PF00579: tRNA-synt_1b: 1.
DR Pfam: PF00458: WHEP-TFS: 1.
DR PRINTS: PR01030: TPNASYNTHPTP
DR TIGRFAMS: TIGR00233: tfs: 1
DR PROSITE: PS00178: AA_IPNA_LIGASE_I: 1
DR PROSITE: PS00762: WHEP-TFS: 1.
KW Amidacyl-tRNA synthetase
SQ SEQUENCE 481 AA; 54325 MW; A754E1ED0F582EF3 CRC64.

Query Match 93.8%; Score 30; DP 11; Length 481.
Best Local Similarity 100.0%; Prod. No. 1 556c-79.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYRN 7
DB 250 GFYRN 254

RESULT 30
Q91XK0 PRELIMINARY: PRT; 523 AA.
AC Q91XK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 0 day neonatal skin cDNA, EMBL full-length cDNA library;
DE clone:463340207, full insert sequence.
GN TYR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
PC TISSUE=SKIN;
RA Akahira S., Carninci P., Fukuda S., Fujinishi Y., Furuno M.,
Hanaoka T., Hara A., Hayatsu M., Hiramoto K., Hiraoka T., Hori F.,
Kamada H., Ishii Y., Itoh H., Iwata M., Kato H., Kawai M., Kojima Y.,
Kondo M., Koyu S., Kurihara S., Matsuyama T., Miyazaki A.,
Mizui Y., Muraoka K., Nishikawa K., Oh M., Okazaki Y., Okido T.,
Owada T., Saito F., Saito T., Sakai F., Sano H., Suzuki D.,
Shibata K., Shibata Y., Shikawa A., Shiraki T., Sodabe Y.,
Suzuki H., Tawara M., Tagawa A., Takahashi F., Tanaka T., Tojima Y.,
Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
EL Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
PC TISSUE=SKIN;
RA STELLINE-2195560; PubMed=11217851;
RA EKEN FANTOM Consortium.;
RT Functional annotation of a full length mouse cDNA collection.;
RN [3]
RP SEQUENCE FROM N.A.
PC TISSUE=SKIN;
RA STELLINE-99279452; PubMed=1049636;
RA Carninci P., Hayashizaki Y.;
RT High efficiency full length cDNA cloning.;
EL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
PC TISSUE=SKIN;
RA STELLINE-20499374; PubMed 11242159;
RA Carninci P., Shibata Y., Hayatsu M., Sugihara Y., Shibata K., Itoh M.,
Zhuo R., Ishii Y., Murakata M., Hayashizaki Y.;
RT Normalization and subtraction of cap-trapper selected cDNAs to
prepare full length cDNA libraries for rapid discovery of new genes.;
RN [5]
RP SEQUENCE FROM N.A.
PC TISSUE=SKIN;
RA STELLINE 20530913; PubMed=11076861;
RA Shibata K., Itoh M., Akawa K., Sasaki S., Sasaki N., Carninci P.,
Kondo M., Akiyama Y., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
Sami N., Ishii Y., Nakamura S., Hozumi M., Nishino T., Harada A.,
Yamamoto H., Matsumoto H., Sakaguchi S., Ikegami T., Kashikawa K.,
Fujisake S., Inoue K., Tojima Y., Izawa M., Ohara E., Watabiki M.,
Tanaka Y., Takikawa T., Goto F., Tanaka T., Matsuda S., Kawai J.,
Akahira Y., Matsuda S., Inoue Y., Fira A., Hayashizaki Y.;
RT "EKEN integrated sequence analysis (EISA) system" (84-format
sequence) pipeline with 384 multicapillary sequencer.;
EL EMBL: BC014619; BAB29466.1; 5.
DR MGD: MGI:98880; TYR.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR002227; Tyrosinase.
DR Pfam: PF00264; tyrosinase; 1.
DR PROSITE: PS00022; EGF_1; UNKN-WN_1.
DR PROSITE: PS01248; LAMININ_TYR_EGF; UNKN-WN_1.
DR PROSITE: PS00497; TYROSINASE_1; UNKN-WN_1.
DR PROSITE: PS00498; TYROSINASE_2; UNKN-WN_1.
SQ SEQUENCE 533 AA; 60606 MW; AAC109A973B05D6A CRC64.

Query Match 93.8%; Score 30; DP 11; Length 533.
Best Local Similarity 100.0%; Prod. No. 2 16-02.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYRN 7
DB 159 GFYRN 462

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Db      283 GFEYN 287

RESULT 33
Q9L127      PRELIMINARY, PRI: 611 AA.
AC      Q9L127
DT      01-OCT-2000 (TrEMBLrel_15, Created)
DT      01-OCT-2000 (TrEMBLrel_15, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel_17, Last annotation update)
DE      Netrin.
DE      C1-Netrin.
OS      Clona intestinalis.
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Ascidacea; Enteromorpha;
OC      Phlebobranchia; Cloniidae; Clona.
CX      RefSeqTaxID-7719;
KN      [1]
PE      SEQUENCE FROM N.A.
RA      Takamura K.;
FT      "Expression patterns of ascidian netrin homologues."
FL      PubMed 11507199; by the EMBL, GenBank, DDBP databases.
ER      EMBL: AB053352; FAY94 403.1;
DR      InterPro: IPR000561; EGF-like.
DR      InterPro: IPR002049; Laminin_EGF.
DR      InterPro: IPR001886; LamNT.
DR      InterPro: IPR001134; Netrin_C.
DR      Pfam: PF00053; laminin_EGF_2.
DR      Pfam: PF00055; laminin_Nterm; 1.
DR      Pfam: PF01759; NTR; 1.
DR      ProDom: PROD02082; LamNT; 1.
DR      SMART: SM00186; EGF_Lam_2.
DR      SMART: SM00136; LamNT; 1.
DR      ProSite: PS00022; PEP_1; UNPKNWN_1.
DR      ProSite: PS01248; LAMININ_TYPE_EGF; UNKNKNWN_1.
SQ      SEQUENCE 600 AA; 68312 MW; 227DS324D170CFB CRC64;

Query Match      93.8%; Score 40; DB 5; Length 600;
Best Local Similarity 100.0%; Pred. No. 2,4e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GFEYN 7
      [111]
DB      438 GFEYN 442

RESULT 34
Q9L175      PRELIMINARY, PRI: 611 AA.
AC      Q9L175;
DT      01-OCT-2000 (TrEMBLrel_15, Created)
DT      01-OCT-2000 (TrEMBLrel_15, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel_20, Last annotation update)
DE      Tyrosine phosphatase like protein (putative tyrosine
DE      phosphatase).
DE      ATG19420.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
CX      RefSeqTaxID-7719; by the EMBL, GenBank, DDBP databases.
KN      [1]
PE      SEQUENCE FROM N.A.
RA      Takamura Y.;
FT      "Structural analysis of Arabidopsis thaliana chromosome 4. I. Sequence
FT      features of the regions of 4,564,864 bp covered by sixty F1 and F2
      [2]
DB      438 GFEYN 442

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RT clones."
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,
  Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
  Yamamura Y., Yu G., Yu S., Bowser T., Kamaya A., Karlin-Neumann G.,
  Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
  Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
  Narasaka M., Nguyen M., Palm C.F., Sakurai T., Satou M., Seki M.,
  Shinn P., Srinivasan A., Shimozaki K., Davis F.W., Ecker J.P.,
  Theologis A.
PT "Full length cDNA of gene At3g19420 (GI:15240479)."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB025624; BAB02466.1;
DR EMBL: AY070042; AA49799.1;
DR InterPro: IP000340; PS_phosphatase
DR InterPro: IP000347; TYP_phosphatase
DR SMART: SM00012; TYP_DSPEC; 1.
DR PROSITE: PS00393; TYP_PHOSPHATASE_1; 1.
DR PROSITE: PS00556; TYP_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 611 AA: 66430 MW: 6474306577 CRC64;

Query Match 93.8%, Score 30; DR 10; Length 611;
Best Local Similarity 120.0%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7
DB 183 GYRN 187

RESULT 35
QY1W8 PRELIMINARY; PRI: 650 AA.
AC QY1W8
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DI 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DI 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Netrin.
GN CI-NET1A.
OS Clona intestinalis.
CC Eukaryota; Metazoa; Chordata; Vertebrata; Ascidiacea; Enteropneusta.
CC Phlebobranchia; Cloniidae; Clona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Takamura K.
RT "Expression patterns of ascidian netrin homologues."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases
DR EMBL: AB033331; BA034302.1;
DR HSP: P02468; 1KLO.
DR InterPro: IP000561; FGF-like.
DR InterPro: IP002049; laminin_EGF.
DR InterPro: IP001886; Lamnt.
DR InterPro: IP001134; Netrin_C.
DR Pfam: PF00053; laminin_EGF_3.
DR Pfam: PF00055; laminin_Nterm; 1.
DR Pfam: PF01759; RTR; 1.
DR PRINTS: PR00011; EGFAMININ
DR ProDom: PD002082; Lamnt; 1.
DR SMART: SM00180; EGF_Lam; 3.
DR SMART: SM00136; Lamnt; 1.
DR PROSITE: PS00022; EGF_L1; UNKOWN_1.
DR PROSITE: PS01248; LAMININ_TYFP_EGF; UNKOWN_1.
SQ SEQUENCE 450 AA: 73407 MW: 75200153416420 CRC64;

Query Match 93.8%, Score 30; DR 5; Length 450;
Best Local Similarity 160.0%; Pred. No. 2.6e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7
DB 183 GYRN 187

RESULT 36
QY1U9 PRELIMINARY; PRI: 692 AA.
AC QY1U9
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DI 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NADH.
OS Cryptantha flavoculata.
CC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; easterids 1; easterids 1; Solanales; Hydrophyllales; Phacelia.
OX NCBI_TaxID=79334;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferguson D.M.
RT "Phylogenetic analysis and characterization of hydrophyllaceae based on
  ndhF sequence data."
RL Syst. Bot. 0:0-0(1998).
CC Eukaryota; Viridiplantae; NADH.
CC EMBL: AF047803; AA22410.1;
DR InterPro: IP001750; oxidored_q1.
DR InterPro: IP002128; oxidored_q1_C.
DR InterPro: IP001516; oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1; 1.
DR Pfam: PF01010; oxidored_q1_C; 1.
DR Pfam: PF00662; oxidored_q1_N; 1.
KW Chloroplast; NAD; oxidoreductase; Plastocyanone.
FT NON_TER 1
FT NON_TER 692
SQ SEQUENCE 692 AA: 78529 MW: 6917223341733AC CRC64;

Query Match 94.8%, Score 30; DR 8; Length 692;
Best Local Similarity 100.0%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7
DB 329 GYRN 333

RESULT 37
QY1W8 PRELIMINARY; PRI: 696 AA.
AC QY1W8
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DI 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NADH.
OS Phacelia rotundifolia.
CC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; easterids 1; Solanales; Hydrophyllales; Phacelia.
OX NCBI_TaxID=79395;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferguson D.M.
RT "Phylogenetic analysis and characterization of hydrophyllaceae based on
  ndhF sequence data."
RL Syst. Bot. 0:0-0(1998).
CC Eukaryota; Viridiplantae; NADH.
CC EMBL: AF047779; AA22406.1;
DR InterPro: IP001750; oxidored_q1.
DR InterPro: IP002128; oxidored_q1_C.

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DE  Shearwaterpepla, Maculirostrata, Coliidae, penguins, core eukaryotes;
OC  Astoridae; euasterids 1; euasterids 1 incertae sedis; Bacterozoa;
OC  Cordia.
EX  NCBI_LaxID 79442;
KN  [1]
RP  SEQUENCE FROM N.A.
KA  Porcouson D.M.;
KT  "Phylogenetic analysis and circumscription of Hydrophyllaceae based on
RT  ndhF sequence data.";
RL  Syst. Bot. 0:0-0(1998);
GC  C1 CATALYTIC ACIDITY; RABH - PLASMAQUINONE RABH(-) - PLASOQUINONE.
DE  DML; AF547938; AF522415.1;
DR  InterPro: IPR001750; oxidorel_q1;
DR  InterPro: IPR001218; oxidorel_q1_N;
DR  InterPro: IPR001516; oxidorel_q1_C;
DR  Pfam: PF03361; oxidorel_q1; 1;
DR  Pfam: PF01010; oxidorel_q1_C; 1;
DR  Pfam: PF00662; oxidorel_q1_N; 1;
DR  Chloroplast; NAD; oxidoreductase; Plastocyanine.
FT  NIN_TER 1
FT  NIN_LEN 698 698
SQ  SEQUENCE 698 AA; 79203 MW; 182391388FEFE2FB C6764;

Query Match 93.8%; Score 30; DB 8; Length 698;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYFN 7
DL 325 GIVEN 333
[1111]

RESULT 40
Q20046 PRELIMINARY; PRI: 747 AA.
ID Q20046 AC Q20046;
AC Q20046;
DI 01-NOV-1996 (TREMBLrel. 01; Created)
DI 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19; Last annotation update)
DE F502.4 protein.
DE F502.4
GN F502.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
EX NCBI_LaxID:6249;
KN [1]
RP SEQUENCE FROM N.A.
KA MEDLINE=94150718; PubMed=7906498;
KA Wilson P., Ainsworth P., Anderson K., Raynes C., Parks M.,
KA Benfield J., Burton J., Connell M., Guppy T., Kader J., Maltsev A.,
KA Craxton M., Dear S., Du Z., Durbin R., Fayello A., Fulton L.,
KA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
KA Jones M., Kershak P., Kingston J., Lister N., Lottridge P.,
KA Lachring J., Lloyd C., Murray A., Mortimore R., O'Callaghan M.,
KA Parsons J., Percy C., Rikken L., Ropra A., Sanders D., Shownkeen R.,
KA Shalden N., Smith A., Sommer E., Staden R., Sulston J.,
KA Thierry-Mieg J., Thomas K., Vardiu M., Vaughan K., Waterston R.,
KA Watson A., Winkstock L., Wilkinson Sreat J., Wohlman P.;
FT #2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
FT elegans."
RL Nature 368: 42-38(1994).
KN [2]
RP SEQUENCE FROM N.A.
KA STRAIN-BRISTOL N2;
RC STRAIN-BRISTOL N2;
KA Connell M.;
RT "The sequence of C. elegans cosmid F5042."
RT F5042 (contig) and F5043 (contig) from F5042 and F5043.
KN [3]
RP SEQUENCE FROM N.A.
KA STRAIN-BRISTOL N2;
RC STRAIN-BRISTOL N2;
KA Waterston R.;
RT F5042 (contig) and F5043 (contig) from F5042 and F5043.
KN [3]

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[illegible]

230	9	91.8	7	23	ABJ03841	Human VEGF-targeted	403	9	91.8	7	23	ABJ03440	Human VEGF-targeted
231	9	81.8	7	23	ABJ03844	Human VEGF-targeted	404	9	81.8	7	23	ABJ03441	Human VEGF-targeted
232	9	81.8	7	23	ABJ03847	Human VEGF-targeted	405	9	81.8	7	23	ABJ03442	Human VEGF-targeted
233	9	81.8	7	23	ABJ03848	Human VEGF-targeted	406	9	81.8	7	23	ABJ03457	Human VEGF-targeted
234	9	81.8	7	23	ABJ03849	Human VEGF-targeted	407	9	81.8	7	23	ABJ03460	Human VEGF-targeted
235	9	81.8	7	23	ABJ03854	Human VEGF-targeted	408	9	81.8	7	23	ABJ03462	Human VEGF-targeted
236	9	81.8	7	23	ABJ03855	Human VEGF-targeted	409	9	81.8	7	23	ABJ03463	Human VEGF-targeted
237	9	81.8	7	23	ABJ03857	Human VEGF-targeted	410	9	81.8	7	23	ABJ03467	Human VEGF-targeted
238	9	81.8	7	23	ABJ03859	Human VEGF-targeted	411	9	81.8	7	23	ABJ03470	Human VEGF-targeted
239	9	81.8	7	23	ABJ03859	Human VEGF-targeted	412	9	81.8	7	23	ABJ03472	Human VEGF-targeted
240	9	81.8	7	23	ABJ03862	Human VEGF-targeted	413	9	81.8	7	23	ABJ03474	Human VEGF-targeted
241	9	81.8	7	23	ABJ03861	Human VEGF-targeted	414	9	81.8	7	23	ABJ03475	Human VEGF-targeted
242	9	81.8	7	23	ABJ03862	Human VEGF-targeted	415	9	81.8	7	23	ABJ03476	Human VEGF-targeted
243	9	81.8	7	23	ABJ03864	Human VEGF-targeted	416	9	81.8	7	23	ABJ03477	Human VEGF-targeted
244	9	81.8	7	23	ABJ03864	Human VEGF-targeted	417	9	81.8	7	23	ABJ03478	Human VEGF-targeted
245	9	81.8	7	23	ABJ03866	Human VEGF-targeted	418	9	81.8	7	23	ABJ03478	Human VEGF-targeted
246	9	81.8	7	23	ABJ03867	Human VEGF-targeted	419	9	81.8	7	23	ABJ03479	Human VEGF-targeted
247	9	81.8	7	23	ABJ03868	Human VEGF-targeted	420	9	81.8	7	23	ABJ03480	Human VEGF-targeted
248	9	81.8	7	23	ABJ03869	Human VEGF-targeted	421	9	81.8	7	23	ABJ03481	Human VEGF-targeted
249	9	81.8	7	23	ABJ03870	Human VEGF-targeted	422	9	81.8	7	23	ABJ03482	Human VEGF-targeted
250	9	81.8	7	23	ABJ03871	Human VEGF-targeted	423	9	81.8	7	23	ABJ03483	Human VEGF-targeted
251	9	81.8	7	23	ABJ03872	Human VEGF-targeted	424	9	81.8	7	23	ABJ03484	Human VEGF-targeted
252	9	81.8	7	23	ABJ03873	Human VEGF-targeted	425	9	81.8	7	23	ABJ03485	Human VEGF-targeted
253	9	81.8	7	23	ABJ03875	Human VEGF-targeted	426	9	81.8	7	23	ABJ03486	Human VEGF-targeted
254	9	81.8	7	23	ABJ03876	Human VEGF-targeted	427	9	81.8	7	23	ABJ03487	Human VEGF-targeted
255	9	81.8	7	23	ABJ03877	Human VEGF-targeted	428	9	81.8	7	23	ABJ03488	Human VEGF-targeted
256	9	81.8	7	23	ABJ03878	Human VEGF-targeted	429	9	81.8	7	23	ABJ03489	Human VEGF-targeted
257	9	81.8	7	23	ABJ03879	Human VEGF-targeted	430	9	81.8	7	23	ABJ03490	Human VEGF-targeted
258	9	81.8	7	23	ABJ03880	Human VEGF-targeted	431	9	81.8	7	23	ABJ03491	Human VEGF-targeted
259	9	81.8	7	23	ABJ03881	Human VEGF-targeted	432	9	81.8	7	23	ABJ03882	Human VEGF-targeted
260	9	81.8	7	23	ABJ03882	Human VEGF-targeted	433	9	81.8	7	23	ABJ03883	Human VEGF-targeted
261	9	81.8	7	23	ABJ03883	Human VEGF-targeted	434	9	81.8	7	23	ABJ03884	Human VEGF-targeted
262	9	91.8	7	23	ABJ03884	Human VEGF-targeted	435	9	91.8	7	23	ABJ03885	Human VEGF-targeted
263	9	81.8	7	23	ABJ03885	Human VEGF-targeted	436	9	81.8	7	23	ABJ03886	Human VEGF-targeted
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270	9	81.8	7	23	ABJ03892	Human VEGF-targeted	443	9	81.8	7	23	ABJ03893	Human VEGF-targeted
271	9	81.8	7	23	ABJ03893	Human VEGF-targeted	444	9	81.8	7	23	ABJ03894	Human VEGF-targeted
272	9	81.8	7	23	ABJ03894	Human VEGF-targeted	445	9	81.8	7	23	ABJ03895	Human VEGF-targeted
273	9	81.8	7	23	ABJ03895	Human VEGF-targeted	446	9	81.8	7	23	ABJ03896	Human VEGF-targeted
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277	9	81.8	7	23	ABJ03899	Human VEGF-targeted	450	9	81.8	7	23	ABJ03900	Human VEGF-targeted
278	9	81.8	7	23	ABJ03900	Human VEGF-targeted	451	9	81.8	7	23	ABJ03901	Human VEGF-targeted
279	9	81.8	7	23	ABJ03901	Human VEGF-targeted	452	9	81.8	7	23	ABJ03902	Human VEGF-targeted
280	9	81.8	7	23	ABJ03902	Human VEGF-targeted	453	9	81.8	7	23	ABJ03903	Human VEGF-targeted
281	9	81.8	7	23	ABJ03903	Human VEGF-targeted	454	9	81.8	7	23	ABJ03904	Human VEGF-targeted
282	9	81.8	7	23	ABJ03904	Human VEGF-targeted	455	9	81.8	7	23	ABJ03905	Human VEGF-targeted
283	9	81.8	7	23	ABJ03905	Human VEGF-targeted	456	9	81.8	7	23	ABJ03906	Human VEGF-targeted
284	9	81.8	7	23	ABJ03906	Human VEGF-targeted	457	9	81.8	7	23	ABJ03907	Human VEGF-targeted
285	9	81.8	7	23	ABJ03907	Human VEGF-targeted	458	9	81.8	7	23	ABJ03908	Human VEGF-targeted
286	9	81.8	7	23	ABJ03908	Human VEGF-targeted	459	9	81.8	7	23	ABJ03909	Human VEGF-targeted
287	9	81.8	7	23	ABJ03909	Human VEGF-targeted	460	9	81.8	7	23	ABJ03910	Human VEGF-targeted
288	9	81.8	7	23	ABJ03910	Human VEGF-targeted	461	9	81.8	7	23	ABJ03911	Human VEGF-targeted
289	9	81.8	7	23	ABJ03911	Human VEGF-targeted	462	9	81.8	7	23	ABJ03912	Human VEGF-targeted
290	9	81.8	7	23	ABJ03912	Human VEGF-targeted	463	9	81.8	7	23	ABJ03913	Human VEGF-targeted
291	9	81.8	7	23	ABJ03913	Human VEGF-targeted	464	9	81.8	7	23	ABJ03914	Human VEGF-targeted
292	9	81.8	7	23	ABJ03914	Human VEGF-targeted	465	9	81.8	7	23	ABJ03915	Human VEGF-targeted
293	9	81.8	7	23	ABJ03915	Human VEGF-targeted	466	9	81.8	7	23	ABJ03916	Human VEGF-targeted
294	9	81.8	7	23	ABJ03916	Human VEGF-targeted	467	9	81.8	7	23	ABJ03917	Human VEGF-targeted
295	9	81.8	7	23	ABJ03917	Human VEGF-targeted	468	9	81.8	7	23	ABJ03918	Human VEGF-targeted
296	9	81.8	7	23	ABJ03918	Human VEGF-targeted	469	9	81.8	7	23	ABJ03919	Human VEGF-targeted
297	9	81.8	7	23	ABJ03919	Human VEGF-targeted	470	9	81.8	7	23	ABJ03920	Human VEGF-targeted
298	9	81.8	7	23	ABJ03920	Human VEGF-targeted	471	9	81.8	7	23	ABJ03921	Human VEGF-targeted
299	9	81.8	7	23	ABJ03921	Human VEGF-targeted	472	9	81.8	7	23	ABJ03922	Human VEGF-targeted
300	9	81.8	7	23	ABJ03922	Human VEGF-targeted	473	9	81.8	7	23	ABJ03923	Human VEGF-targeted
301	9	81.8	7	23	ABJ03923	Human VEGF-targeted	474	9	81.8	7	23	ABJ03924	Human VEGF-targeted
302	9	81.8	7	23	ABJ03924	Human VEGF-targeted	475	9	81.8	7	23	ABJ03925	Human VEGF-targeted

476	9	81.8	7	23	APB48366	Zinc finger protein	449	9	81.8	7	23	APB48314	Zinc finger protein
477	9	81.8	7	23	APB98670	Zinc finger protein	450	9	81.8	7	23	APB48315	Zinc finger protein
478	9	81.8	7	23	APB98671	Zinc finger protein	451	9	81.8	7	23	APB48316	Zinc finger protein
479	9	81.8	7	23	APB18204	Zinc finger protein	452	9	81.8	7	23	APB48317	Zinc finger protein
480	9	81.8	7	23	APB48205	Zinc finger protein	453	9	81.8	7	23	APB48319	Zinc finger protein
481	9	81.8	7	23	APB48207	Zinc finger protein	454	9	81.8	7	23	APB48320	Zinc finger protein
482	9	81.8	7	23	APB48208	Zinc finger protein	455	9	81.8	7	23	APB48322	Zinc finger protein
483	9	81.8	7	23	APB48210	Zinc finger protein	456	9	81.8	7	23	APB48323	Zinc finger protein
484	9	81.8	7	23	APB18211	Zinc finger protein	457	9	81.8	7	23	APB48325	Zinc finger protein
485	9	81.8	7	23	APB18213	Zinc finger protein	458	9	81.8	7	23	APB48326	Zinc finger protein
486	9	81.8	7	23	APB48214	Zinc finger protein	459	9	81.8	7	23	APB48327	Zinc finger protein
487	9	81.9	7	23	APB48216	Zinc finger protein	460	9	81.9	7	23	APB48328	Zinc finger protein
488	9	81.8	7	23	APB48218	Zinc finger protein	461	9	81.8	7	23	APB48329	Zinc finger protein
489	9	81.8	7	23	APB48220	Zinc finger protein	462	9	81.8	7	23	APB48330	Zinc finger protein
490	9	81.8	7	23	APB48222	Zinc finger protein	463	9	81.8	7	23	APB48332	Zinc finger protein
491	9	81.8	7	23	APB48223	Zinc finger protein	464	9	81.8	7	23	APB48333	Zinc finger protein
492	9	81.8	7	23	APB48225	Zinc finger protein	465	9	81.8	7	23	APB48335	Zinc finger protein
493	9	81.8	7	23	APB48226	Zinc finger protein	466	9	81.8	7	23	APB48336	Zinc finger protein
494	9	81.8	7	23	APB48227	Zinc finger protein	467	9	81.8	7	23	APB48338	Zinc finger protein
495	9	81.8	7	23	APB48228	Zinc finger protein	468	9	81.8	7	23	APB48340	Zinc finger protein
496	9	81.8	7	23	APB48229	Zinc finger protein	469	9	81.8	7	23	APB48344	Zinc finger protein
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498	9	81.8	7	23	APB48232	Zinc finger protein	471	9	81.8	7	23	APB48343	Zinc finger protein
499	9	81.8	7	23	APB48233	Zinc finger protein	472	9	81.8	7	23	APB48346	Zinc finger protein
500	9	81.8	7	23	APB48235	Zinc finger protein	473	9	81.8	7	23	APB48348	Zinc finger protein
501	9	81.8	7	23	APB48237	Zinc finger protein	474	9	81.8	7	23	APB48349	Zinc finger protein
502	9	81.8	7	23	APB48240	Zinc finger protein	475	9	81.8	7	23	APB48353	Zinc finger protein
503	9	81.8	7	23	APB48242	Zinc finger protein	476	9	81.8	7	23	APB48351	Zinc finger protein
504	9	81.8	7	23	APB48243	Zinc finger protein	477	9	81.8	7	23	APB48353	Zinc finger protein
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506	9	81.8	7	23	APB48245	Zinc finger protein	479	9	81.8	7	23	APB48355	Zinc finger protein
507	9	81.9	7	23	APB48246	Zinc finger protein	480	9	81.8	7	23	APB48356	Zinc finger protein
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516	9	81.8	7	23	APB48255	Zinc finger protein	489	9	81.8	7	23	APB48365	Zinc finger protein
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528	9	81.8	7	23	APB48285	Zinc finger protein	501	9	81.8	7	23	APB48383	Zinc finger protein
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531	9	81.8	7	23	APB48291	Zinc finger protein	504	9	81.8	7	23	APB48387	Zinc finger protein
532	9	81.8	7	23	APB48292	Zinc finger protein	505	9	81.8	7	23	APB48389	Zinc finger protein
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544	9	81.8	7	23	APB48305	Zinc finger protein	517	9	81.8	7	23	APB48405	Zinc finger protein
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547	9	81.8	7	23	APB48310	Zinc finger protein	520	9	81.8	7	23	APB48427	Zinc finger protein
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526	7	23	ABP48133	zinc finger protein	559	7	23	ABP48555	zinc finger protein
527	9	81.8	ABP48134	zinc finger protein	560	9	81.8	ABP48556	zinc finger protein
528	7	23	ABP48135	zinc finger protein	561	7	23	ABP48557	zinc finger protein
529	9	81.8	ABP48136	zinc finger protein	562	9	81.8	ABP48558	zinc finger protein
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531	9	81.8	ABP48138	zinc finger protein	564	9	81.8	ABP48560	zinc finger protein
532	7	23	ABP48139	zinc finger protein	565	7	23	ABP48561	zinc finger protein
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534	7	23	ABP48141	zinc finger protein	567	7	23	ABP48563	zinc finger protein
535	9	81.8	ABP48142	zinc finger protein	568	9	81.8	ABP48564	zinc finger protein
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537	9	81.8	ABP48144	zinc finger protein	570	9	81.8	ABP48566	zinc finger protein
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539	9	81.8	ABP48146	zinc finger protein	572	9	81.8	ABP48568	zinc finger protein
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541	9	81.8	ABP48148	zinc finger protein	574	9	81.8	ABP48570	zinc finger protein
542	7	23	ABP48149	zinc finger protein	575	7	23	ABP48571	zinc finger protein
543	9	81.8	ABP48150	zinc finger protein	576	9	81.8	ABP48572	zinc finger protein
544	7	23	ABP48151	zinc finger protein	577	7	23	ABP48573	zinc finger protein
545	9	81.8	ABP48152	zinc finger protein	578	9	81.8	ABP48574	zinc finger protein
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547	9	81.8	ABP48154	zinc finger protein	580	9	81.8	ABP48576	zinc finger protein
548	7	23	ABP48155	zinc finger protein	581	7	23	ABP48577	zinc finger protein
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553	9	81.8	ABP48160	zinc finger protein	586	9	81.8	ABP48582	zinc finger protein
554	7	23	ABP48161	zinc finger protein	587	7	23	ABP48583	zinc finger protein
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556	7	23	ABP48163	zinc finger protein	589	7	23	ABP48585	zinc finger protein
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570	7	23	ABP48177	zinc finger protein					
571	9	81.8	ABP48178	zinc finger protein					
572	7	23	ABP48179	zinc finger protein					
573	9	81.8	ABP48180	zinc finger protein					
574	7	23	ABP48181	zinc finger protein					
575	9	81.8	ABP48182	zinc finger protein					
576	7	23	ABP48183	zinc finger protein					
577	9	81.8	ABP48184	zinc finger protein					
578	7	23	ABP48185	zinc finger protein					
579	9	81.8	ABP48186	zinc finger protein					
580	7	23	ABP48187	zinc finger protein					
581	9	81.8	ABP48188	zinc finger protein					
582	7	23	ABP48189	zinc finger protein					
583	9	81.8	ABP48190	zinc finger protein					
584	7	23	ABP48191	zinc finger protein					
585	9	81.8	ABP48192	zinc finger protein					
586	7	23	ABP48193	zinc finger protein					
587	9	81.8	ABP48194	zinc finger protein					
588	7	23	ABP48195	zinc finger protein					
589	9	81.8	ABP48196	zinc finger protein					
590	7	23	ABP48197	zinc finger protein					
591	9	81.8	ABP48198	zinc finger protein					
592	7	23	ABP48199	zinc finger protein					
593	9	81.8	ABP48200	zinc finger protein					
594	7	23	ABP48201	zinc finger protein					

960 9 81.8 7 23 ARP4998 Zinc finger protein

961 9 81.8 7 23 ARP4999 Zinc finger protein

962 9 81.8 7 23 ARP49100 Zinc finger protein

963 9 81.8 7 23 ARP49102 Zinc finger protein

964 9 81.8 7 23 ARP49104 Zinc finger protein

965 9 81.8 7 23 ARP49105 Zinc finger protein

966 9 81.8 7 23 ARP49108 Zinc finger protein

967 9 81.8 7 23 ARP49109 Zinc finger protein

968 9 81.8 7 23 ARP49110 Zinc finger protein

969 9 81.8 7 23 ARP49111 Zinc finger protein

970 9 81.8 7 23 ARP49116 Zinc finger protein

971 9 81.8 7 23 ARP49122 Zinc finger protein

972 9 81.8 7 23 ARP49124 Zinc finger protein

973 9 81.8 7 23 ARP49125 Zinc finger protein

974 9 81.8 7 23 ARP49127 Zinc finger protein

975 9 81.8 7 23 ARP49128 Zinc finger protein

976 9 81.8 7 23 ARP49130 Zinc finger protein

977 9 81.8 7 23 ARP49131 Zinc finger protein

978 9 81.8 7 23 ARP49133 Zinc finger protein

979 9 81.8 7 23 ARP49136 Zinc finger protein

980 9 81.8 7 23 ARP49137 Zinc finger protein

981 9 81.8 7 23 ARP49138 Zinc finger protein

982 9 81.8 7 23 ARP49140 Zinc finger protein

983 9 81.8 7 23 ARP49143 Zinc finger protein

984 9 81.8 7 23 ARP49144 Zinc finger protein

985 9 81.8 7 23 ARP49146 Zinc finger protein

986 9 81.8 7 23 ARP49147 Zinc finger protein

987 9 81.8 7 23 ARP49148 Zinc finger protein

988 9 81.8 7 23 ARP49149 Zinc finger protein

989 9 81.8 7 23 ARP49150 Zinc finger protein

990 9 81.8 7 23 ARP49152 Zinc finger protein

991 9 81.8 7 23 ARP49153 Zinc finger protein

992 9 81.8 7 23 ARP49155 Zinc finger protein

993 9 81.8 7 23 ARP49156 Zinc finger protein

994 9 81.8 7 23 ARP49157 Zinc finger protein

995 9 81.8 7 23 ARP49159 Zinc finger protein

996 9 81.8 7 23 ARP49161 Zinc finger protein

997 9 81.8 7 23 ARP49162 Zinc finger protein

998 9 81.8 7 23 ARP49163 Zinc finger protein

999 9 81.8 7 23 ARP49169 Zinc finger protein

1000 9 81.8 7 23 ABA47816 GATA 15,5 zinc fin

ALIGNMENTS

RESULT 1
AAW4194
ID AAW4194 standard; peptide; 4 AA.

XX AAW4194;
XX 25 MAR 1999 (first entry)
XX Peptide comprising a proteinase site.
DE
XX
XX
XX
XX Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW bone morphogenetic protein; transforming growth factor beta;
KW active fragment; wound healing; bone growth.
XX
XX Unidentified.
XX
XX W0905517 AL.
XX
XX 16 DEC 1998.
XX
XX
XX 02 JUN 1998; 98WO-US11189.
XX
XX 03 JUN 1997; 97US-0868452.
XX
XX (HALL/) HALL F L.
XX (HARR/) HARR B.
XX (HARR/) HARR M E.

PA (SHAR/) SHARRS E C.
PA (WILL/) WILL L.
XX
XX Hall F L, Harr B, Rimm M E, Sharrs E C, Will L;
XX WFL, 1999 059875/05.
XX New bone morphogenetic fusion proteins - comprising a putative fusion
XX tag and a bone morphogenetic active fragment, used for enhancing
XX wound healing or bone growth
XX Claim 8, Page 34; 64pp; English.
XX The present peptide represents a proteinase site used in the creation
XX of the bone morphogenetic fusion proteins of the invention. The bone
XX morphogenetic fusion protein may contain some or all of the following
XX elements: a purification tag, a proteinase site, an ECM/bone binding
XX site, a second proteinase site, and a bone morphogenetic protein
XX active fragment. The fusion proteins of the invention also includes
XX proteins that have transforming growth factor beta active fragments
XX instead of bone morphogenetic protein active fragments. The bone
XX morphogenetic fusion proteins can be used for enhancing wound healing
XX or bone growth.
XX
XX Sequence 4 AA;
SQ
Query Match 81.8%; Score 9; DB 20; Length 4;
Best Local Similarity 66.7%; Pos. No. 7,70000;
Matches 2; Conserved Pro. 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EXR 3
DB 1 LTR 3

RESULT 2
AAW48182
ID AAW48182 standard; peptide; 4 AA.

XX AAW48182;
XX
XX 03 JUN 1998 (first entry)
XX
XX Conantokin peptide derivative.
DE
XX
XX Conantokin; predatory cone snail; treatment; neurological disorder;
KW psychiatric disorder; antidepressant; non-preserved; analgesic.
KW HIV infection; ophthalmic indication; memory; learning defect;
KW cognitive defect.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 4
XX Zwitter "gamma-carboxyglutamic acid"
XX
XX W09803541 AL.
XX
XX 29 JAN 1998.
XX
XX 21 JUL 1997; 97WO-US12618.
XX
XX 22 JUL 1996; 96US-0684742.
XX
XX (COGN-) CORNETIX INC.
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Abexadole FC, Colledge C, Cruz LJ, Hillyard DR, Jimenez E;
XX Laylor RI, Moschis RI, Oliveto RM, Rivier JE, Shen GS;
XX Walker C, Zhou L;
XX WFL, 1998 120604/11.
XX

PI New conantokin peptide(s) - useful for treating neurologic or
 PI psychiatric disorders; or the management of pain
 XX
 PS Claim 15: Page 98; 123pp. English.

XX The present sequence is a conantokin peptide derivative, which can
 CC be used to treat neurologic and psychiatric disorders, e.g. as an
 CC anticonvulsant, neuroprotective or analgesic agent. Neurologic and
 CC psychiatric disorders include epilepsy, convulsions, pain, stroke
 CC injury (associated with conditions of hypoxia, anoxia or ischemia,
 CC which typically follow stroke, cerebrovascular accident, brain or
 CC spinal cord trauma, myocardial infarct, physical trauma, drowning,
 CC suffocation, perinatal asphyxia or hypoglycemic events),
 CC neurodegeneration (associated with Alzheimer's disease, senile
 CC dementia, Amyotrophic Lateral Sclerosis, Multiple Sclerosis,
 CC Parkinson's disease, Huntington's disease, Down's Syndrome,
 CC Kretschmer's disease, schizophrenia, AIDS dementia, multi-infarct
 CC dementia, Binswanger dementia and neuronal damage associated with
 CC uncontrolled seizures), chemical toxicity (such as addiction, and
 CC morphine, opiate, opioid and barbiturate tolerance), pain (acute,
 CC chronic, migraine), anxiety, major depression, manic-depressive
 CC illness, obsessive compulsive disorder, schizophrenia and mood
 CC disorders (such as bipolar disorder, unipolar depression, dysthymia
 CC and seasonal affective disorder) and dementia (concurrent disorder),
 CC sleep disorder, muscle relaxation and urinary incontinence. The
 CC peptide can also be used to treat HIV infection, ophthalmic
 CC indication and memory, learning or cognitive defects.

XX Sequence 4 AA:

Query Match 81.8%; Score 9; DB 19; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 Db 1 LAR 3

RESULT 3

AAW49964

ID AAW49964 standard; peptide: 4 AA.

AC AAW49964:

DT 30-JUN-1998 (first entry)

XX conantokin peptide derivative.

XX Conantokin: predatory cone snail; treatment, neurologic disorder,
 KW psychiatric disorder; anticonvulsant; neuroprotective; analgesic,
 KW HIV infection, ophthalmic indication, memory, learning defects,
 KW cognitive defect.

XX Synthetic.

OS Key Location/Qualifiers

XX Modified-site 4 /note: "gamma-carboxyglutamic acid"

FT

FN W09803189-A1.

XX

PD 29-JAN-1998.

XX

PF 21-JUL-1997; 97WA-US12652.

XX

PR 06-DEC-1996; 96US-0762377.

XX

PR 22-JUL-1996; 96US-0684750.

XX

PA (COGN-) COGNETIX INC.

XX

PI Layer RT, McCabe RT, Zhou L;

XX

XX Wt. 1992 123456711.

XX Use of conantokin peptide(s) - for treating disorders involving
 PI excessive excretion of amino acids by excitatory amino acids or
 PI agonists of the N-methyl D-aspartate receptor

XX Claim 27: Page 69; 123pp. English.

XX The present sequence is a conantokin peptide derivative, which can
 CC be used to treat neurologic and psychiatric disorders, e.g. as an
 CC anticonvulsant, neuroprotective or analgesic agent. Neurologic and
 CC psychiatric disorders include epilepsy, convulsions, neurodegeneration,
 CC injury (associated with conditions of hypoxia, anoxia or ischemia,
 CC which typically follow stroke, cerebrovascular accident, brain or
 CC spinal cord trauma, myocardial infarct, physical trauma, drowning,
 CC suffocation, perinatal asphyxia or hypoglycemic events),
 CC neurodegeneration (associated with Alzheimer's disease, senile
 CC dementia, Amyotrophic Lateral Sclerosis, Multiple Sclerosis,
 CC Parkinson's disease, Huntington's disease, Down's Syndrome,
 CC Kretschmer's disease, schizophrenia, AIDS dementia, multi-infarct
 CC dementia, Binswanger dementia and neuronal damage associated with
 CC uncontrolled seizures), chemical toxicity (such as addiction, and
 CC morphine, opiate, opioid and barbiturate tolerance), pain (acute,
 CC chronic, migraine), anxiety, major depression, manic-depressive
 CC illness, obsessive compulsive disorder, schizophrenia and mood
 CC disorders (such as bipolar disorder, unipolar depression, dysthymia
 CC and seasonal affective disorder) and dementia (concurrent disorder),
 CC sleep disorder, muscle relaxation and urinary incontinence. The
 CC peptide can also be used to treat HIV infection, ophthalmic
 CC indication and memory, learning or cognitive defects.

XX Sequence 4 AA:

Query Match 81.8%; Score 9; DB 19; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3

Db 1 LAR 3

RESULT 4

AAG79019

Id AAG79019 standard; peptide: 4 AA.

AC AAG79019:

DT 10-DEC-2001 (first entry)

XX conantokin peptide derivative.

XX Conantokin: predatory cone snail; treatment, neurologic disorder,
 KW psychiatric disorder; anticonvulsant; neuroprotective; analgesic,
 KW HIV infection, ophthalmic indication, memory, learning defects,
 KW cognitive defect.

XX Synthetic.

OS Key Location/Qualifiers

XX Modified-site 4 /note: "gamma-carboxyglutamic acid"

FT

FN US6277825-B1.

XX

PD 21-AUG-2001.

XX

PR 20-JUL-1999; 99US-0457141.

XX

PK 22 JUL-1996; 96DS-0684750.
 PK 06-DEC-1996; 96DS-0762477.
 PK 21 JUL-1997; 96DS-0819652.
 PK 10 FEB-1999; 96DS-0142926.
 PK 01-APR-1999; 96DS-0283277.
 XX (JIAH) UNIV UTAB RES FOUND.
 FA (CHGR) CAGNETIX INC.
 XX
 PK Oliveira BM, McIntosh JM, McBride RT, Layer RT, Zhou L;
 DB WPI: 2001-601477/69.
 XX
 XX Use of conantokin peptide in the derivation of a conantokin peptide
 PT chimera for treating disorders e.g. migraine
 XX
 XX Claim 9; Column 80; 60pp; English.
 XX
 XX AA674012-43 and AA6740054-56 represent domains of conantokin peptides.
 CC Conantokins differ from conotoxins, in that they contain
 CC gamma-carboxyglutamic acid. The conantokins are derived from the venom
 CC of cone snails. They are used for the treatment of disorders in which
 CC the pathophysiology involves excessive excitation of nerve cells by
 CC excitatory amino acids or analogs of N-methyl-D-aspartate (NMDA)
 CC receptors. The conantokin peptides are used for the treatment of
 CC disorders such as pain, neurologic or psychiatric disorders such
 CC as epilepsy, for reducing neurotoxic injury associated with conditions of
 CC hypoxia, anoxia or ischemia; for treating neurodegeneration; for
 CC treating chemical toxicity such as addiction, drug craving, alcohol
 CC abuse, morphine, opiod and barbiturate tolerance; for treating
 CC psychiatric disorders such as anxiety, major depression, manic-depression
 CC illness, obsessive compulsive disorder, schizophrenia or mood disorder;
 CC for treating ophthalmic disorders; for treating additional neurological
 CC disorders e.g. dystonia, sleep disorder, muscle relaxation and urinary
 CC incontinence; for memory/cognition enhancement; for treating HIV
 CC infection.
 XX
 SQ Sequence 4 AA:
 Query Match 81.8%; Score 9; DB 23; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.7e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 DB 1 1
 DB 1 LXR 3
 RESULT 5
 AA624457 standard; peptide; 4 AA.
 AC AAE24457;
 XX
 XX 04-JUL-2002 (first entry)
 XX
 XX BONT/A N-glycosylation site #1
 DE
 XX Botulinum toxin; Clostridium botulinum; Clostridial petstiferous; blepharospasm; pain; therapy;
 KW neuromuscular disorder; cervical dystonia; oromandibular dystonia;
 KW spasmodic dysphonia; laryngeal dystonia; muscular tension; asthma;
 KW hyperhidrosis; autonomic nervous system disorder; sweating; salivation;
 KW headache; neuropathy; botulinum toxin serotype A; BONT/A.
 XX
 XX Clostridium botulinum.
 OS
 XX W0200249506-A2.
 IN
 XX
 XX 23 MAY-2002.
 XX
 XX 16-NOV-2001; 2001W024954040.
 XX
 XX 17-NOV-2000; 2000W02495404P.
 XX

XX
 PA (ALLI) ALLERGAN SALES INC.
 XX
 XX Steward LB, Spangarudis A, Liu W, Ack EK;
 XX WPI: 2002-479904/91.
 DR
 XX
 XX Modified neurotoxin especially clostridial toxins, useful for treatment
 PT neuromuscular and autonomic nervous system disorder and pain, comprises
 PT structural modification to alter biological persistence of neurotoxin
 PT
 PS Disclosure; Page 19; 55pp; English.
 XX
 XX The invention related to modified neurotoxins especially
 CC clostridial botulinum toxins with altered biological persistence.
 CC These toxins comprise a structural modification which is effective to
 CC alter the biological persistence. Modified neurotoxins of the invention
 CC are used for treating biological disorders which include neuromuscular
 CC disorder e.g. strabismus, blepharospasm, spasmodic torticollis (cervical
 CC dystonia), oromandibular dystonia and spasmodic dysphonia (laryngeal
 CC dystonia), autonomic nervous system disorders e.g. excessive salivation
 CC and sweating, asthma etc. and pain e.g. headache, muscular tension,
 CC neuralgia and neuropathy. The present sequence is botulinum toxin
 CC serotype A (BONT/A) N-glycosylation site. This peptide is derived from
 CC C. botulinum.
 XX
 SQ Sequence 4 AA:
 Query Match 81.8%; Score 9; DB 23; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.7e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 DB 1 1
 DB 2 LXR 4
 RESULT 5
 AA620561 standard; peptide; 4 AA.
 ID AAE20561
 XX
 XX AAE20561;
 AC
 XX 01-JUL-2002 (first entry)
 DI
 XX
 XX Soybean diverged delta 9 fatty acid desaturase peptide #2.
 DE
 XX
 XX Soybean; diverged delta 9 fatty acid desaturase; enzyme; cellular lipid;
 KW oil; transgenic plant; gene mapping; immunisation.
 KW
 XX
 XX glycerol max.
 OS
 XX W0200216565 A2.
 IN
 XX
 XX 28-FEB-2002.
 PD
 XX
 XX 22-AUG-2001; 2001W0226246.
 XX
 XX 22-AUG-2000; 2000W0226696P.
 XX
 XX (2000) 10 PAT 13 BOMB005 & Co E 1.
 XX
 XX Bont A, Cabaud RE, Hill WB, Kinney AL, Yadav RS;
 PT WPI: 2002-269353/91.
 XX
 XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
 PT useful in creating transgenic plants having altered levels of mono-,
 PT poly- and unsaturated fatty acids and in increasing the unsaturation
 PT levels in cellular lipids.
 XX
 XX claim 12; Page 48; 77pp; English.
 PT

XX The present invention relates to diverged delta 9 fatty acid desaturase
 CC proteins and polynucleotides encoding such proteins. The nucleic acid
 CC sequences may be used to increase the level of unsaturation in cellular
 CC lipids, including oil, in tissues when the enzyme is absent or rare-
 CC limiting, to isolate cDNAs and genes encoding homologous proteins from
 CC the same or other plant species and to create transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found,
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in
 CC those cells. They are useful as probes for genetic and physical gene
 CC mapping and as markers, e.g. restriction fragment length polymorphism
 CC (RFLP) markers. The peptides can be used to immunise animals to produce
 CC antibodies specific for the peptides and proteins. The present sequence
 CC is soybean diverged delta-9 fatty acid desaturase peptide (residues
 CC 256-256).

XX Sequence 4 AA:

Query Match 91.8%, Score 9, LP 23, Length 1,
 Best Local Similarity 66.7%, Pred. No. 7.7e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 2 LAR 4

RESULT 7

AAEI4417

ID AAEI4417 standard; peptide; 4 AA.

XX AAEI4417;

XX 26-MAR-2002 (first entry)

XX C-terminal sequence of an arginine-containing peptide.

XX Protein quantification; protein identification; signature peptide;
 FW mass spectrometric analysis; proteolytic peptide; affinity ligand;
 KW arginine; isobaric peptide.

XX Unidentified.

XX W200186306-A2.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US14418.

XX 05-MAY-2000; 2000US-203227P.

XX 31-MAY-2000; 2000US-208184P.

XX 31-MAY-2000; 2000US-208372P.

XX (PUD) PURDUE RES. FOUND.

XX (RCGN) REIGNER F. E.

XX (CHAK) CHAKRABORTY A. B.

XX (DJRM) DORMADY S. J.

XX (GENG) G'ENG M.

XX (JHJ) JI J.

XX (KJG) KONGS L. D.

XX (SIOW) SIOWA C. S.

XX (WANG) WANG S.

XX (ZHAN) ZHANG X.

XX Reigner FF, Chakraborty AB, Dormady SJ, Cheng M, Ji J, Piggis LP;

XX Sioma CS, Wang S, Zhang X;

XX WPI: 2002-089812/12

PI peptides

XX Example 9; Page 73; 106pp; English.

XX the invention relates to analysing differences in protein content among
 CC plural protein samples comprising employing mass spectrometric analysis
 CC of proteolytic peptide fragments. The method comprises
 CC fragmenting at least a first protein sample and a second protein
 CC sample to produce a first peptide pool and a second peptide pool;
 CC isotopically labelling at least a portion of the peptides in at
 CC least one of the pools so as to permit resolution of otherwise
 CC identical peptides in the first and second peptide pools by mass
 CC analysis; contacting peptides from at least a portion of both of the
 CC peptide pools with a capillary electrophoretic affinity selected peptides
 CC comprising an affinity ligand, where the capillary selected peptides for the
 CC affinity ligand; and analysing the affinity selected peptides by mass
 CC spectrometry to determine one or more differences between the first and
 CC second samples. The method of the invention is useful for identifying one
 CC or more proteins in the sample, and is typically useful for identifying one
 CC or more peptides in a sample or several samples. The advantages
 CC for quantifying proteins in a sample or several samples. The advantages
 CC of the novel method are that it is easier to separate peptides than
 CC proteins; native structure of the protein does not have to be maintained
 CC during the analysis; structural variants do not interfere; and
 CC putative proteins suggested from LIA database can be recognised by
 CC using a signature peptide probe. The present method permits
 CC identification of a protein in a complex sample without purifying the
 CC protein or obtaining its composite peptide signature. The present
 CC sequence is C-terminal fragment of a differentially acetylated
 CC arginine-containing peptide which is used to generate fragment ions for
 CC distinguishing isobaric peptides.

XX Sequence 4 AA:

Query Match 61.8%, Score 9, LP 23, Length 4;
 Best Local Similarity 66.7%, Pred. No. 7.7e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 2 LAR 4

RESULT 8

AAAM51953

ID AAM51953 standard; peptide; 4 AA.

XX AAM51953;

XX 01-FEB-2002 (first entry)

XX PSA antibody preparation immunogen peptide #5.

XX PSA: prostate-specific antigen; prostatic carcinoma; pro-kallikrein 2;
 KW human; antibody; immunogen.

XX Homo sapiens.

XX P010042040 A1.

XX 29-NOV-2001.

XX 05-JUL-2000; 2000OE-1942040.

XX 24-MAY-2000; 2000OE-1925487.

XX (GCOFF) RECHIE DIAGN-SIUS GMPH.

XX WPI: 2002-042533/06.

XX Antibody comprising specificity for each truncated forms of
 PT pro prostate specific antigen, useful in immunoassays for differential
 PT diagnosis of prostatic carcinoma

```

XX PS Disclosure: Page 11; 16pp; German.
XX CC
XX CC The present invention relates to an antibody specific for (-5,-6 and
XX CC 7)-proPSA (prostate specific antigen), but with no reactivity with (-4)
XX CC or shorter forms of the protein. The antibody can be used to diagnose
XX CC prostate carcinoma and to detect human pro-kallikrein 2. The present
XX CC sequence is a peptide which forms part of a peptide-containing immunogen
XX CC described in the exemplification of the invention.
XX SQ Sequence 4 AA:
XX
XX Query Match 81.8%; Score 9; DB 23; Length 4;
XX Best Local Similarity 66.7%; Pred. No. 7.7e+05;
XX Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LXR 4
XX 1 1
XX 2 LSR 4
XX
XX RESULT 9
XX AAM51957
XX ID AAM51957 standard; peptide; 4 AA.
XX AC AAM51957;
XX XX
XX 01 FEB-2002 (first entry)
XX PS PSA antibody preparation immunogen peptide #9.
XX CC
XX CC PSA: prostate specific antigen; prostatic carcinoma; pro-kallikrein 2;
XX CC human; antibody; immunogen.
XX CC B-mo sapiens.
XX CC
XX CC DE10032040-A1.
XX CC
XX CC 29-NOV-2001.
XX CC
XX CC 05-JUL-2000; 2000DE-1042040.
XX CC
XX CC 24 MAY-2000; 2000DE-1025487.
XX CC
XX CC (BOFF) ROCHE DIAGNOSTICS GMBH.
XX CC
XX CC WPI: 2002-042644706.
XX CC
XX CC Antibody comprising specificity for some truncated forms of
XX CC pro-prostate specific antigen, useful in immunoassays for differential
XX CC diagnosis of prostate carcinoma.
XX CC
XX PS Disclosure: Page 11; 16pp; German.
XX CC
XX CC The present invention relates to an antibody specific for (-5,-6 and
XX CC 7)-proPSA (prostate-specific antigen), but with no reactivity with (-4)
XX CC or shorter forms of the protein. The antibody can be used to diagnose
XX CC prostate carcinoma and to detect human pro-kallikrein 2. The present
XX CC sequence is a peptide which forms part of a peptide-containing immunogen
XX CC described in the exemplification of the invention.
XX SQ Sequence 4 AA:
XX
XX Query Match 81.8%; Score 9; DB 23; Length 4;
XX Best Local Similarity 66.7%; Pred. No. 7.7e+05;
XX Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LXR 4
XX 1 1
XX 2 LSR 4
XX
XX RESULT 10

```

```

AAR03446
XX ID AAR03446 standard; protein; 5 AA.
XX AC AAR03446;
XX XX
XX 02-AUG-1990 (first entry)
XX CC
XX CC Accessory moiety derived from transferrin receptor.
XX CC
XX CC Accessory moiety; transferrin receptor; tumour therapy.
XX CC
XX CC Synthetic.
XX CC
XX CC EP059447-A.
XX CC
XX CC 21-MAR-1990.
XX CC
XX CC 14-AUG-1989; 89EP-0250014.
XX CC
XX CC 15-AUG-1988; 88US-0232337.
XX CC
XX CC (NEER) NBERX CORP.
XX CC
XX CC Anderson DC, Mordan AC, Abrams PG, Nichols EJ, Filtzberg AK;
XX CC WPI: 1990 085154/12.
XX CC
XX CC Covalently linked complex for tumour treatment - comprises
XX CC treating with protein, cytotoxic agent and anchored moiety.
XX CC
XX CC claim 13; Page 22; 24pp; English.
XX CC
XX CC the sequence is one of several possible accessory moieties which can be
XX CC attached to the C-terminus of an anchoring moiety which in turn is
XX CC linked to a targeting protein and a cytotoxic agent. When the anchoring
XX CC peptide intercalates into the target cell plasma membrane the accessory
XX CC moiety is translocated across the membrane and protrudes into the
XX CC cytoplasm. It can then be phosphorylated by cellular kinases at neutral
XX CC pH. This irreversibly anchors the complex to the membrane and may
XX CC enhance the translocation into the cytoplasm. The complex is useful for
XX CC treatment and diagnosis of tumours.
XX CC See also AAR03435-60.
XX SQ Sequence 5 AA:
XX
XX Query Match 81.8%; Score 9; DB 11; Length 5;
XX Best Local Similarity 66.7%; Pred. No. 7.7e+05;
XX Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LXR 3
XX 1 1
XX 3 LSR 5
XX
XX RESULT 11
XX AAR48999
XX ID AAR48999 standard; Protein; 5 AA.
XX AC AAR48999;
XX XX
XX 02-SEP-1994 (first entry)
XX CC
XX CC Sequence of portion of wild type murine erythropoietin receptor
XX CC (rEPOR).
XX CC
XX CC Erythropoietin receptor; EPO; ss.
XX CC
XX CC Mus musculus.
XX CC
XX CC Key Location/Qualifiers
XX CC Misc-difference 3
XX CC Note "cys in rEPOR"
XX CC

```


PN US9292654 A.
 XX
 PD 08-MAR-1994.
 XX
 PF 13-DEC-1990: 900S-0626923.
 XX
 PR 13-DEC-1990: 900S-0626923.
 XX
 PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Lodish H, Longmore GD, Yoshimura A;
 XX
 DE WPI: 1994-082236/10.
 XX
 DR N-PSDR: AAR48666.
 XX
 PT Mutant erythropoietin (EPO) receptor gene - hypersensitive to
 PT EPO, useful in assay for identifying compounds, mimicking EPO
 PT action
 XX
 PS Disclosure; Flu 10; 13pp; English.
 XX
 CC cEPOR is wild-type EPO. cEPOR is a constitutive PPO. It contains
 CC a point mutation (4 transition from C to T at nucleotide 484) which
 CC causes one substitution (Arg to Cys) in the exoplasmic domain of
 CC EPO at position 129 of the predicted N-terminus. The Arg to Cys point
 CC mutation in cEPOR is sufficient to induce factor-independent
 CC growth.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DE 1 LAR 3
 XX
 RESULT 12
 AAR50145
 ID AAR50135 standard; peptide; 5 AA.
 AC AAR50135;
 XX
 DT 23-SEP-1994 (first entry)
 XX
 DE Ovine growth hormone residues 92-96.
 XX
 KW Bovine; ovine; porcine; growth hormone; bGH; oGH; pGH; antigen;
 KW growth hormone activity; potentiate; enhance; increase.
 XX
 OS Bos taurus.
 OS Ovis aries.
 OS Sus scrofa.
 XX
 PN W09405697-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 07-SEP-1993: 93WO-GB01887.
 XX
 PR 07-SEP-1992: 92GB-0018907.
 PR 04-AUG-1993: 93GB-0016508.
 XX
 PA (ASRI) AGRIC & FOOD RES COUNCIL.
 PA (HANN) HANNAH RES INST.
 XX
 PI Beattie J, Holder AT;
 XX
 DE WPI: 1994-101122/12.
 XX
 PT New antigenic molecules derived from growth hormone - and derived
 PT antibodies, used to stimulate the activity of growth hormone
 XX
 PS Claim 4; Page 7; 64pp; English.
 XX
 CC This peptide corresponds to residues 94-97 of bovine, ovine and
 CC porcine growth hormone. The peptide is rendered antigenic and is
 CC then capable of stimulating the production of antibodies which,
 CC when in the appropriate formulation, potentiate the effect of
 CC growth hormone.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DE 1 LAR 3
 XX
 RESULT 13
 AAR50136
 ID AAR50136 standard; peptide; 5 AA.
 AC AAR50136;
 XX
 DT 23-SEP-1994 (first entry)
 XX
 DE Ovine growth hormone residues 94-97.
 XX
 KW Bovine; ovine; porcine; growth hormone; bGH; oGH; pGH; antigen;
 KW growth hormone activity; potentiate; enhance; increase.
 XX
 OS Bos taurus.
 OS Ovis aries.
 OS Sus scrofa.
 XX
 PN W09405697-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 07-SEP-1993: 93WO-GB01887.
 XX
 PR 07-SEP-1992: 92GB-0018907.
 PR 04-AUG-1993: 93GB-0016508.
 XX
 PA (ASRI) AGRIC & FOOD RES COUNCIL.
 PA (HANN) HANNAH RES INST.
 XX
 PI Beattie J, Holder AT;
 XX
 DE WPI: 1994-101122/12.
 XX
 PT New antigenic molecules derived from growth hormone - and derived
 PT antibodies, used to stimulate the activity of growth hormone
 XX
 PS Claim 4; Page 7; 64pp; English.
 XX
 CC This peptide corresponds to residues 94-97 of bovine, ovine and
 CC porcine growth hormone. The peptide is rendered antigenic and is
 CC then capable of stimulating the production of antibodies which,
 CC when in the appropriate formulation, potentiate the effect of
 CC growth hormone.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DE 1 LAR 3
 XX
 RESULT 14
 AAR50137
 ID AAR50137 standard; peptide; 5 AA.
 AC AAR50137;
 XX
 DT 23-SEP-1994 (first entry)
 XX
 DE Ovine growth hormone residues 94-97.
 XX
 KW Bovine; ovine; porcine; growth hormone; bGH; oGH; pGH; antigen;
 KW growth hormone activity; potentiate; enhance; increase.
 XX
 OS Bos taurus.
 OS Ovis aries.
 OS Sus scrofa.
 XX
 PN W09405697-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 07-SEP-1993: 93WO-GB01887.
 XX
 PR 07-SEP-1992: 92GB-0018907.
 PR 04-AUG-1993: 93GB-0016508.
 XX
 PA (ASRI) AGRIC & FOOD RES COUNCIL.
 PA (HANN) HANNAH RES INST.
 XX
 PI Beattie J, Holder AT;
 XX
 DE WPI: 1994-101122/12.
 XX
 PT New antigenic molecules derived from growth hormone - and derived
 PT antibodies, used to stimulate the activity of growth hormone

PT antibodies, used to stimulate the activity of growth hormone
 XX
 PS Claim 4; Page 7; 64pp; English.
 XX
 CC This peptide corresponds to residues 92-96 of bovine, ovine and
 CC porcine growth hormone. The peptide is rendered antigenic and is
 CC then capable of stimulating the production of antibodies which,
 CC when in the appropriate formulation, potentiate the effect of
 CC growth hormone.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DE 1 LAR 4
 XX
 RESULT 14
 AAR50136
 ID AAR50136 standard; peptide; 5 AA.
 AC AAR50136;
 XX
 DT 23-SEP-1994 (first entry)
 XX
 DE Ovine growth hormone residues 94-97.
 XX
 KW Bovine; ovine; porcine; growth hormone; bGH; oGH; pGH; antigen;
 KW growth hormone activity; potentiate; enhance; increase.
 XX
 OS Bos taurus.
 OS Ovis aries.
 OS Sus scrofa.
 XX
 PN W09405697-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 07-SEP-1993: 93WO-GB01887.
 XX
 PR 07-SEP-1992: 92GB-0018907.
 PR 04-AUG-1993: 93GB-0016508.
 XX
 PA (ASRI) AGRIC & FOOD RES COUNCIL.
 PA (HANN) HANNAH RES INST.
 XX
 PI Beattie J, Holder AT;
 XX
 DE WPI: 1994-101122/12.
 XX
 PT New antigenic molecules derived from growth hormone - and derived
 PT antibodies, used to stimulate the activity of growth hormone
 XX
 PS Claim 4; Page 7; 64pp; English.
 XX
 CC This peptide corresponds to residues 94-97 of bovine, ovine and
 CC porcine growth hormone. The peptide is rendered antigenic and is
 CC then capable of stimulating the production of antibodies which,
 CC when in the appropriate formulation, potentiate the effect of
 CC growth hormone.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DE 1 LAR 4
 XX

```

DB      1 LSR 4
RESULT 14
AAK50134
ID      AAK50134 standard; peptide: 5 AA.
XX
AC      AAK50134:
XX
DT      24-SEP-1994 (first entry)
XX
DE      ovine growth hormone residues 91-95.
XX
KW      bovine; ovine; porcine; growth hormone; bGH; oGH; pGH; antigen;
PW      growth hormone activity; potentiate; enhance; increase.
XX
OS      Bos taurus.
OS      Ovis aries.
OS      Sus scrofa.
XX
IN      W09405697-A.
XX
PD      17-MAR-1994.
XX
PF      07-SEP-1993; 93WO-GR01887.
XX
PR      07-SEP-1992; 92GB-0018907.
PR      09-AUG-1993; 93GB-0016508.
XX
PA      (AERI-) AGRIC & FOOD RES COUNCIL.
PA      (HANN) HANNAH RES INST.
XX
PI      Beattie J, Holder AT;
XX
DE      WPI: 1994-101122/12.
XX
XX      New antigenic molecules derived from growth hormone - and derived
PT      antibodies, used to stimulate the activity of growth hormone
XX
PS      Claim 4; Page 7; 64pp; English.
XX
CC      This peptide corresponds to residues 91-95 of bovine, ovine and
CC      porcine growth hormone. The peptide is rendered antigenic and is
CC      then capable of stimulating the production of antibodies which,
CC      when in the appropriate formulation, potentiate the effect of
CC      growth hormone.
XX
SQ      Sequence 5 AA.
Query Match 81.8%; Score 9; DB 15; Length 5;
Best local Similarity 66.7%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LSR 4
DB      1 LSR 5
DE      4 LSR 5
RESULT 15
AAK77433
ID      AAK77433 standard; peptide: 5 AA.
XX
AC      AAK77433:
XX
DT      06-FEB-1996 (first entry)
XX
DE      Human apolipoprotein (a) (apo(a)) antigenic peptide.
XX
KW      Human; old world monkey; apolipoprotein (a); apo(a); primer; probe;
PW      antigenic peptide; immunoassay; detection; quantitation.
XX
OS      Homo sapiens.
XX

Query Match 81.8%; Score 9; DB 16; Length 5;
Best local Similarity 66.7%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LSR 3
DB      1 LSR 3
DE      1 LSR 3
RESULT 16
AAW09695
ID      AAW09695 standard; peptide: 5 AA.
XX
AC      AAW09695:
XX
DT      24-MAY-1997 (first entry)
XX
DE      Cyclic pentapeptide having thrombolytic activity.
XX
KW      thrombolysis; arteriosclerosis; cyclic.
XX
OS      Synthetic.
XX
PI      Key Location/Qualifiers
PI      Modified-site 1 /note "this residue forms part of a cyclic
PI      peptide, being condensed with the amino acid
PI      at position 5. It is not an N-terminal site."
PI      Modified-site 5 /note "this residue forms part of a cyclic
PI      peptide, being condensed with the amino acid
PI      at position 1. It is not a C-terminal site."
PI      Misc-difference 1 /note "p term residue."
PI      Misc-difference 3 /note "p term residue."
PI      Misc-difference 5 /note "p term residue."
PI      Misc-difference 5 /note "p term residue."
XX
IN      JF08217794 A.
XX
PD      27-AUG-1996.
XX

```

PF 15-FEB-1995; 95JP-0026674.
 XX
 PR 15-FEB-1995; 95JP-0026674.
 XX (BIOC-) BIOCSMOS YG.
 XX
 XX WPI: 1996-425431/44;
 XX

PF New cyclic penta-peptide exhibits thrombolytic and
 PT anti-arteriosclerosis activity
 XX
 XX Disclosure: Page 8: 9pp; Japanese.
 XX
 XX The invention relates to new cyclic pentapeptides of formula
 CC cyclo(A-B-C-D-E) in which A is Val, Leu, Ile, Phe, Lys, Arg, Glu, Ala or Ser; C is Leu,
 CC Ser; B is Leu, Val, Phe, Lys, Arg, His, Glu, Glu, Ala or Ser; D is Leu,
 CC Val, Ile, Phe, Lys, Arg, Glu, Glu, Ala or Ser; E is Phe, Val, Leu, Tyr,
 CC Lys, Arg, His, Glu, Glu, Ala or Ser; and E is Arg, Val, Leu, Phe, Lys,
 CC His, Glu, Asn, Ala or Ser. The amino acids may be in D- or L-form.
 CC The peptides have thrombolytic activity and anti-arteriosclerotic
 CC activity.
 CC The present sequence is a specific example of the new peptides.
 XX
 XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Post-Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 DB 3 LAR 5

RESULT 17
 AAW09696
 ID AAW09696 standard; peptide; 5 AA.
 XX
 AC AAW09696;

DI 23-MAY-1997 (first entry)

XX Cyclic pentapeptide having thrombolytic activity.

XX Thrombolysis, arteriosclerosis; cyclic.

XX Synthetic.

PH Key location/qualifiers

FT Modified-site 1

FT /note= "this residue forms part of a cyclic
 peptide, being condensed with the amino acid
 at position 5. It is not an N-terminal site"

FT Modified-site 5

FT /note= "this residue forms part of a cyclic
 peptide, being condensed with the amino acid
 at position 1. It is not a C-terminal site"

FT Misc-difference 1

FT /note= "p-form residue"

FT Misc-difference 3

FT /note= "p-form residue"

FT Misc-difference 5

FT /note= "p-form residue"

XX JP08217794-A.

XX 27-AUG-1996.

XX 15-FEB-1995; 95JP-0026674.

XX 15-FEB-1995; 95JP-0026674.

XX (BIOC-) BIOCSMOS YG.

XX WPI: 1996-425431/44.
 DR

XX New cyclic pentapeptide exhibits thrombolytic and
 PT anti-arteriosclerosis activity

XX Disclosure: Page 8: 9pp; Japanese.

XX the invention relates to new cyclic pentapeptides of formula
 CC cyclo(A-B-C-D-E) in which A is Val, Leu, Ile, Phe, Lys, Arg, Glu, Ala or Ser; C is Leu,
 CC Ser; B is Leu, Val, Phe, Lys, Arg, His, Glu, Glu, Ala or Ser; D is Leu,
 CC Val, Ile, Phe, Lys, Arg, Glu, Glu, Ala or Ser; E is Phe, Val, Leu, Tyr,
 CC Lys, Arg, His, Glu, Glu, Ala or Ser; and E is Arg, Val, Leu, Phe, Lys,
 CC His, Glu, Asn, Ala or Ser. The amino acids may be in D- or L-form.
 CC The peptides have thrombolytic activity and anti-arteriosclerotic
 CC activity.
 CC The present sequence is a specific example of the new peptides.
 XX
 XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;

Post-Local Similarity 66.7%; Pred. No. 7.7e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 DB 3 LSR 5

RESULT 18

AAW00251

ID AAW00251 standard; Peptide; 5 AA.

XX AC AAW00251;

XX 16-DEC-1996 (first entry)

XX Subtilisin N62D/G166D substrate peptide.

XX Subtilisin BPN'. Protease, enzyme engineering; protein engineering;
 KW Bacillus amyloliquefaciens, mutagenesis, substrate specificity;
 KW phase display.

XX Synthetic.

XX W66627671-A1.

XX 12-SEP-1996.

XX 27-FEB-1996; 96WI-0502861.

XX 19-JUN-1995; 95US-0504245.

XX 03-MAR-1995; 95US-0398038.

XX (GUTH) GUNTER-H INC.

XX Ballinger MD, Wells JA;

XX WPI: 1996-425431/42.

XX Subtilisin variants for cleaving substrates containing basic residues -
 PT allow effective cleavage of fused proteins with basic linker
 sequences

XX Example 4, Page 27; 93pp; English.

XX A phase display system was used to screen 5 residue substrate
 CC linkers for cleavage by subtilisin BPN' (P225516P deBr mutant
 CC (AAW00247). The library was subjected to 9 rounds of selection, and
 CC clones that were increasingly sensitive or resistant to cleavage
 CC were selected. of 21 clones in the sensitive pool, 3 were monobasic
 CC (AAW00249) and 19 dibasic (AAW00249-5). The substrate given in
 CC AAW00251 was selected once from the pool of 21. of 10 substrates

CC selected from the resistant pool (AAW00254-63), 7 contained no basic
 CC sites, 2 were monobasic and 1 was dibasic. The N620/G1660 double mutant
 CC specifically cleaves protein substrates contg. basic amino acid
 CC residues at positions P1 and P2.
 XX
 SQ Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 1 LXR 3

RESULT 19
 AAW00252
 ID AAW00252 standard; peptide; 5 AA.
 XX
 AC AAW00252;
 XX
 DT 16-DEC-1996 (first entry)
 XX
 DE Subtilisin B620/G1660 substrate peptide.
 XX

KW Subtilisin BPN'; protease; enzyme engineering; protein engineering;
 KW bacillus amyloliquefaciens; mutagenesis; substrate specificity;
 KW phase display.
 XX
 CS Synthetic.
 XX
 DN W-96-27671-A1.
 XX
 PD 12 SEP-1996.
 XX
 PF 27-FEB-1996; 96W0-0502861.
 XX

PR 19-JUL-1995; 95US 0504265.
 PR 03-MAR-1995; 95US-0398028.
 XX
 PA (CETH) GENENTECH INC.
 XX
 PI Bollinger MD, Wells JA;
 XX
 DK WPI: 1996-425431/42.
 XX

PT Subtilisin variants for cleaving substrates contg. basic residues -
 PT allow effective cleavage of fusion proteins with basic linker
 PI sequences
 XX
 PS Example 4; Page 27; 84pp; English.
 XX

CC A phage display system was used to screen 5-residue substrate
 CC linkers for cleavage by subtilisin BPN' B620/G1660 double mutant
 CC (AAW00247). The library was subjected to 9 rounds of selection, and
 CC clones that were increasingly sensitive to restriction enzyme cleavage
 CC were selected. Of 21 clones in the sensitive pool, 3 were monobasic
 CC (AAW00248) and 18 dibasic (AAW00249-53). The substrate given in
 CC AAW00252 was selected once from the pool of 21, of 10 substrates
 CC selected from the resistant pool (AAW00254-63), 7 contained no basic
 CC sites, 2 were monobasic and 1 was dibasic. The N620/G1660 double mutant
 CC specifically cleaves protein substrates contg. basic amino acid
 CC residues at positions P1 and P2.
 XX
 SQ Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 1 LXR 3

DB 2 LXR 4

RESULT 20
 AAW37417
 ID AAW37417 standard; peptide; 5 AA.
 XX
 AC AAW37417;
 XX
 DT 10 MAR-1998 (first entry)
 XX
 DE Mammalian haemoglobin tryptic peptide C-terminal sequence.
 XX
 KW Mammalian; haemoglobin; tryptic peptide; bovine; porcine; equine;
 KW immune enhancer; microbial psoriasis; blood contracting; food;
 KW powdered milk; cow; pig; horse.
 XX
 CS Bos taurus.
 CS Equus caballus.
 CS Sus scrofa.
 CS Synthetic.
 XX
 PN JP09262094 A.
 XX
 PD 07-OCT-1997.
 XX
 PF 27 MAR-1996; 96JP 0072797.
 XX
 PR 27 MAR-1996; 96JP-0072797.
 XX
 CS (FIOH-) ITO HAM KK.
 XX
 DN WPI: 1997-544157/50.
 XX

PT New mammalian haemoglobin tryptic peptide(s) - useful as immune
 PT enhancers and to prevent microbial psoriasis
 XX
 PS Claim 1; Page 1; 7pp; Japanese.
 XX

CC The present sequence represents a C-terminal peptide used in low
 CC mammalian haemoglobin tryptic peptides, consisting of 5-12 amino
 CC acids. The peptides can be produced from bovine, swine or equine
 CC haemoglobin by hydrolysis with an enzyme (e.g. trypsin) and subsequent
 CC purification. They can also be produced by chemical synthesis. The
 CC peptides correspond to the partial amino acid sequence with length of
 CC the beta-chain of bovine, swine or equine haemoglobin and have
 CC immun-contracting and immune enhancing activities. They may be used
 CC in prevention of microbiological psoriasis or as immune enhancers,
 CC functional foods or powdered milk for infants.
 XX
 SQ Sequence 5 AA;

Query Match 81.8%; Score 9; DB 18; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 3 LXR 5

RESULT 21
 AAY51458
 ID AAY51458 standard; peptide; 5 AA.
 XX
 AC AAY51458;
 XX

DT 11 MAY-2000 (first entry)

DE AAV VP3 derived peptide fragment #14.

KW VP3; structural protein; capsid; tropism; diagnosis; gene therapy.
 XX

OS Adeno associated virus.
 PN W09967393-A2.
 XX
 PD 24-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-EP04288.
 XX
 PR 19-JUN-1999; 99DE 1927457.
 XX
 PA (MEDI-) MEDIGENE AG
 XX
 PI Hillek M, Ried M, DeLage G, Girard A,
 XX
 PF WPI: 2000 16056/14
 XX
 PR Structure proteins of adeno-associated virus with at least one mutation
 PT have increased infectiveness -
 XX
 PS Claim 15; Page 31; 43pp; German.
 XX
 CC This invention describes novel structural proteins of adeno associated
 CC virus (AAV) especially AAV-capsids with at least one mutation and which
 CC have an increased infectiveness. The structural proteins are used to
 CC alter the tropism of AAV, to transform cells, for diagnosis and for
 CC effectivity studies for gene therapy and/or for stochastic targeting.
 CC AAV51446-Y51467 represent AAV derived peptides used to illustrate the
 CC method of the invention.
 XX
 SQ Sequence 5 AA:
 Query Match 91.9%; Score 9; IP 23; Length 5;
 Best local Similarity 66.7%; Prod No 7 76-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 J I
 Db 3 LSR 5
 RESULT 22
 AAE11109
 ID AAE11109 standard; peptide: 5 AA.
 XX
 AC AAE11109;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Tryptic peptide #11 of phAR fusion protein.
 XX
 KW Phenylalanine hydroxylase; PAH; pHA; 4a-carbinolamine dehydratase; phhB;
 KW aromatic aminotransferase; phhC; milk protein; animal protein; casein;
 KW proteinaceous food product; metabolite; whey protein; phenylketonuria;
 KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
 KW cell therapy; chymotryptic peptide.
 XX
 OS Unidentified.
 XX
 PN W0200169822 A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-DE00172.
 XX
 PR 14-MAR-2000; 2000US-0525116.
 XX
 PA (NIIA-) NIIAH APS.
 XX
 PI Johnson M, Ravn P, Madsen SM, Vrang A, Israelson H, Brodmose L;
 PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
 XX
 DR WPI: 2001-590055/66.
 XX
 PT Novel recombinant cells comprising a nucleic acid encoding a gene

PT Novel recombinant cells comprising a nucleic acid encoding a gene
 PT product having phenylalanine hydroxylase activity, that is derived from
 PT a prokaryotic organism, is useful for treating phenylketonuria in
 PT mammals -
 XX
 PS Example 8; Page 47; 91pp; English.
 XX
 CC The patent discloses novel cells comprising a nucleic acid encoding
 CC a gene product having phenylalanine hydroxylase (PAH) activity such
 CC as phenylalanine hydroxylase (phhA), 4a-carbinolamine dehydratase
 CC (phhB) and aromatic aminotransferase (phhC), which are derived
 CC from a prokaryotic organism. The patent also relates to fusion
 CC proteins comprising a protein subunit and/or stabilising the
 CC PAH activity in addition to PAH activity, the cells are useful
 CC for producing PAH. The sequences of the invention are also useful
 CC for preparing a proteinaceous food product (animal protein such
 CC as a milk protein derived from casein, whey protein or a whey protein)
 CC having reduced content of phenylalanine. The method involves contacting
 CC the food product starting material with the cells or fusion proteins
 CC such that at least part of the phenylalanine content of the starting
 CC material is converted into compounds that do not cause phenylketonuria
 CC (PKU) by the enzymatically active product. PAH enzyme is useful for
 CC manufacturing a medicament for treating PKU, which is an inherited
 CC metabolic disorder resulting in an accumulation in the body of
 CC a phenylalanine and metabolites that can cause impaired brain
 CC function. The present sequence is tryptic peptide of phhAR fusion
 CC protein.
 XX
 SQ Sequence 5 AA:
 Query Match 41.9%; Score 9; IP 22; Length 5;
 Best local Similarity 55.7%; Prod No 7 76-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 J I
 Db 3 LAR 5
 RESULT 23
 AAE11144
 ID AAE11144 standard; peptide: 5 AA.
 XX
 AC AAE11144;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Chymotryptic peptide #14 of phhAR fusion protein.
 XX
 KW Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; phhB;
 KW aromatic aminotransferase; phhC; milk protein; animal protein; casein;
 KW proteinaceous food product; metabolite; whey protein; phenylketonuria;
 KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
 KW cell therapy; chymotryptic peptide.
 XX
 OS Unidentified.
 XX
 PN W0200169822-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-DE00172.
 XX
 PR 14-MAR-2000; 2000US-0525116.
 XX
 PA (NIIA-) NIIAH APS.
 XX
 PI Johnson M, Ravn P, Madsen SM, Vrang A, Israelson H, Brodmose L;
 PI Arnau J, Jensen SH, Gjetting T, Nielsen E;
 XX
 DR WPI: 2001-590055/66.
 XX
 PT Novel recombinant cells comprising a nucleic acid encoding a gene

PT product having phenylalanine hydroxylase activity, that is derived from
PT a prokaryotic organism, is useful for treating phenylketonuria in
XX mammals

PS Example B- Page 46- 9pp: English

XX the patent discloses novel cells comprising a nucleic acid encoding
XX a gene product having phenylalanine hydroxylase (PAH) activity such
XX as phenylalanine hydroxylase (pHA), 4a carbinolamine dehydratase
XX (qHA) and aromatic aminotransferase (pHC), which are derived
XX from a prokaryotic organism. The patent also relates to fusion
XX proteins comprising a protein enhancer and/or stabilising the
XX PAH activity in addition to PAH activity. The cells are useful
XX for producing PAH. The sequences of the invention are also useful
XX for preparing a proteinaceous food product (animal protein such
XX as a milk protein derived from casein, globulin or a whey protein)
XX having reduced content of phenylalanine. The method includes contacting
XX the food product starting material with the cells or fusion proteins
XX such that at least part of the phenylalanine content of the starting
XX material is converted into compounds that do not cause phenylketonuria
XX (PKU) by the enzymatically active product. PAH enzyme is useful for
XX manufacturing a medicament for treating PKU, which is an inherited
XX metabolic disorder resulting in an accumulation in the body of
XX L-phenylalanine and metabolites that can cause retarded brain
XX function. The present sequence is chymotryptic peptide of pHA-B fusion
XX protein.

XX Sequence 5 AA;

Query Match 81.99; Score 9; DB 22; Length 5;
Best Local Similarity 66.7%; Pred. No. 7.7e-05;

Matches 2; Conservative 6; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3

DB 1 LAR 3

RES011 24

AAR05461

XX ID AAR05461 standard; peptide: 5 AA.

XX AC AAR05461;

XX 24-SEP-2001 (first entry)

XX MASP substrate #3.

XX Mannan binding protein-associated serine protease; MASP substrate;
XX complement activation; C-activation; microbial infection;
XX cytomegalovirus; CMV; hepatitis virus; human immunodeficiency virus;
XX HIV; organ transplant rejection; tissue injury; autoimmune disease;
XX rheumatoid arthritis; systemic lupus erythematosus; SLE; mouse,
XX inflammatory response; Alzheimer's disease; anaphylatoxin.

XX Synthetic.

XX Key location/Qualifiers

XX Modified-site 1

XX Note "N-terminal acetyl"

XX Modified-site 5

XX Note: "Conjugated to para-nitroaniline (PNA)"

XX US623544 B1.

XX 22-MAY 2001.

XX 08-FEB-1999; 9905 0246500.

XX 08-FEB-1999; 9905-0246500.

XX (Seri) SCHIPPS RES INST.

PI Huqli TE;

XX WPI: 2001-45082/48.

XX Method for determining in vivo levels of activated mannan binding

PT protein-associated serine protease enzyme, and new peptide derivatives

XX

XX Claim 47: Column 59, 9pp: English.

XX The invention relates to assays for monitoring in vivo levels of
XX activated mannan-binding protein-associated serine protease (MASP-1 and
XX MASP-2) activity. The assay comprises contacting a sample of blood or
XX plasma comprising a metal ion chelator with a substrate of tomosin
XX R peptide Y, wherein the peptide comprises at least 4 residues from the
XX C-terminus of an anaphylatoxin selected from C3a, C4a and C5a; R is a
XX peptide backbone protected at C-terminus by a group Z and Y is a group
XX cleavable from the substrate by MASP and comprises a labelled tag. The
XX substrate of the invention is also useful for monitoring in vitro and
XX in vivo complement activation (C-activation) by classical alternative
XX or lectin pathways. The assays of MASP activity can be used for
XX detecting or monitoring a condition associated with complement
XX activation; the conditions include microbial infections
XX caused by particularly cytomegalovirus (CMV), hepatitis virus and
XX human immunodeficiency virus (HIV), organ transplant rejection, tissue
XX injury, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
XX erythematosus (SLE)) and inflammatory responses (e.g. in Alzheimer's
XX disease and bacterial diseases). The assay of MASP is also useful for
XX assessing the toxicity or injury of therapeutic treatments or screening
XX test compounds as agents for treatment of viral diseases, parasitic
XX infections, tissue injury, organ transplant rejection, autoimmune
XX diseases or inflammatory responses. The present sequence is a
XX mannan-binding protein-associated serine protease (MASP) substrate.

XX Sequence 5 AA;

Query Match 81.88; Score 9; DB 22; Length 5;
Best Local Similarity 66.7%; Pred. No. 7.7e-05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LTR 5

RES011 25

AAM51952

XX ID AAM51952 standard; peptide: 5 AA.

XX AC AAM51952;

XX 01-FEB-2002 (first entry)

XX PSA antibody preparation immunogen peptide #4.

XX PSA; prostate-specific antigen; prostatic carcinoma; pro kallikrein 2;
XX human; antibody; immunogen.

XX Homo sapiens.

XX DE10032040-A1.

XX 29-NOV 2001.

XX 05-JUL-2000; 2000E-1032040.

XX 24-MAY 2000; 2000E-1025467.

XX (HOF) ROCHE DIAGNOSTICS GMBH.

XX WPI: 2002 042634/06.

PT Antibody comprising specificity for some truncated forms of

PI pro-prostate specific antigen, useful in immunoassays for differential
 PI diagnosis of prostatic carcinoma
 XX
 PS Disclosure; Page 10; 16pp; German.
 XX
 CC The present invention relates to an antibody specific for (-5,-6 and
 CC -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4)
 CC or shorter forms of the protein. The antibody can be used to diagnose
 CC prostatic carcinoma and to detect human pro-kallikrein 2. The present
 CC sequence is a peptide which forms part of a peptide-containing immunogen
 CC described in the exemplification of the invention.
 XX
 SQ Sequence 5 AA;

Query Match 81.8%; Score 9; DB 23; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 3 LSR 5

RESULT 26
 AAM51956
 ID AAM51956 standard; peptide; 5 AA
 XX
 AC AAM51956;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE PSA antibody preparation immunogen peptide #9.
 XX
 KW PSA: prostate specific antigen; prostatic carcinoma; pro-kallikrein 2;
 KW human; antibody; immunogen.
 XX
 OS Homo sapiens.
 XX
 FN DE10032040-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 05-JUL-2000; 2000EE 1032049.
 XX
 PP 24-MAY-2000; 2000PF 1025387
 XX
 PA (HOFF) POCHÉ DIAGNOSTICS GMRH
 XX
 DP WPI: 2000-042632/06
 XX
 PT Antibody comprising specificity for prostate carcinoma forms of
 PT pro prostate specific antigen, useful in immunoassays for differential
 PT diagnosis of prostatic carcinoma
 XX
 PS Disclosure; Page 11; 16pp; German.
 XX
 CC The present invention relates to an antibody specific for (-5,-6 and
 CC -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4)
 CC or shorter forms of the protein. The antibody can be used to diagnose
 CC prostatic carcinoma and to detect human pro-kallikrein 2. The present
 CC sequence is a peptide which forms part of a peptide-containing immunogen
 CC described in the exemplification of the invention.
 XX
 SQ Sequence 5 AA;

Query Match 81.8%; Score 9; DB 23; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 2 LSR 4

RESULT 27
 AAR46808
 ID AAR46808 standard; Protein; 6 AA.
 XX
 AC AAR46808;
 XX
 DT 19-AUG-1994 (first entry)
 XX
 DE Phytase derived peptide 794(9 phy).
 XX
 KW pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid;
 KW phytate degrading enzyme; pH; chemical; insoluble hexaphosphoric acid;
 KW plant; feed composition; filtration.
 XX
 OS Synthetic.
 XX
 PN W09403612-A.
 XX
 PD 17-FEB-1994.
 XX
 PF 30-JUL-1993; 93WO-FI00410.
 XX
 PP 31-JUL-1992; 92US-0924724.
 XX
 PP (AIKO-) AIKO LTD.
 XX
 FA Cantrell M., Fagerström RB., Miettinen-Oinonen ASK;
 PI Hockliffe MP., Pihlajama MT., Pihlajonen O., Pahlsson JA;
 PI Hockell TK., Turunen MK;
 XX
 DE WPI: 1994 055700/08.
 XX
 KW Comensal, host; phytate degrading enzyme; solid; by expression
 KW of their genes in Trichoderma, used partic. for producing animal
 KW feed composit.

Example 4. Page 43, 144pp; English.
 XX
 PS The sequences given in AAR46794-824 are peptides derived from the
 PS phytase protein. The phytase protein may be used in the composition
 CC of the invention. The RNA encoding the phytase protein may be
 CC introduced into a Trichoderma host which then expresses it and the
 CC protein is collected from the culture medium. By using Trichoderma as
 CC a host for Aspergillus phytase biotransformation, such as this, a
 CC totally different enzyme composition compared to that secreted from
 CC Aspergillus results. The enzyme composition can be used for removal
 CC of phytic acid or inositol hexaphosphoric acid from raw material,
 CC particularly plant material. The composition is used in feed
 CC compositions for animals. By using Trichoderma as a source of a
 CC composition containing phytate degrading enzymes some difficult
 CC downstream processing problems, e.g. filtration, that occur with
 CC similar Aspergillus compositions are avoided and yields are improved.
 XX
 SQ Sequence 6 AA;

Query Match 61.8%; Score 9; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 4 LTR 6

RESULT 28
 AAR50141
 ID AAR50141 standard; peptide; 6 AA.
 XX
 AC AAR50141;
 XX
 DT 24-SEP-1994 (first entry)
 XX

SQ Sequence 6 AA:
 Query Match 81.8%; Score 9; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 Db 1 LSR 3
 RESULT 31
 AAR55741
 ID AAR55741 standard; peptide; 6 AA.
 AC AAR55741;
 XX 16-NOV-1994 (first entry)
 DI dsRNA-dependent kinase inhibitor.
 DE dsRNA dependent kinase inhibitor; fatty acyl-peptide; conjugate;
 KW anticelliferative; tumor; psoriasis; docosahexaenoic acid; DHA;
 KW eicosapentaenoic acid; EPA; anti-tumor.
 XX Synthetic.
 GS WO9412530-A.
 FN 06-JUN-1994
 PD 29-NOV-1993; 93WO-H000065.
 PF 30-NOV-1992; 92US-0984293.
 XX (BIOS-) BIOSIGNAL KUTATO FEJESZTO KFT.
 PA (SYNT-) SYNTHETIC PEPTIDES INC.
 XX Balogh A., Csachia PJ., Hodges PS., Horvath A., Keri G;
 PI Szederkenyi E., Vadász Z.
 XX WI: 1994-280194/24.
 XX New fatty acyl-peptide conjugates for inhibiting cell
 PT proliferation more active than free peptide; particle for
 PT treating tumours, virus-infected cells, psoriasis, etc.
 XX Disclosure; Fig. 1; 45pp; English.
 PS The peptides given in AAR55718 18 can each be conjugated through an
 CC amide linkage with a polyunsaturated fatty acid moiety, such as
 CC docosahexaenoic acid or eicosapentaenoic acid, to improve
 CC antiproliferative activity. The dsRNA-dependent kinase
 CC inhibitor given in AAR55741 modulates protein kinases associated
 CC with cell proliferation.
 XX Sequence 6 AA:
 Query Match 81.8%; Score 9; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 Db 3 LSR 5
 RESULT 32
 AAR90511
 ID AAR90511 standard; peptide; 6 AA.
 AC AAR90511;
 XX

DI 03-SEP-1996 (first entry)
 XX Hybridoma ATCC HB-11884 antibody displacing peptide #9.
 DE Antibody displacement cell separation system, cell surface antigen; Aa;
 XX random peptide display library; complementarity determining region; CDR;
 FW antibody; Ab; peptide; CD34 cell; haematopoietic cell; tumour cell;
 KW lymphocyte; high dose therapy; immune system; chemotherapy;
 KW patient specific vaccine.
 XX Synthetic.
 GS WO9534817-A1.
 FN 21-DEC-1995.
 PD 14-JUN-1995; 95WO-0807491.
 XX 14 JUN 1994. 94US 0259427.
 PF (BAXT) BAXTER INT INC.
 XX Al Abady EA, Fuda EZ, Giffelton E, Hefprich SL;
 FI Kozori JA, Isner JW J;
 XX WI: 1996-049866/05.
 DR Selecting target cells by reacting specific antibody to surface
 PT antigen - then disrupting the complex formed with peptide displacer.
 PT for selecting CD34 cells for reconstitution of immune system
 PT after anticancer treatment
 XX Claim 27; Page 158; 170pp; English.
 PS AAR90503-R90511 represent antibody displacing peptides. These sequences
 CC displace the antibody produced by the hybridoma ATCC HB-11884 (9187).
 CC These sequences can be used in a method to select target cells from a
 CC heterologous cell suspension. In the suspension, there is at least one
 CC complex of a cell separation system, linked to a primary antibody (Ab)
 CC which is bound to the cell surface antigen (Aa). The complex is
 CC separated from the rest of the suspension, and contacted with a peptide
 CC (such as this sequence) that binds to the Ab, displacing it from the Aa
 CC and releasing the cell. These sequences can be identified by biopanning
 CC random peptide display libraries with the Ab, by analysis of potential
 CC antigenic parts of the cell surface antigen, or by analysis of the
 CC complementarity determining regions of the Ab. These sequences can also
 CC be used in a method for determining the number of specific cells in a
 CC reposition. The methods can be used for positive selection of CD4
 CC haematopoietic cells, and removal of undesired tumour cells or
 CC lymphocytes from the selected cells. The pure CD34 cells are released
 CC into a cancer patient after high dose therapy to reconstitute the immune
 CC system. Tumor cells can also be isolated to determine their
 CC chemotherapeutic susceptibility, or for the production of
 CC patient specific vaccines or antibodies. These sequences allow for the
 CC recovery of cells from solid supports, in high yield, without enzymatic
 CC cleavage. They are relatively inexpensive and safe, and leave cell
 CC surface proteins intact.
 XX Sequence 6 AA:
 Query Match 81.8%; Score 9; DB 17; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 Db 1 LTR 3
 RESULT 33
 AAR74602
 ID AAR74602 standard; peptide; 6 AA.
 XX

AC AAB74602;
 XX
 DT 21-MAY-2001 (first entry)
 XX
 DE 4-methylcholanthrene (MCA) peptide substrate.
 XX
 KW 4-methylcholanthrene; MCA; substrate; metalloproteinase inhibitor;
 KW cancer; metastasis; arthritis.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 FT /note= "Pro in N-terminally modified to
 FT 7-methoxycoumarin-4-yl-acetyl-pro"
 FT Modified-site 5
 FT /note= "Ala is N-terminally modified to
 FT 3-(2,4-dichlorophenyl)-2,2-dimethylpropyl-ala"
 FT Modified-site 6
 FT /note= "amidated"
 XX
 GN W09720824 AL.
 XX
 DT 12-JUN-1997.
 XX
 PE 05-DEC-1996; 66W0-0519328
 XX
 PR 08-DEC-1995; 95US-0569766
 XX
 PA (AG00-) AG00FON PHARM INC.
 XX
 PI Zook SE, Iannino E, Deason ME, Bender SL, Melnick MJ;
 XX
 DE WFL: 1997-532465/30
 XX
 XX New N-hydroxy benzoxasulphonyl carbamate derivatives - are
 PT metalloproteinase inhibitors, useful for treating cancer, metastasis,
 PT and arthritis
 XX
 PS Example 22: Page 109, 151pp. English.
 XX
 CC The present invention describes metalloproteinase inhibitors and
 CC pharmaceutical compositions containing them. Also described are methods
 CC and intermediates useful in the preparation of the metalloproteinase
 CC inhibitors. R¹-hydroxy benzoxasulphonyl (thiazole or piperazine)
 CC carbamate derivatives are metalloproteinase (MP) inhibitors. The
 CC present sequence represents a 3-methylcholanthrene (MCA) peptide
 CC substrate which is used in the exemplification of the present invention.
 CC The metalloproteinase inhibitors are useful for treating cancer,
 CC metastasis and arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 81.8%; Score 9; DB 18; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 OY 1 LXR 3
 DB 4 LAR 6
 RESULT 64
 ID AAW43665 standard; peptide; 6 AA.
 XX
 AC AAW43665;
 XX
 DT 24-APR-1998 (first entry)
 XX
 DE Complement antagonising peptide.
 XX
 KW Factoriothapep; capsid protein; mutant; half-life; phage therapy;

KW bacterial infection; antibacterial; complement antagonising peptide.
 XX
 OS Synthetic.
 XX
 GN W09739118-AL.
 XX
 DT 27-OCT-1997.
 XX
 PE 03-APR-1997; 97W0-0804714.
 XX
 PR 12-APR-1996; 96US-0641427.
 XX
 PA (EXPO-) EXPONENTIAL BIOTHERAPIES INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES
 XX
 PI Adhya SL, Carlton RM, Merrill CR;
 XX
 DE WFL: 1997-526457/48.
 XX
 PT Amplifying gene to extend half-life of phage in circulation - gene
 PT encodes modified capsid protein; useful for therapy of bacterial
 PT infections
 XX
 PS Example 4: Page 23; 49pp. English.
 XX
 CC This is a complement antagonising peptide. A double stranded DNA encoding
 CC this peptide was synthesised. This nucleotide sequence is fused at the 3'
 CC end of a gene encoding a phage coat surface protein. This is used in the
 CC construction of a phage that can express molecules antagonising the host
 CC defence system. This enables the phage to delay inactivation by the host
 CC defence system. This is used in the construction of a modified phage with
 CC extended half-life. The phage has a modified capsid protein, having an
 CC acidic amino acid replaced by a basic amino acid, and extended half-life
 CC (at least 15%). The modified phages are used to treat a very wide range
 CC of bacterial infections, optionally in conjunction with antibiotics, in
 CC human or veterinary medicine. The modified phages are more resistant to
 CC inactivation by the host's immune system, so are more efficient
 CC antibacterial agents than wild-type phages. Phage therapy has fewer side
 CC effects than treatment with antibiotics or other drugs. It is suitable
 CC for patients allergic to conventional therapy and is especially valuable
 CC for treating infections caused by drug resistant bacteria.
 XX
 SQ Sequence 6 AA;
 Query Match 91.0%; Score 9; DB 18; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 OY 1 LXR 3
 DB 1 LAR 3
 RESULT 35
 ID AAW77324 standard; peptide; 6 AA.
 XX
 AC AAW77324;
 XX
 DT 10-MAR-1998 (first entry)
 XX
 DE Mammalian haemoglobin tryptic peptide bovine derived sequence.
 XX
 KW Mammalian; haemoglobin; tryptic peptide; bovine; porcine; equine;
 KW immune enhancer; microbial psoriasis; thrombocontracting food;
 KW powdered milk; cow; pig; horse.
 XX
 OS Synthetic.
 OS Bos taurus.
 XX
 GN JP09262094-A.
 XX
 DT 07-OCT-1997.

XX 27-MAR-1996; 96JP-0072797.
 XX 27-MAR-1996; 96JP-0072797.
 PR (ITOH-) ITO HAM KK.
 XX WPI: 1997-544157/50.
 XX
 PT New mammalian haemoglobin tryptic peptide(s) - useful as immune
 PT enhancers and to prevent microbial psoriasis
 XX
 PS Example 5; Page 4; 7pp: Japanese.
 XX
 CC The present sequence represents a bovine haemoglobin derived tryptic
 CC peptides. The peptide can be produced from bovine haemoglobin by
 CC hydrolysis with an enzyme (e.g. trypsin) and subsequent purification.
 CC It can also be produced by chemical synthesis. The peptide corresponds
 CC to the partial amino acid sequence 105th-116th of the beta-chain of
 CC bovine haemoglobin and has haem-concentrating and immune enhancing
 CC activities. It may be used in prevention of microbiological psoriasis
 CC or as in immune enhancers, functional foods or powdered milk for
 CC infants.
 XX
 SQ Sequence 6 AA:
 Query Match 81.8%; Score 9; BB 18; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 QY 1 LXR 3
 I I
 Db 4 LAR 6
 RESULT 36
 AAW26572
 ID AAW26572 standard; Peptide: 6 AA.
 XX
 AC AAW26572;
 XX
 PT 19-JAN-1998 (first entry)
 XX
 DE Peptide immunoreactive with HuMAb L94.
 XX
 KW Tumour associated antigen, melanoma, cancer, therapy, immunotherapy;
 KW diagnosis; prognosis; vaccine.
 XX
 OS Synthetic.
 XX
 PN W09714795-A1.
 XX
 PD 24-APR-1997.
 XX
 PF 19-OCT-1995; 95WO-US13331.
 XX
 PE 19-OCT-1995; 95WO-US13331.
 XX
 PA (WAYN-) WAYNE CANCER INST JOHN.
 XX
 PI Irie RF, Kikumoto Y;
 XX
 DR WPI: 1997-245112/22.
 XX
 PT Antibody against polypeptide having C-terminal amino acid sequence
 PT comprising Ala-Pro, Gly-Pro or Phe-Pro - useful to purify
 PT polypeptide which can be useful in human melanoma treatment
 XX
 PS Claim 3; Page 71; 87pp: English.
 XX
 CC This peptide is immunoreactive with human monoclonal antibody JWC
 CC L94 that reacts to a human melanoma cell line. Claimed peptides
 CC (AAW26566-73) that are immunoreactive with L94 share a C-terminal

CC Ala-Pro sequence. They can be used in an antigen composition to
 CC elicit an immune response, particularly a cytotoxic T lymphocyte
 CC response, specifically as a polyvalent tumour cell vaccine in
 CC conjunction with a cancer whole cell vaccine therapy for human
 CC melanoma. The peptides can also be used to enhance an immune
 CC response, treat and diagnose cancer.
 XX
 SQ Sequence 6 AA:
 Query Match 81.8%; Score 9; BB 18; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 QY 1 LXR 3
 I I
 Db 1 LAR 3
 RESULT 37
 AAW76723
 ID AAW76723 standard; Peptide: 6 AA.
 XX
 AC AAW76723;
 XX
 PT 13 JAN 1999 (first entry)
 XX
 CC Pancreatic polypeptide C-terminal fragment for NIDDM treatment.
 XX
 KW Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
 KW pancreatic polypeptide; PP; treatment; GS protein alpha subunit;
 KW inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion;
 KW exocrine pancreas; beta cell; pancreatic islet hyperplasia; insulin;
 KW neuropeptide Y; hyperglycaemia.
 XX
 OS Homo sapiens.
 XX
 FN US5840434-A.
 XX
 PD 03-NOV-1998.
 XX
 PF 26-FEB-1997; 97US-0306203.
 XX
 PE 26-FEB-1997; 97US-0306203.
 XX
 PA (UYSC) UNIV SOUTH CAROLINA MEDICAL RES FOUND.
 XX
 PI Gettys T, Taylor IL;
 XX
 DR WPI: 1998-609185/51.
 XX
 XX Treatment of non-insulin-dependent diabetes mellitus with
 XX pancreatic polypeptide or C-terminal fragment
 XX
 PS Claim 1; Column 3; 11pp: English.
 XX
 CC This human pancreatic polypeptide C-terminal fragment is used in a method
 CC for treating non-insulin dependent diabetes mellitus (NIDDM). The method
 CC involves administering a composition comprising pancreatic polypeptide or
 CC C-terminal pancreatic polypeptide fragment in a carrier. Screening a
 CC composition for the ability to treat NIDDM is also possible and involves
 CC determining if the composition decreases hepatic expression of the
 CC alpha subunit of a GS protein in a liver cell plasma membrane, thereby
 CC inhibiting stimulation of cyclic adenosine monophosphate (cAMP) by
 CC glucagon, determined if the composition binds the vacuolar nuclear complex
 CC and inhibits secretions of digestive enzymes by the exocrine pancreas,
 CC thereby inhibiting beta cell and pancreatic islet hyperplasia or
 CC determining if the composition binds the arcuate nucleus in the
 CC hypothalamus and potentiates the effect of leptin in reducing
 CC neuropeptide Y synthesis, thereby enhancing insulin sensitivity and
 CC reversing the effects of neuropeptide Y. The NIDDM treatment method
 CC decreases hepatic glucose and increases insulin sensitivity without
 CC additional detrimental effects.
 XX

SQ Sequence 6 AA;
 Query Match 81.8%; Score 9; Dh 19; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 4
 1 1
 Dh 1 LXR 4
 1 1
 RESULT 39
 AAW76725
 ID AAW76725 standard; peptide: 6 AA.
 XX
 AC AAW76725;
 XX
 DT 13-JAN-1999 (first entry)
 XX
 DE Pancreatic polypeptide C-terminal fragment analogue #1.
 XX
 KW Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
 KW pancreatic polypeptide; PP; treatment; GS protein alpha subunit;
 KW inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion;
 KW exocrine pancreas; beta cell; pancreatic islet hyperplasia; insulin;
 KW neuropeptide Y; hyperglycaemia.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note "D-form residue"
 FT FT Misc-difference 5 /note "D-form residue"
 FT FT Modified-site 6 /note "C-terminal amide group"
 FT FT
 IN US5830444-A.
 XX
 XX 03-NOV-1998.
 XX
 PF 26-FEB-1997; 97US-0806203.
 XX
 PR 26-FEB-1997; 97US-0806203.
 XX
 PA (USPC) UNIV SOUTH CAROLINA MEDICAL RES FUND.
 XX
 PI Gettys T. Taylor II;
 XX
 DR WPI: 1998-609185/51.
 XX
 PT Treatment of non-insulin-dependent diabetes mellitus - with
 PT pancreatic polypeptide or C-terminal fragment
 XX
 PS Disclosure: Column 6; 11pp; English.
 XX
 CC This human pancreatic polypeptide analogue C-terminal fragment is used in
 CC a method for treating non-insulin-dependent diabetes mellitus (NIDDM).
 CC The method involves administering a composition comprising pancreatic
 CC polypeptide or C-terminal pancreatic polypeptide fragment in a carrier.
 CC Screening a composition for the ability to treat NIDDM is also possible
 CC and involves determining if the composition decreases hepatic expression
 CC of the alpha subunit of a GS protein in a liver cell plasma membrane.
 CC thereby inhibiting stimulation of cyclic adenosine monophosphate (cAMP)
 CC by glucagon, determined if the composition binds the vular nuclear
 CC complex and inhibits secretions of digestive enzymes by the exocrine
 CC pancreas, thereby inhibiting beta cell and pancreatic islet hyperplasy
 CC or determining if the composition binds the arcuate nucleus in the
 CC hypothalamus and potentiates the effect of leptin in reducing
 CC neuropeptide Y synthesis, thereby enhancing insulin sensitivity and
 CC reversing the effects of neuropeptide Y. The NIDDM treatment method
 CC decreases hyperglycaemia and increases insulin sensitivity without
 CC additional detrimental effects.
 XX
 SQ Sequence 6 AA;
 Query Match 81.8%; Score 9; Dh 19; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 4
 1 1
 Dh 1 LXR 4
 1 1
 RESULT 39
 AAW76725
 ID AAW76725 standard; peptide: 6 AA.
 XX
 AC AAW76725;
 XX
 DT 13-JAN-1999 (first entry)
 XX
 DE Pancreatic polypeptide C-terminal fragment analogue #2.
 XX
 KW Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
 KW pancreatic polypeptide; PP; treatment; GS protein alpha subunit;
 KW inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion;
 KW exocrine pancreas; beta cell; pancreatic islet hyperplasia; insulin;
 KW neuropeptide Y; hyperglycaemia.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note "D-form residue"
 FT FT Misc-difference 5 /note "D-form residue"
 FT FT Modified-site 6 /note "C-terminal amide group"
 FT FT
 IN US5830444-A.
 XX
 XX 03-NOV-1998.
 XX
 PF 26-FEB-1997; 97US-0806203.
 XX
 PR 26-FEB-1997; 97US-0806203.
 XX
 PA (USPC) UNIV SOUTH CAROLINA MEDICAL RES FUND.
 XX
 PI Gettys T. Taylor II;
 XX
 DR WPI: 1998-609185/51.
 XX
 PT Treatment of non-insulin-dependent diabetes mellitus - with
 PT pancreatic polypeptide or C-terminal fragment
 XX
 PS Disclosure: Column 6; 11pp; English.
 XX
 CC This human pancreatic polypeptide analogue C-terminal fragment is used in
 CC a method for treating non-insulin-dependent diabetes mellitus (NIDDM).
 CC The method involves administering a composition comprising pancreatic
 CC polypeptide or C-terminal pancreatic polypeptide fragment in a carrier.
 CC Screening a composition for the ability to treat NIDDM is also possible
 CC and involves determining if the composition decreases hepatic expression
 CC of the alpha subunit of a GS protein in a liver cell plasma membrane.
 CC thereby inhibiting stimulation of cyclic adenosine monophosphate (cAMP)
 CC by glucagon, determined if the composition binds the vular nuclear
 CC complex and inhibits secretions of digestive enzymes by the exocrine
 CC pancreas, thereby inhibiting beta cell and pancreatic islet hyperplasy
 CC or determining if the composition binds the arcuate nucleus in the
 CC hypothalamus and potentiates the effect of leptin in reducing
 CC neuropeptide Y synthesis, thereby enhancing insulin sensitivity and
 CC reversing the effects of neuropeptide Y. The NIDDM treatment method
 CC decreases hyperglycaemia and increases insulin sensitivity without
 CC additional detrimental effects.
 XX

SQ Sequence 6 AA;

Query Match 81.8%; Score 9; DB 19; Length 6;
Best Local Similarity 66.7%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
| |
Db 1 LTR 3

RESULT 40

AAW76726

AAW76726 standard; peptide; 6 AA.

XX AAW76726;

AC AAW76726;

XX 13-JAN-1999 (first entry)

DE Pancreatic polypeptide C-terminal fragment analogue #3.

XX Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
KW pancreatic polypeptide; P; treatment; Gs protein alpha subunit;
KW inhibitor; cyclic adenosine monophosphate, cAMP; glucagon secretion;
KW exocrine pancreas; beta cell; pancreatic islet hypertrophy; insulin;
KW neuropeptide Y; hyperglycaemia.

XX Synthetic.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 5

FT /note= "D-form residue"

FT Modified-site 6

FT /note= "C-terminal amide group"

XX US5830434-A.

PN 03-NOV-1998.

XX 26-FEB-1997; 97US-0806203.

XX 26-FEB-1997; 97US-0806203.

XX (USC-) UNIV SOUTH CAROLINA MEDICAL RES FOUND.

PA Gettys T. Taylor IL;

PI WPI; 1998-609185/51.

XX Treatment of non-insulin-dependent diabetes mellitus - with

PT pancreatic polypeptide or C-terminal fragment

XX Disclosure; Column 6; 11pp; English.

XX This human pancreatic polypeptide C-terminal fragment is used in

CC a method for treating non-insulin-dependent diabetes mellitus (NIDDM).

CC The method involves administering a composition comprising pancreatic

CC polypeptide or C-terminal pancreatic polypeptide fragment in a carrier,

CC screening a composition for the ability to treat NIDDM is also possible,

CC and involves determining if the composition decreases hepatic expression

CC of the alpha subunit of Gs protein in a liver cell plasma membrane,

CC thereby inhibiting stimulation of cyclic adenosine monophosphate (cAMP)

CC by glucagon. Determined if the composition binds the cyclic adenosine

CC complex and inhibits secretions of all active enzymes by the exocrine

CC pancreas, thereby inhibiting beta cell and pancreatic islet hypertrophy

CC or determining if the composition binds the arcuate nucleus in the

CC hypothalamus and potentiates the effect of leptin in reducing

CC neuropeptide Y synthesis, thereby enhancing insulin sensitivity and

CC reversing the effects of neuropeptide Y. The NIDDM treatment method

CC decreases hyperglycaemia and increases insulin sensitivity without

CC additional detrimental effects.

XX Sequence 6 AA;

SQ

Query Match

Best Local Similarity 66.7%;

Pred. No. 7.7e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

| |

Db 1 LTR 3

RESULT 41

AAW52139

AAW52139 standard; Peptide; 6 AA.

XX AAW52139;

AC AAW52139;

XX 20-JUL-1998 (first entry)

DE Matrix metalloproteinase MMP-9 substrate B.

XX Membrane-type matrix metalloproteinase; MT-MMP; MT1-MMP;

KW matrix metalloproteinase; MMP-9; osteoarthritis; osteoporosis;

KW osteoclast; inhibitor; metabolic bone disease; osteoporosis;

KW bone resorption; metastasis; tumor; cancer; ulcer; arthritis;

KW periodontal disease; therapy.

XX Synthetic.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Mca-proline"

FT Cleavage-site 3.4

FT Modified-site 5

FT /note= "Ipa-alanine"

XX W09804287-A1.

PN 05-FEB-1998.

XX 29 JUL 1997; 97WO-EP04110.

XX 30-JUL-1999; 96GR-0015976.

XX (CLIN-) CINT CLINICAL & BASIC RES.

PA Delaisse J. Faged NI. Molital M;

PI WPI; 1998-130425/12.

XX Use of inhibitors of protease(S) involved in osteoclast activity -

PT useful for, e.g. treating metabolic bone disease such as

XX osteoporosis

XX Example 6b; Page 44; 110pp; English.

XX Peptide B is a sub-fragment of matrix metalloproteinase MMP-9. A gel

CC peptide substrate mimicking MMP-inhibitors (see AAW52132-33) are

CC remaining agents for use in treatment of bone metabolic disease.

CC They can be used to inhibit proteolysis involved in the

CC recruitment, proliferation, differentiation or migration of

CC osteoclast precursor cells or in the migration, fusion, attachment,

CC polarisation, removal of mineralised osseous substance or death of

CC osteoclasts. The inhibitors reduce the rate of bone resorption

CC and are used to treat a patient, e.g. osteoporosis and osteolytic

CC bone metastases. They are also useful in, e.g. treatment of

CC cancer, ulcers, arthritis and periodontal disease

XX Sequence 6 AA;

SQ

Query Match

Best Local Similarity 66.7%;

Pred. No. 7.7e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

| |

Db 1 LTR 3

XX 14-MAR-1994; 94US 0212546.
 PR 15-JAN-1991; 91US 0641720.
 PR 13-OCT-1992; 92US-0959560.
 PR 01-JUN-1993; 93US-0069891.
 PR 12-JUN-1996; 96US-0747137.
 XX (HEMO-) HEMOSPHERE INC.
 XX Yen FCK;
 XX WPI: 1999-508153/42.
 PT Non-crosslinked protein particles for therapeutic and diagnostic use
 XX Example 22; Colcan 83 84; 65pp, English.
 CC This invention describes a novel aqueous suspension of non-crosslinked particles on non-crosslinked, non-denatured albumin (30-500 nm) which is stable against dissolving upon filtration with an alcohol-free aqueous medium. The method involves (a) forming an aqueous solution containing albumin and hemoglobin and (b) treating the aqueous solution with an alcohol to cause the solution to become turbid. The particles are useful as agents for in vivo administration, either of their own administration or as a vehicle for other therapeutic or diagnostic agents. The method permits the formation of albumin and hemoglobin particles in the nanometer and micrometer size range, in a form closer to their natural form than the forms of the prior art. The particles therefore constitute a more closely controlled agent for in vivo administration, with greater ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention.
 XX Sequence 6 AA;
 SQ Query Match 81.88; Score 9; DB 20; Length 6;
 Best Local Similarity 56.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 4 LAR 6
 RESULT 45
 AAY23392
 ID AAY23392 standard; Peptide: 6 AA.
 XX AAY23392;
 AC AAY23392;
 XX 02-SEP-1999 (first entry)
 DT V beta 6 clone found in MS patients after vaccination with TCR.
 DE
 DE
 KW Vaccines, T cell receptor, TCR, T cell, V beta 6.2/3, V beta 5/5,
 KW V beta 6.7, V beta 2; V beta 5/1, V beta 7, V beta 13; V beta 6,
 KW multiple sclerosis.
 XX Synthetic.
 OS Homo sapiens.
 OS
 FN WO9927957-A1.
 XX 10-JUN-1999.
 PD
 XX 03-DEC-1997; 97WO-US23147.
 PF
 XX 03-DEC-1997; 97WO-US23147.
 XX (IMMUN-) IMMUNE RESPONSE CORP.
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 XX
 PI Brostoff SW, Carlo DJ, Gold DP, Smith LR, Wilson DB;
 XX

DR WPI: 1999-404801/34.
 XX TO cell receptor peptide derived vaccines
 XX Example 11; Page 84; 104pp; English.
 XX The specification describes vaccines which comprise immunologically effective amounts of T cell receptor (TCR) peptides. The TCRs are present on the surface of T cells. The TCRs are chosen from V beta 5.2/1, V beta 5/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta TCR peptide-based vaccines are useful for prevention or treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears to be particularly associated with multiple sclerosis and can be used to determine an individual's susceptibility to multiple sclerosis. CC Vaccinating, rather than passively administering heterologous antibodies, allows the host's own immune system to mobilize and suppress auto aggressive T cells. Therefore, the suppression is persistent and may involve any and all immunological mechanisms in effecting that suppression. Such a multi targeted response is more effective than the non-immunological suppressions achieved by passive administration of monoclonal antibodies or extract-derived regulatory T cell clones.
 CC AAY30952-Y31135 represent peptides derived from the V beta 6 clones found in the cerebrospinal fluid (CSF) of MS patients after vaccination with V beta 6.
 XX Sequence 6 AA;
 SQ Query Match 81.88; Score 9; DB 20; Length 6;
 Best Local Similarity 56.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 1 LAR 3
 Search completed: April 30, 2003, 13:34:14
 Job time : 28.5455 secs

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